

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 9.51087 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336A-149
Perfect score: 171
Sequence: 1 NNILRAIEAQHLLQLTWQIKQLQARILAVERYL 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	95.9	357	2 S21996	env polypeptide -
2	164	95.9	851	2 S33985	env polypeptide -
3	164	95.9	853	2 S54384	env polypeptide -
4	164	95.9	854	2 S13288	env polypeptide - huma
5	164	95.9	855	1 VCLJ2R	env polypeptide pr
6	164	95.9	856	1 VCLJH3	env polypeptide pr
7	164	95.9	856	1 VCLJVL	env polypeptide pr
8	164	95.9	861	1 VCLJIV	env polypeptide pr
9	163	95.3	357	2 S22006	env polypeptide g
10	163	95.3	357	2 S21994	env polypeptide g
11	163	95.3	357	2 S22004	env polypeptide g
12	163	95.3	358	2 S22002	env polypeptide g
13	163	95.3	358	2 S22000	env polypeptide g
14	163	95.3	358	2 S70417	env polypeptide g
15	163	95.3	443	2 C41621	env polypeptide p
16	163	95.3	443	2 A41621	env polypeptide p
17	163	95.3	843	1 H44001	env polypeptide M
18	163	95.3	846	1 VCLJND	env polypeptide pr
19	163	95.3	852	1 T12016	env polypeptide pr
20	163	95.3	855	1 VCLJ2A	env polypeptide pr
21	163	95.3	856	1 VCLJ3W	env polypeptide pr
22	163	95.3	859	2 T01672	env polypeptide pr
23	163	95.3	861	1 VCLJ5C	env polypeptide pr
24	161	94.2	357	2 S21990	env polypeptide g
25	161	94.2	859	1 B41621	env polypeptide D
26	160	93.6	454	2 VCLJ2K	env polypeptide pr
27	160	93.6	729	1 VCLJ2K	env polypeptide pr
28	160	93.6	856	1 A4963	env polypeptide pr
29	160	93.6	861	1 VCLJ2B	env polypeptide pr

30	160	93.6	868	1 VCLJ2A	env polypeptide -
31	156	91.2	358	2 S21998	env polypeptide g
32	155	90.6	357	2 S21992	env polypeptide g
33	153	89.5	847	2 T09448	env polypeptide g
34	153	89.5	847	2 S13289	env polypeptide - huma
35	153	89.5	854	1 VCLJ2I	env polypeptide pr
36	152	88.9	852	1 VCLJ2B	env polypeptide -
37	120	70.2	104	2 S52930	env polypeptide -
38	117	68.4	877	2 S49197	env polypeptide p
39	113	66.1	864	1 VCLJ2A	env polypeptide -
40	113	66.1	877	2 C46356	env polypeptide -
41	109	63.7	863	2 A53034	env polypeptide -
42	108	63.2	732	2 S46352	env polypeptide -
43	99	57.9	366	2 B41665	env polypeptide -
44	99	57.9	858	1 VCLJ2G	env polypeptide pr
45	97	56.7	68	2 S60695	env polypeptide - huma
46	97	56.7	68	2 S60696	env polypeptide - huma
47	97	56.7	68	2 S60705	env polypeptide - huma
48	97	56.7	68	2 S60707	env polypeptide - huma
49	97	56.7	68	2 S60694	env polypeptide - huma
50	97	56.7	69	2 S60706	env polypeptide - huma
51	97	56.7	712	1 VCLJ2A	env polypeptide pr
52	97	56.7	851	2 S12159	env polypeptide - huma
53	97	56.7	852	1 VCLJ2G	env polypeptide pr
54	97	56.7	859	1 VCLJ2G	env polypeptide pr
55	97	56.7	859	2 S53098	env polypeptide pr
56	96	56.1	859	1 VCLJ2G	env polypeptide pr
57	95	55.6	855	2 A45713	env polypeptide pr
58	95	55.6	881	2 S03068	env polypeptide - huma
59	95	55.6	885	2 S04322	env polypeptide - huma
60	95	55.6	886	2 T11555	env polypeptide - simi
61	95	55.6	889	1 VCLJ2G	env polypeptide -
62	94	55.0	881	1 VCLJ2G	env polypeptide -
63	93	54.4	859	2 S24571	env polypeptide - huma
64	93	54.4	869	2 A47665	env polypeptide gp120(
65	92	53.8	68	2 S60693	env polypeptide - huma
66	92	53.8	68	2 S60687	env polypeptide - huma
67	92	53.8	880	1 VCLJ2G	env polypeptide - huma
68	91	53.2	151	2 S30458	env polypeptide pr
69	91	53.2	786	2 S28084	env polypeptide - huma
70	90	52.6	68	2 S60692	env polypeptide - huma
71	90	52.6	887	2 T11566	env polypeptide - huma
72	89	52.0	68	2 S60688	env polypeptide - huma
73	89	52.0	151	2 S30458	env polypeptide - huma
74	89	52.0	151	2 S30452	env polypeptide - huma
75	89	52.0	151	2 S30450	env polypeptide - huma
76	89	52.0	151	2 S30451	env polypeptide - huma
77	89	52.0	151	2 S30459	env polypeptide - huma
78	87	50.9	151	2 S30457	env polypeptide - huma
79	87	50.9	151	2 S30456	env polypeptide - huma
80	87	50.9	151	2 S30455	env polypeptide - huma
81	87	50.9	151	2 S30454	env polypeptide - huma
82	87	50.9	151	2 S60690	env polypeptide - huma
83	86	50.3	69	2 S60689	env polypeptide - huma
84	86	50.3	69	2 S60691	env polypeptide - huma
85	86	48.0	294	2 S60525	env polypeptide - huma
86	82	48.0	297	2 S60538	env polypeptide - huma
87	82	48.0	372	2 S46344	env polypeptide -
88	82	48.0	372	2 S46345	env polypeptide -
89	75	43.9	394	2 S60545	env polypeptide -
90	73	42.7	294	2 S60545	env polypeptide -

ALIGNMENTS

RESULT 1
S21996
env polypeptide gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence #revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422, S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A/Reference number: S70417; MUID:92144209; PMID:1736940

A/Accession: S70422

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-357 <STR2>

A/Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:g1067129

A/Experimental source: patient 27L

A/Note: submitted to the EMBL Data Library, July 1991

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.9%; Score 164; DB 2; Length 357;

Best Local Similarity 97.1%; Pred. No. 5.5e-15;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 35

54 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 88

RESULT 2

S33985

env polypeptide - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C/Accession: S33985

R/Carlino, F.

submitted to the EMBL Data Library, November 1991

A/Reference number: S33979

A/Accession: S33985

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-851 <CAR>

A/Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA7628.1; PID:g60199

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.9%; Score 164; DB 2; Length 851;

Best Local Similarity 97.1%; Pred. No. 1.4e-14;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 35

548 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 582

RESULT 3

S54384

envelope polypeptide - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C/Accession: S54384

R/Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A/Reference number: S54377

A/Accession: S54384

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-853 <THE>

A/Cross-references: EMBL:M26639; NID:9329377; PIDN:AAA45370.1; PID:9329385

C/Superfamily: type E retrovirus env polypeptide

C/Keywords: polypeptide

Query Match 95.9%; Score 164; DB 2; Length 853;

Best Local Similarity 97.1%; Pred. No. 1.4e-14;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 35

550 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 584

RESULT 4

S13288

env polypeptide - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C/Accession: S13288

R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 349, 69-73, 1990

A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A/Reference number: S13288; MUID:91043044; PMID:2172853

A/Accession: S13288

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-854 <OBR>

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.9%; Score 164; DB 2; Length 854;

Best Local Similarity 97.1%; Pred. No. 1.4e-14;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 35

551 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 585

RESULT 5

VCLJH3

env polypeptide precursor - human immunodeficiency virus Zr-6

N/Alternate names: coat polypeptide

C/Species: human immunodeficiency virus Zr-6

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C/Accession: D26192

R/Stinafaan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cui

Gene 52, 71-82, 1987

A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic

A/Reference number: A26192; MUID:87248097; PMID:3036660

A/Accession: D26192

A/Molecule type: DNA

A/Residues: 1-855 <SRI>

A/Cross-references: GB:X03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:9329403

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polypeptide

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-855/Product: env polypeptide #status predicted <MAT>

F/501-855/Product: transmembrane glycoprotein #status predicted <TM>

F/87,129,140,145,154,158,186,189,199,236,243,254,278,291,297,333,340,355,386,392,398,404,

Query Match 95.9%; Score 164; DB 1; Length 855;

Best Local Similarity 97.1%; Pred. No. 1.4e-14;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 35

552 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYL 586

RESULT 6

VCLJH3

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N/Alternate names: coat polypeptide

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C/Accession: A03973

R/Katner, U.; Haezelte, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar

nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A/Reference number: A93353; MUID:85111123; PMID:2578655

A/Accession: A03973

A/Molecule type: DNA

A;Residues: 1-856 <RAT>
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326383; PIDN:AAA442
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 1,4e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 35
Db 553 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 587
RESULT 7
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03974
R;Meising, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A;Reference number: A93355; MUID:5511157; PMID:2982104
A;Molecule type: DNA
A;Residues: 1-856 <MOE>
A;Cross-references: GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 1,4e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 35
Db 553 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 587
RESULT 8
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <MA1>
A;Cross-references: GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C;Genetics:

A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 95.9%; Score 164; DB 1; Length 861;
Best Local Similarity 97.1%; Pred. No. 1,4e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 35
Db 558 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 592
RESULT 9
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 41)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S70420; S22006
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
Aids Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <STE1>
A;Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
A;Experimental source: patient 1
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type B retrovirus env polyprotein
Query Match 95.3%; Score 163; DB 2; Length 357;
Best Local Similarity 94.3%; Pred. No. 7,6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 35
Db 54 NNTLRATIEAOQHLLQLTWQIKQLQARILAVERYL 88
RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 27B
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C;Accession: S21994; S70421
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A;Reference number: S21990
A;Accession: S21994
A;Molecule type: DNA
A;Residues: 1-357 <STE1>
A;Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
Aids Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140,'X',142-312,'X',314-357 <STE2>
A;Cross-references: EMBL:X61355; NID:G60179
C;Superfamily: type E retrovirus env polyprotein
Query Match 95.3%; Score 163; DB 2; Length 357;

Best Local Similarity 94.3%; Pred. No. 7.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 35
Db 54 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 88

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22004
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 4B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:960186; PIDN:CAA43614.1; PID:960189
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:960188
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 357;
Best Local Similarity 94.3%; Pred. No. 7.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 35
Db 54 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 88

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22002
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43614.1; PID:960187
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:960186
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 7.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 35
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 89

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22000
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 7.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 35
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 89

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
S70417
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 7.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 35
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYL 89

RESULT 15

env polyprotein P - human immunodeficiency virus type 1 (fragment)
C41621
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: C41621
R/Burger, H.; Weisner, B.; Flaherty, K.; Guila, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; MUID:92107924; PMID:1763038
A/Accession: C41621
A/Molecule type: DNA

A;Residues: 1-443 <BUR>
A;Cross-references: GB:M77230; NID:g328631; PIDN:AA03792.1; PID:g555015
A;Note: this virus was isolated from the mother's sexual partner
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polypeptide
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;424-443/DNA: transmembrane #status predicted <TM>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 95.3%; Score 163; DB 2; Length 443;
Best Local Similarity 94.3%; Pred. No. 9.6e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 35
Db 293 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 327

RESULT 16
A41621
env polypeptide M - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polypeptide
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: A41621
R;Burger, H.; Weisner, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Glibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
A;Accession: A41621
A;Molecule type: DNA
A;Residues: 1-445 <BUR>
A;Cross-references: GB:M77228; NID:g328627; PIDN:AA03790.1; PID:g555013
A;Note: this virus was isolated from the mother
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polypeptide
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/DNA: transmembrane #status predicted <TM>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 95.3%; Score 163; DB 2; Length 445;
Best Local Similarity 94.3%; Pred. No. 9.7e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 35
Db 295 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 329

RESULT 17
H44001
env polypeptide precursor - human immunodeficiency virus type 1 (strain YU-2)
N;Alternate names: coat polypeptide
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C;Accession: H44001
J;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
A;Title: Complete nucleotide sequence, genome organization, and biological properties of
A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Molecule type: DNA
A;Residues: 1-843 <LiY>

A;Cross-references: GB:M93258
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polypeptide
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/DNA: signal sequence #status predicted <SIG>
F;19-35/Region: hydrophobic
F;30-489/Product: coat protein gp120 #status predicted <GP1>
F;490-843/Product: coat protein gp41 #status predicted <GP2>
F;499-515/Region: hydrophobic
F;673-689/Region: hydrophobic
F;738-755/DNA: transmembrane #status predicted <TM>
F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 95.3%; Score 163; DB 1; Length 843;
Best Local Similarity 94.3%; Pred. No. 1.9e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 35
Db 540 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 574

RESULT 18
VCLND
env polypeptide precursor - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: coat polypeptide
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: J00066
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV-1 NDK, a highly cytopathic strain of the human immunoc
A;Reference number: J00065; MUID:90034200; PMID:2806917
A;Accession: J00066
A;Molecule type: DNA
A;Residues: 1-846 <SPI>
A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A;Note: the authors translated the codon GCG for residue 523 as Arg
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polypeptide
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-29/DNA: signal sequence #status predicted <SIG>
F;30-501/Product: coat protein gp120 #status predicted <GP1>
F;502-846/Product: coat protein gp41 #status predicted <GP2>
F;502-520/DNA: transmembrane #status predicted <TM>
F;674-692/DNA: transmembrane #status predicted <TM2>
F;87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606,

Query Match 95.3%; Score 163; DB 1; Length 846;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 35
Db 543 NNTLRATEAQQHLLQTLTWGIKQLQARVLAVERYL 577

RESULT 19
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12016
R;McCuchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Shepard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in St
A;Reference number: Z17379; MUID:9818716; PMID:9519894
A;Accession: T12016
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-852 <MCC>
A;Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 852;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 35
Db 549 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 583

RESULT 20
VCLJAZ
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03976
R;Sanchez-Bescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-SH
Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A;Reference number: A04003; MUID:85090453; PMID:2578227
A;Accession: A03976
A;Molecule type: DNA
A;Residues: 1-855 <SAN>
A;Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-509/Product: exterior membrane glycoprotein #status predicted <TM>
F;510-855/Product: transmembrane glycoprotein #status predicted <TM>
F;87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.3%; Score 163; DB 1; Length 855;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 35
Db 552 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 586

RESULT 21
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMU1)
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parke, E.
Cell 45, 637-648, 1986
A;Title: Identification and characterization of conserved and variable regions in the en
A;Reference number: A24774; MUID:86218077; PMID:2423250
A;Accession: A24774
A;Molecule type: DNA
A;Residues: 1-856 <STR>
A;Cross-references: GB:K03455; GB:M38432; NID:g1906382
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-501/Product: coat protein gp120 #status predicted <GP1>
F;502-847/Product: coat protein gp41 #status predicted <GP2>

F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,
Query Match 95.3%; Score 163; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 35
Db 553 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 587

RESULT 22
T01672
envelope polyprotein precursor - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01672
R;Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-859 <ADL>
A;Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
C;Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 859;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 35
Db 555 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 589

RESULT 23
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
R;Gargio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Stat
Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Accession: B28922
A;Molecule type: DNA
A;Residues: 1-861 <GUR>
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396,

Query Match 95.3%; Score 163; DB 1; Length 861;
Best Local Similarity 94.3%; Pred. No. 2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 35
Db 558 NNILRAIEAQOHLQLTWGIRKQARILAVERYL 592

RESULT 24
S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate 20
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C;Accession: S21990, S70423
 R;Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A;Reference number: S21990
 A;Accession: S21990
 A;Molecule type: DNA
 A;Residues: 1-357 <STE1>
 A;Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
 R;Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
 A;Reference number: S70417; MUID:92144209; PMID:1736940
 A;Accession: S70423
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-332, 'X', 334-357 <STE2>
 A;Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
 C;Superfamily: type E retrovirus env polypeptide

Query Match 94.2%; Score 161; DB 2; Length 357;
 Best Local Similarity 91.4%; Pred. No. 1.4e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 35
 Db 54 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 88

RESULT 25
 VCLJMN
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)
 N;Alternate names: coat polypeptide
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C;Accession: A28922
 R;Gurgoo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
 Virology 164, 531-536, 1988
 A;Title: Envelope sequences of two new United States HIV-1 isolates.
 A;Reference number: A28922; MUID:88219542; PMID:3369091
 A;Accession: A28922
 A;Molecule type: DNA
 A;Residues: 1-859 <GUR>
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polypeptide
 C;Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-859/Product: env polypeptide #status predicted <EP>
 F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.2%; Score 161; DB 1; Length 859;
 Best Local Similarity 91.4%; Pred. No. 3.7e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 35
 Db 557 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 591

RESULT 26
 B41621
 env polypeptide D - human immunodeficiency virus type 1 (fragment)
 N;Alternate names: coat polypeptide
 N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
 C;Accession: B41621
 R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A;Reference number: A41621; MUID:92107924; PMID:1763038
 A;Accession: B41621
 A;Molecule type: DNA
 A;Residues: 1-454 <BUR>
 A;Cross-references: GB:W77279
 A;Note: this virus was isolated from the daughter
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polypeptide
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polype
 F;1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F;263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F;435-454/Domain: transmembrane #status predicted <TM>
 F;9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo

Query Match 93.6%; Score 160; DB 2; Length 454;
 Best Local Similarity 91.4%; Pred. No. 2.6e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 35
 Db 304 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 338

RESULT 27
 VCLJMX
 env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
 N;Alternate names: coat polypeptide
 N;Contains: coat protein gp120; coat protein gp32
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
 C;Accession: B42995
 R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
 A;Reference number: A42995; MUID:92351552; PMID:1322587
 A;Accession: B42995
 A;Molecule type: mRNA
 A;Residues: 1-729 <SHI>
 A;Cross-references: GB:S41266; GB:D01206
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polypeptide
 C;Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
 F;1-689/Domain: extracellular #status predicted <EXT>
 F;1-33/Domain: signal sequence #status predicted <SIG>
 F;17-33/Region: hydrophobic #status predicted
 F;34-517/Product: coat protein gp120 #status predicted <CP1>
 F;514-517/Region: cleavage processing #status predicted
 F;518-729/Product: coat protein gp32 #status predicted
 F;518-534/Region: hydrophobic #status predicted
 F;690-711/Domain: transmembrane #status predicted <TM1>
 F;712-729/Domain: intracellular #status predicted <INT>
 F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414,

Query Match 93.6%; Score 160; DB 1; Length 729;
 Best Local Similarity 91.4%; Pred. No. 4.3e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 35
 Db 559 NNLRAIEAQOHLQTLTWQIKQLQARVLAVERYL 593

RESULT 28
 A44963
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate Z321)
 N;Alternate names: coat polypeptide
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
 C/Accession: A44963
 R/Stinivaasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989
 A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
 A/Reference number: A44963; MUID:89228766; PMID:2713163
 A/Accession: A44963
 A/Molecule type: DNA
 A/Residues: 1-856 <SHI>
 A/Cross-references: GB:M15896; NID:g329392; PIDN:AA53948.1; PID:g3293924
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-520/Product: coat protein gp120 #status predicted <CP1>
 F:521-856/Product: coat protein gp41 #status predicted <CP2>
 F:884-705/Domain: transmembrane #status predicted <TMN>
 F:87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611

Query Match 93.6%; Score 160; DB 1; Length 856;
 Best Local Similarity 94.3%; Pred. No. 5.1e-14;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 35
 Db 553 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 587

RESULT 29

VCLJKB
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
 N/Alternate names: coat polyprotein
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
 C/Accession: A42995
 R/Shimizu, H.; Hasebe, F.; Teuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
 A/Reference number: A42995; MUID:92351552; PMID:1322587
 A/Accession: A42995
 A/Molecule type: mRNA
 A/Residues: 1-861 <SHI>
 A/Cross-references: GB:S41266; GB:D01206
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F:1-689/Domain: extracellular #status predicted <EXT>
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:1-33/Region: hydrophobic #status predicted
 F:34-517/Product: coat protein gp120 #status predicted <CP1>
 F:514-517/Region: cleavage processing #status predicted
 F:518-861/Product: coat protein gp41 #status predicted <CP2>
 F:518-534/Region: hydrophobic #status predicted
 F:690-711/Domain: transmembrane #status predicted <TM1>
 F:712-861/Domain: intracellular #status predicted <INT>
 F:756-772/Region: hydrophobic #status predicted
 F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.6%; Score 160; DB 1; Length 861;
 Best Local Similarity 91.4%; Pred. No. 5.2e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 35
 Db 559 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 593

RESULT 30

VCLJTH4
 env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
 N/Alternate names: coat polyprotein
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
 C/Accession: C25523
 R/Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Stinivaasan, A.; Andersen, P.R.; Devare, S.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
 A/Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human J
 A/Reference number: A94136; MUID:87041461; PMID:3490666
 A/Accession: C25523
 A/Molecule type: DNA
 A/Residues: 1-868 <DES>
 A/Cross-references: GB:M13137; NID:g326460; PIDN:AAA44311.1; PID:g326467
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
 F:1-521/Product: coat protein gp120 #status predicted <GP1>
 F:522-868/Product: coat protein gp41 #status predicted <GP2>
 F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match 93.6%; Score 160; DB 1; Length 868;
 Best Local Similarity 94.3%; Pred. No. 5.2e-14;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 35
 Db 565 NNLLRAIEAQOHLQTLTWQIKQLQARILAVERYL 599

Search completed: June 2, 2004, 11:50:09
 Job time: 9.51087 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 5.70652 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-149
Perfect score: 171
Sequence: 1 NMLRAIEAQOHDLQLTWQIKQLQARIILAVERYL 35

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	95.9	853	1	ENV_HV1EL
2	164	95.9	853	1	ENV_HV1MP
3	164	95.9	853	1	ENV_HV122
4	164	95.9	855	1	ENV_HV126
5	164	95.9	856	1	ENV_HV1B1
6	164	95.9	856	1	ENV_HV1H2
7	164	95.9	856	1	ENV_HV1H3
8	164	95.9	856	1	ENV_HV1H4
9	164	95.9	856	1	ENV_HV1H5
10	164	95.9	856	1	ENV_HV1H6
11	163	95.3	843	1	ENV_HV1H7
12	163	95.3	846	1	ENV_HV1H8
13	163	95.3	847	1	ENV_HV1H9
14	163	95.3	852	1	ENV_HV1H10
15	163	95.3	855	1	ENV_HV1H11
16	163	95.3	855	1	ENV_HV1H12
17	163	95.3	856	1	ENV_HV1H13
18	163	95.3	856	1	ENV_HV1H14
19	163	95.3	859	1	ENV_HV1H15
20	163	95.3	865	1	ENV_HV1H16
21	161	94.2	848	1	ENV_HV1H17
22	161	94.2	856	1	ENV_HV1H18
23	160	93.6	847	1	ENV_HV1H19
24	160	93.6	851	1	ENV_HV1H20
25	160	93.6	856	1	ENV_HV1H21
26	160	93.6	861	1	ENV_HV1H22
27	160	93.6	867	1	ENV_HV1H23
28	160	93.6	868	1	ENV_HV1H24
29	155	90.6	863	1	ENV_HV1H25
30	153	89.5	854	1	ENV_HV1H26
31	152	88.9	852	1	ENV_HV1H27
32	113	66.1	865	1	ENV_HV1H28
33	113	66.1	877	1	ENV_HV1H29

34	110	64.3	854	1	ENV_HV1H30
35	106	62.0	768	1	ENV_HV1H31
36	99	57.9	858	1	ENV_HV1H32
37	97	56.7	712	1	ENV_HV1H33
38	97	56.7	846	1	ENV_HV1H34
39	97	56.7	851	1	ENV_HV1H35
40	97	56.7	851	1	ENV_HV1H36
41	97	56.7	856	1	ENV_HV1H37
42	97	56.7	859	1	ENV_HV1H38
43	97	56.7	860	1	ENV_HV1H39
44	96	56.1	859	1	ENV_HV1H40
45	95	55.6	380	1	ENV_HV1H41
46	95	55.6	881	1	ENV_HV1H42
47	95	55.6	885	1	ENV_HV1H43
48	95	55.6	889	1	ENV_HV1H44
49	94	55.0	882	1	ENV_HV1H45
50	93	54.4	857	1	ENV_HV1H46
51	93	54.4	859	1	ENV_HV1H47
52	92	53.8	880	1	ENV_HV1H48
53	91	53.2	821	1	ENV_HV1H49
54	53	31.0	2564	1	SPCQ_HUMAN
55	50.5	29.5	1411	1	BEAL_HUMAN
56	50	29.2	1938	1	MYH4_HUMAN
57	50	28.9	581	1	FRIZ_DROME
58	49.5	28.9	583	1	FRIZ_DROVI
59	49	28.7	1938	1	MYH4_HUMAN
60	49	28.7	1939	1	MYH4_HUMAN
61	49	28.7	4349	1	DYHC_FUSO
62	48.5	28.4	790	1	BEAL_MOUSE
63	48	28.1	551	1	YD25_YEAST
64	48	28.1	8797	1	SNEI_HUMAN
65	47.5	27.8	253	1	CYSH_VIBCH
66	47.5	27.8	303	1	ALB3_MAIZE
67	47.5	27.8	467	1	EUTE_ECOLI
68	47.5	27.8	467	1	EUTE_SALTY
69	47.5	27.8	962	1	ARVC_HUMAN
70	47.5	27.8	969	1	ARVC_MOUSE
71	47.5	27.8	1955	1	PUMA_PARUN
72	47	27.5	376	1	O43A_DROME
73	47	27.5	684	1	RPOC_MARPO
74	47	27.5	906	1	CTNI_HUMAN
75	47	27.5	906	1	CTNI_MOUSE
76	47	27.5	1379	1	M3KS_MOUSE
77	47	27.5	1935	1	MYSS_CYPCA
78	46.5	27.2	1093	1	AE17_HUMAN
79	46.5	27.2	1319	1	SOSI_MOUSE
80	46.5	27.2	1333	1	SOSI_HUMAN
81	46.5	27.2	1755	1	PEPL_MOUSE
82	46.5	27.2	2022	1	ANTI_ONCVO
83	46	26.9	70	1	RL15_BRUPA
84	46	26.9	286	1	IN35_HUMAN
85	46	26.9	358	1	YCCF_BACSU
86	46	26.9	743	1	ANAG_HUMAN
87	46	26.9	839	1	IF2_HAEDU
88	46	26.9	1867	1	MOT1_YEAST
89	46	26.9	1941	1	MYH2_HUMAN
90	45.5	26.6	669	1	UVRB_SYNY3

ALIGNMENTS

RESULT 1
ENV_HV1EL
ID ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).

CC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86245056; PubMed=2424612;
 RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 of two isolates from African patients";
 RL Cell 46:63-74(1986).
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 CC -----
 CC EMBL; K03454; AAA44329.1; -;
 DR EMBL; A07108; CAA00616.1; -;
 DR HIV; K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 31 BY SIMILARITY.
 FT SIGNAL 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
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 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MM; P9CDB64DAAD007A5 CMC64;
 Query Match 95.9%; Score 164; DB 1; Length 853;

Best Local Similarity 97.1%; Pred. No. 9e-16;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLLQLTWQIKQLQARILLAVERYL 35
 Db 550 NNLRAIEAQOHLLQLTWQIKQLQARILLAVERYL 584
 RESULT 2
 ENV_HVIMF STANDARD; PRT; 853 AA.
 ID ENV_HVIMF AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MRA isolate) (HIV-1).
 CC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
 RA Wasik A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1
 RT variants diminished in the ability to induce syncytium-independent
 RT cytolysis";
 RL J. Virol. 64:3792-3803(1990).
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 CC -----
 CC EMBL; M33943; AAA44850.1; -;
 DR PDB; 1A1K; 16-JUN-97.
 DR HIV; M33943; ENVSMRA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT CHAIN 1 30
 FT SIGNAL 31 509
 FT CHAIN 510 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 329 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).


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FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22A8A CRC64;

Query Match 95.9%; Score 164; DB 1; Length 853;
Best Local Similarity 97.1%; Pred. No. 9e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIIVERYL 35
Db 551 NNLRAIEAQOHLQLTWGIKOLQARIIVERYL 585

RESULT 3
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22639; AAA45370.1; -.
DR PIR; S54384; S54384.
DR HIV; M22639; ENV52226.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.

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FT DISULFID 383 415 BY SIMILARITY.
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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08CBFAFF7008 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 853;
Best Local Similarity 97.1%; Pred. No. 9e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIIVERYL 35
Db 550 NNLRAIEAQOHLQLTWGIKOLQARIIVERYL 584

RESULT 4
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luthi P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82 (1987).
CC -----
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CC -----
DR EMBL; K03458; AAA45380.1; -.
DR PIR; D26192; VCLJZR.
DR HIV; K03458; ENV526.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane;
  Signal.
KW Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 1 510 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 207 BY SIMILARITY.
FT DISULFID 125 198 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 220 249 BY SIMILARITY.
FT DISULFID 230 241 BY SIMILARITY.
FT DISULFID 298 332 BY SIMILARITY.
FT DISULFID 378 444 BY SIMILARITY.
FT DISULFID 385 417 BY SIMILARITY.
FT CARBOHYD 87 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 264 264 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 673 673 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 855 AA; 96971 MW; 3B4D3D6E239C3457 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 855;
Best Local Similarity 97.1%; Pred. No. 9e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
  Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
  Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
  Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
  Wong-Staal F.;
  "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
  Nature 313:277-284(1985).
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
  Gregory T.J.;
  "Assignment of intrachain disulfide bonds and characterization of
  potential glycosylation sites of the type 1 recombinant human
  immunodeficiency virus envelope glycoprotein (gp120) expressed in
  Chinese hamster ovary cells.";
  J. Biol. Chem. 265:10373-10382(1990).
RL J. Biol. Chem. 265:10373-10382(1990).
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CC -----
DR EMBL; M15654; AAA44205.1; -.
DR PIR; A03973; VCLJH3.
DR HIV; M15654; ENV5BH102.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .)

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FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931B27 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 9e-16; Mismatches 0; Gaps 0;
Matches 34; Conservative 0; Indels 1;

Db 1 NNTLRAIEAOQHLLQLTWGIKOLQARILAVERYL 35
553 NNTLRAIEAOQHLLQLTWGIKOLQARILAVERYL 587

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID _ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF038419; AAC82596.1; -
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DL8; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
FM 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 511
FT 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
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FT CARBOHYD 88 88
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FT CARBOHYD 141 141
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FT CARBOHYD 160 160
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FT CARBOHYD 197 197
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FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107F80 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 9e-16; Mismatches 0; Gaps 0;
Matches 34; Conservative 0; Indels 1;

Db 1 NNTLRAIEAOQHLLQLTWGIKOLQARILAVERYL 35
553 NNTLRAIEAOQHLLQLTWGIKOLQARILAVERYL 587

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
ID _ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.

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RX	MEDLINE=85528248; PubMed=2988795;
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
RA	Shaw G.M., Wong-Staal P., Reddy E.P.
RT	"HIV-III env gene products synthesized in E. coli are recognized by
RT	antibodies present in the sera of AIDS patients."
RL	Cell 41:979-986(1985).
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CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL, M14100; AAA44679.1; --
DR	PDB; 1JAU; 17-OCT-01.
DR	PDB; 1JAV; 17-OCT-01.
DR	HIV; M14100; ENVSHXB3.
DR	InterPro; IPR000328; Env GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120_1.
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
FT	SIGNAL 1 30
FT	CHAIN 31 511
FT	DISULFID 512 856
FT	DISULFID 119 205
FT	DISULFID 126 196
FT	DISULFID 131 157
FT	DISULFID 218 247
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Query Match	95.9%; Score 164; DB 1; Length 856;
Best Local Similarity	97.1%; Pred No. 9e-16;
Matches 34; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

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DB	553	NNLRRAIEAOQHLLQLTWVGKIQQAIIIVAVERTL	587	
Oy	1	NNLRRAIEAOQHLLQLTWVGKIQQAIIIVAVERTL	35	
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].			
GN	ENV.			
OC	Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).			
OC	Vitruvise; Retroid vitruvise; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=82834;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95127297; PubMed=7826699;			
RA	Reitz M.S., Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.J.			
RT	"Viral variability and serum antibody response in a laboratory virus infected with HIV type 1 (HTLV type IIIB)."			
RL	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).			
CC	-----			
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CC	-----			
DR	EMBL; U12055; AAA76690.1; -. PDB; 1IF3; O2-MAY-01.			
DR	GlycoSuiteDB; Q70626; -. Env GP41.			
DR	InterPro; IPR000328; .			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
KM	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal; 3D-structure.			
KW	SIGNAL			
FT	CHAIN	1	30	
FT	CHAIN	31	511	
FT	CHAIN	512	856	
FT	DISULFID	54	74	
FT	DISULFID	119	205	
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FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	448	
FT	DISULFID	385	418	
FT	CARBOHYD	88		
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FT	CARBOHYD	141	141	
FT	CARBOHYD	156	156	
FT	CARBOHYD	160	160	
FT	CARBOHYD	186	186	
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FT	CARBOHYD	230	230	
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FT	CARBOHYD	241	241	
FT	CARBOHYD	262	262	
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FT	CARBOHYD	295	295	
FT	CARBOHYD	301	301	
FT	CARBOHYD	332	332	
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FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 96938 MM; 0C241332CF7E6687 CRC64;
 Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 9e-16;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAOOHLQLTWQIKOLARILAVERYL 35
 Db 553 NNLRAIEAOOHLQLTWQIKOLARILAVERYL 587
 RESULT 9
 ENV_HVLPV STANDARD; PRT; 856 AA.
 AC P03376; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85111157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
 RT Nature 313:450-458(1985).
 RL -----
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 CC -----
 DR EMBL: K02083; AAB59873.1; -;
 DR EMBL: X01762; CA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT CHAIN 1 30
 FT CHAIN 511 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 556 556 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MM; 5FCBD1DC3C1209B3 CRC64;
 Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 9e-16;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAOOHLQLTWQIKOLARILAVERYL 35
 Db 553 NNLRAIEAOOHLQLTWQIKOLARILAVERYL 587
 RESULT 10
 ENV_HVLPV STANDARD; PRT; 861 AA.
 AC P03377; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85099333; PubMed=2981635;
 RA Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RT Cell 40:9-17(1985).
 RL -----
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 CC -----

[illegible][illegible]

FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 843 AA; 95648 MW; C69DFD971C918971 CRC64;
 Query Match 95.3%; Score 163; DB 1; Length 843;
 Best Local Similarity 94.3%; Pred. No. 1.2e-15;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYL 35
 DB 540 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYL 574

RESULT 12
 ENV_HV1ND STANDARD; PRT; 846 AA.
 AC P18799;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11695;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90034200; PubMed=2806917;
 RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.;
 RT "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
 RL Gene 81:275-284(1985).
 CC -1- MISCELLANEOUS: NDK. ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS. AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
 CC -----
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 CC -----
 CC EMBL; M27323; AAA44673.1; -;
 DR PIR; J00066; VCLND.
 DR HIV; M27323; ENV\$NDK.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 846 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 200 BY SIMILARITY.
 FT DISULFID 125 191 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 213 242 BY SIMILARITY.
 FT DISULFID 223 234 BY SIMILARITY.
 FT DISULFID 291 328 BY SIMILARITY.
 FT DISULFID 374 435 BY SIMILARITY.
 FT DISULFID 381 408 BY SIMILARITY.
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2E83 CRC64;
 Query Match 95.3%; Score 163; DB 1; Length 846;
 Best Local Similarity 94.3%; Pred. No. 1.2e-15;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYL 35
 DB 543 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYL 577

RESULT 13
 ENV_HV1S1 STANDARD; PRT; 847 AA.
 AC P19550;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90347835; PubMed=2384920;
 RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
 RL J. Virol. 64:4390-4398(1990).
 CC -----
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 CC -----
 CC EMBL; M65024; AAA45072.1; -;
 DR PDB; 1OBE; 1S-MAY-97.
 DR HIV; M38428; ENV\$SF162.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 203 BY SIMILARITY.
 FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.

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FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

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Query Match 95.3%; Score 163; DB 1; Length 847;
Best Local Similarity 94.3%; Pred. No. 1.2e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 NNLIRAEAOQHLLQLTWGIKOLARVLAVERYL 35
Db 544 NNLIRAEAOQHLLQLTWGIKOLARVLAVERYL 578

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RESULT 14
ENV_HV1A3 STANDARD; PRT; 852 AA.
ID ENV_HV1A3
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor (contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: AY352275; AAC1701.1; -
CC PDB: 1MEQ; 1I-DEC-02.
DR

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DR HTV, M38427; ENV$SF33.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
SO SEQUENCE 852 AA; 96663 MW; EF7BFBFD23C9910D CRC64;

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Query Match 95.3%; Score 163; DB 1; Length 852;
Best Local Similarity 94.3%; Pred. No. 1.3e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 NNLIRAEAOQHLLQLTWGIKOLARVLAVERYL 35
Db 549 NNLIRAEAOQHLLQLTWGIKOLARVLAVERYL 583

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RESULT 15
ENV_HV1A2 STANDARD; PRT; 855 AA.
ID ENV_HV1A2
AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor (contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]

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FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 855 AA; 97476 MM; 9CF82A607AD62DA CRC64;
 Query Match 95.3%; Score 163; DB 1; Length 855;
 Best Local Similarity 94.3%; Pred. No. 1,3e-15;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRRAIEAOQHLLQITVWGIKQARVLAVERYL 35
 Db 552 NNLRRAIEAOQHLLQITVWGIKQARVLAVERYL 586
 RESULT 17
 ENV_HV1SC STANDARD; PRT; 856 AA.
 ID ENV_HV1SC
 AC P05878;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88219542; PubMed=3369091;
 RA Gurgo C., Guo H.-G., Franchin G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Rietz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates";
 RT Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
 CC 1984 IN SOUTHERN CALIFORNIA.
 CC
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 CC or send an email to license@sib.ch).
 CC
 CC
 CC EMBL, M17450; -; NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.

FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97055 MM; DAF4DA600EBA7A08 CRC64;
 Query Match 95.3%; Score 163; DB 1; Length 856;
 Best Local Similarity 94.3%; Pred. No. 1,3e-15;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRRAIEAOQHLLQITVWGIKQARVLAVERYL 35
 Db 553 NNLRRAIEAOQHLLQITVWGIKQARVLAVERYL 587
 RESULT 18
 ENV_HV1W1 STANDARD; PRT; 856 AA.
 ID ENV_HV1W1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MMJ1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86218077; PubMed=2423250.
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 RT AIDS";
 RT Cell 45:637-648(1986).
 CC -1- MISCELLANEOUS: ISOLATES MMJ1, MMJ2, AND MMJ3 WERE OBTAINED FROM
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 CC WAS PERINATALLY INFECTED BY HER MOTHER.
 DR PIR: A24774; VCLJ3W.
 DR PDB: 1LB0; 04-DEC-02.
 DR PDB: 1LCX; 04-DEC-02.

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DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KM 3D-structure. 1
FT SIGNAL 1 29
FT CHAIN 30 510
FT CHAIN 511 856
FT DISULFID 53 73
FT DISULFID 118 205
FT DISULFID 125 196
FT DISULFID 130 152
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 330
FT DISULFID 376 444
FT DISULFID 383 417
FT CARBOHYD 87 134
FT CARBOHYD 134 140
FT CARBOHYD 140 151
FT CARBOHYD 151 155
FT CARBOHYD 183 197
FT CARBOHYD 197 234
FT CARBOHYD 234 241
FT CARBOHYD 241 262
FT CARBOHYD 262 276
FT CARBOHYD 276 289
FT CARBOHYD 289 295
FT CARBOHYD 295 331
FT CARBOHYD 331 338
FT CARBOHYD 338 354
FT CARBOHYD 354 360
FT CARBOHYD 360 390
FT CARBOHYD 390 394
FT CARBOHYD 394 404
FT CARBOHYD 404 447
FT CARBOHYD 447 459
FT CARBOHYD 459 611
FT CARBOHYD 611 616
FT CARBOHYD 616 625
FT CARBOHYD 625 637
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DB9 CRC64;

Query Match 95.3%; Score 163; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 1.3e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYL 35
Db 553 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYL 587

RESULT 19
ENV_HY1MA STANDARD; PRT; 859 AA.
AC P04583;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MOL isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11697;
RP SEQUENCE FROM N.A.
RX MEDLINE=66245056; PubMed=2424612;
RA Aizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis

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RT Of two isolates from African patients.";
RL Cell 46:63-74(1986).
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CC -----
DR EMBL: X04415; CA28016.1; -.
DR EMBL: A07116; CA00623.1; -.
DR PIR: T01672; T01672.
DR HIV; K03456; ENVSMAL.
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KM AIDS; Signal.
FT SIGNAL 1 30
FT CHAIN 31 513
FT CHAIN 514 859
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 334
FT DISULFID 380 445
FT DISULFID 387 418
FT CARBOHYD 87 129
FT CARBOHYD 129 134
FT CARBOHYD 134 139
FT CARBOHYD 139 146
FT CARBOHYD 146 161
FT CARBOHYD 161 193
FT CARBOHYD 193 202
FT CARBOHYD 202 239
FT CARBOHYD 239 246
FT CARBOHYD 246 267
FT CARBOHYD 267 281
FT CARBOHYD 281 294
FT CARBOHYD 294 300
FT CARBOHYD 300 306
FT CARBOHYD 306 337
FT CARBOHYD 337 357
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FT CARBOHYD 460 467
FT CARBOHYD 467 613
FT CARBOHYD 613 618
FT CARBOHYD 618 627
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FT CARBOHYD 639 819
SQ SEQUENCE 859 AA; 97109 MW; DBCF9A52E3ABF29 CRC64;

Query Match 95.3%; Score 163; DB 1; Length 859;
Best Local Similarity 94.3%; Pred. No. 1.3e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYL 35
Db 555 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYL 589

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RESULT 20
ENV_HV1RH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66218077; PubMed=2423250;
RA Seidlich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS.";
RL Cell 45:637-648(1986).
-----
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-----
DR EMBL; M17451; AAA45057.1; -.
DR HIV; M17451; ENVSRF.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane;
Signal.
KM
FT SIGNAL 1 29
FT CHAIN 30 519
FT CHAIN 520 865
FT DISULFID 53 73
FT DISULFID 118 218
FT DISULFID 125 209
FT DISULFID 130 157
FT DISULFID 231 260
FT DISULFID 241 252
FT DISULFID 309 343
FT DISULFID 389 452
FT DISULFID 396 425
FT CARBOHYD 87 129
FT CARBOHYD 136 136
FT CARBOHYD 139 139
FT CARBOHYD 156 156
FT CARBOHYD 193 193
FT CARBOHYD 194 194
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FT CARBOHYD 314 314
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FT CARBOHYD 367 367
FT CARBOHYD 397 397
FT SIGNAL 1 29
FT CHAIN 30 519
FT CHAIN 520 865
FT DISULFID 53 73
FT DISULFID 118 218
FT DISULFID 125 209
FT DISULFID 130 157
FT DISULFID 231 260
FT DISULFID 241 252
FT DISULFID 309 343
FT DISULFID 389 452
FT DISULFID 396 425
FT CARBOHYD 87 129
FT CARBOHYD 136 136
FT CARBOHYD 139 139
FT CARBOHYD 156 156
FT CARBOHYD 193 193
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FT CARBOHYD 308 308
FT CARBOHYD 314 314
FT CARBOHYD 344 344
FT CARBOHYD 351 351
FT CARBOHYD 367 367
FT CARBOHYD 397 397

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FT CARBOHYD 403 403
FT CARBOHYD 407 407
FT CARBOHYD 413 413
FT CARBOHYD 418 418
FT CARBOHYD 455 455
FT CARBOHYD 471 471
FT CARBOHYD 620 620
FT CARBOHYD 625 625
FT CARBOHYD 634 634
FT CARBOHYD 646 646
FT CARBOHYD 825 825
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;
Query Match 95.3%; Score 163; DB 1; Length 865;
Best Local Similarity 94.3%; Pred. No. 1,3e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 562 NMLRAIEAOQHLLQLTWQIKQLQARVLAVERYL 596
Qy 1 NMLRAIEAOQHLLQLTWQIKQLQARVLAVERYL 35
Db 562 NMLRAIEAOQHLLQLTWQIKQLQARVLAVERYL 596
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RESULT 21
ENV_HV1RH STANDARD; PRT; 848 AA.
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
-----
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DR EMBL; M38429; AAB03749.1; -.
DR PDB; 1CE4; 18-MAR-99.
DR HIV; M38429; ENVSRCSF.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
3D-structure.
KM
FT SIGNAL 1 32
FT CHAIN 33 503
FT CHAIN 504 848
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 154
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 437
FT DISULFID 381 410
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 137 137
FT CARBOHYD 153 153
FT SIGNAL 1 32
FT CHAIN 33 503
FT CHAIN 504 848
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 154
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 437
FT DISULFID 381 410
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 137 137
FT CARBOHYD 153 153

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FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 848 AA; 96475 MW; 207675127EC3F3 CRC64;

Query Match 94.2%; Score 161; DB 1; Length 848;
Best Local Similarity 91.4%; Pred. No. 2.4e-15;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARILAVERYL 35
Db 545 NNLRAIEAQOHLQTLTWQIKQLQARILAVERYL 579

RESULT 22
ENV_HV1M1N STANDARD; PRT; 856 AA.
AC P05877;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reltz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
PATIENT IN 1984.
CC -----
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CC -----
CC EMBL; M17449; AAA44857.1; -.
DR PDB; 1ACJ; 31-JUL-94.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1N1Z; 25-FEB-03.
DR PDB; 1NU0; 25-FEB-03.
DR HIV; M17449; ENVSMN.
DR InterPro; IPR000328; Env_GP41.

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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 513
FT 514 856
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
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FT DISULFID 381 445
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FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 140 140
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 336 336
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FT CARBOHYD 612 612
FT CARBOHYD 617 617
FT CARBOHYD 626 626
FT CARBOHYD 638 638
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97140 MW; D197D809940B732 CRC64;

Query Match 94.2%; Score 161; DB 1; Length 856;
Best Local Similarity 91.4%; Pred. No. 2.4e-15;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLTWQIKQLQARILAVERYL 35
Db 554 NNLRAIEAQOHLQTLTWQIKQLQARILAVERYL 588

RESULT 23
ENV_HV1M2 STANDARD; PRT; 847 AA.
AC P05880;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (NMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]

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[illegible]

OY		1	NNLRRAIEAQQHLLQTLTWVGIKQLAQAILVERYL	35
D8		544	NNLRRATDAQCHILLQTVMGIKQLQAIVLAIVERLT	578
<hr/>				
RESULT_24				
ENV_HVLB8				
ID_ENV_HVLB8	STANDARD;	PRT,	851 AA.	
AC_P04582;				
DT	13-AUG-1987	(Rel. 05, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HTV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.			
OX	[NCBI_TaxID=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=65111123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petway S.R., Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-II.";			
RL	Nature 313:277-284(1985).			
CC	- - - - -			
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CC	- - - - -			
DR	EMBL; KO2011; AAA44661.1; -. .			
DR	PDB; 1DDH; 1J-JAN-99.			
DR	PDB; 1HHG; 3I-OCT-93.			
DR	PDB; 1QQ3; 02-JAN-00.			
DR	PDB; 1S2T; 24-DEC-97.			
DR	HIV; KO2011; ENV/SBH8.			
DR	GlycoSuiteDB; P04582; -. .			
DR	InferPro; IPR000328; Env_GP41.			
DR	InferPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
KM	Pfam; PF00517; GP41; 1.			
AIDS; Coat protein; Polypotein; Glycopoltein; Transmembrane; Signal; 3D-structure.				
KW	SIGNAL	1	30	
FT CHAIN	31	506		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID	507	851		TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID	54	74		BY SIMILARITY.
FT DISULFID	119	205		BY SIMILARITY.
FT DISULFID	126	196		BY SIMILARITY.
FT DISULFID	131	157		BY SIMILARITY.
FT DISULFID	218	247		BY SIMILARITY.
FT DISULFID	228	239		BY SIMILARITY.
FT DISULFID	296	331		BY SIMILARITY.
FT DISULFID	378	440		BY SIMILARITY.
FT DISULFID	385	413		BY SIMILARITY.
FT CARBOHYD	88			N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	136	136		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	141	141		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	141	141		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	156	156		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	160	160		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	186	186		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	197	197		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	230	230		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	234	234		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	241	241		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	262	262		N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 93.6%; Score 160; DB 1; Length 851;
Best Local Similarity 94.3%; Pred. No. 3.4e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLTLTWQIKQARILAVERYL 35
Db 548 NNLRAIEAQOHLTLTWQIKQARILAVERYL 582

RESULT 25
ENV_HV12H STANDARD; PRT; 856 AA.
ID ENV_HV12H
AC P05881;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H321 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11692;
RN SEQUENCE FROM N.A.
RX MEDLINE=89228766; Pubmed=2713163;
RA Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
McCormick J., Ou C.Y., Myers G., Smith T., Chen B.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of hybrid HIV.";
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).

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CC
CC EMBL; M15896; AAB53948.1; -.
DR PIR; A44963; A44963.
DR HIV; M15896; ENVS2321.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KM signal.
FT SIGNAL 1 29
FT CHAIN 30 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.

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FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 153 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 379 445 BY SIMILARITY.
FT DISULFID 386 418 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;

Query Match 93.6%; Score 160; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 3.4e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLTLTWQIKQARILAVERYL 35
Db 553 NNLRAIEAQOHLTLTWQIKQARILAVERYL 587

RESULT 26
ENV_HV12B STANDARD; PRT; 861 AA.
ID ENV_HV12B
AC P31819;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36375;
RN SEQUENCE FROM N.A.
RX MEDLINE=92351552; Pubmed=1322587;
RA Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
Kitamura T.;
RT "Analysis of a human immunodeficiency virus type 1 isolate carrying a
truncated transmembrane glycoprotein.";
RL Virology 189:534-546(1992).
CC -I- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CC THE CODONS FOR 723-ALA AND 730-ARG.
CC
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CC EMBL, D12582; BAA02124.1; ALT_SEQ.

DR PIR; A42995; VCLJKB.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Transmembrane;
KM Signal.

FT CHAIN 1 35 POTENTIAL.

FT CHAIN 36 517 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT TRANSMEM 518 861 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 59 711 POTENTIAL.

FT DISULFID 124 212 BY SIMILARITY.

FT DISULFID 131 203 BY SIMILARITY.

FT DISULFID 136 160 BY SIMILARITY.

FT DISULFID 225 254 BY SIMILARITY.

FT DISULFID 235 246 BY SIMILARITY.

FT DISULFID 303 337 BY SIMILARITY.

FT DISULFID 383 446 BY SIMILARITY.

FT DISULFID 390 419 BY SIMILARITY.

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .)

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)

FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .)

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .)

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .)

FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .)

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .)

FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .)

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .)

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)

FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .)

FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .)

FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .)

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .)

FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .)

FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .)

FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .)

FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .)

FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .)

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)

FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .)

FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .)

FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .)

FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .)

FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .)

FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .)

FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .)

FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .)

FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .)

FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .)

FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .)

FT CARBOHYD 861 861 N-LINKED (GLCNAC. . .)

SO SEQUENCE 861 AA; 98116 MW; 3C06787658F0C9DA CRC64;

Query Match 93.6%; Score 160; DB 1; Length 861;

Best Local Similarity 91.4%; Pred. No. 3.4e-15;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAOOHLQTLTWQIKOARLAVERTL 35

DB 559 NNTLRATDAOQHLLQTLTWGKLOARLAVERTL 593

RESULT 27

ENV_HV1J3

ID_ENV_HV1J3

AC P12489; STANDARD; PRT; 867 AA.

ENV_HV1J3

AC P12489; STANDARD; PRT; 867 AA.

ENV_HV1J3

AC P12489; STANDARD; PRT; 867 AA.

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (HIV-1).

OC Viruses; Retroviridae; Lentivirus.

OC NCBI_TaxID=11694;

RM [1]

RP MEDLINE=89352108; PubMed=2669897;

RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."

RL AIDS Res. Hum. Retroviruses 5:411-419(1989).

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CC or send an email to license@isb-sib.ch).

CC EMBL, M21138; AAB03526.1; -.

DR HIV; M21138; ENV5JH3.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Transmembrane;
KM Signal.

FT CHAIN 1 30

FT CHAIN 31 516

FT DISULFID 53 673

FT DISULFID 118 217

FT DISULFID 125 208

FT DISULFID 130 160

FT DISULFID 230 259

FT DISULFID 240 251

FT DISULFID 308 342

FT DISULFID 388 457

FT DISULFID 395 430

FT CARBOHYD 87 87

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 188 188

FT CARBOHYD 189 189

FT CARBOHYD 199 199

FT CARBOHYD 209 209

FT CARBOHYD 246 246

FT CARBOHYD 253 253

FT CARBOHYD 274 274

FT CARBOHYD 288 288

FT CARBOHYD 307 307

FT CARBOHYD 350 350

FT CARBOHYD 366 366

FT CARBOHYD 372 372

FT CARBOHYD 396 396

FT CARBOHYD 402 402

FT CARBOHYD 408 408

FT CARBOHYD 412 412

FT CARBOHYD 418 418

FT CARBOHYD 423 423

FT CARBOHYD 460 460

FT CARBOHYD 475 475

FT CARBOHYD 622 622

FT CARBOHYD 627 627

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

FT CHAIN 1 30

FT CHAIN 31 516

FT DISULFID 53 673

FT DISULFID 118 217

FT DISULFID 125 208

FT DISULFID 130 160

FT DISULFID 230 259

FT DISULFID 240 251

FT DISULFID 308 342

FT DISULFID 388 457

FT DISULFID 395 430

FT CARBOHYD 87 87

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 188 188

FT CARBOHYD 189 189

FT CARBOHYD 199 199

FT CARBOHYD 209 209

FT CARBOHYD 246 246

FT CARBOHYD 253 253

FT CARBOHYD 274 274

FT CARBOHYD 288 288

FT CARBOHYD 307 307

FT CARBOHYD 350 350

FT CARBOHYD 366 366

FT CARBOHYD 372 372

FT CARBOHYD 396 396

FT CARBOHYD 402 402

FT CARBOHYD 408 408

FT CARBOHYD 412 412

FT CARBOHYD 418 418

FT CARBOHYD 423 423

FT CARBOHYD 460 460

FT CARBOHYD 475 475

FT CARBOHYD 622 622

FT CARBOHYD 627 627

FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;
 Query Match 93.6%; Score 160; DB 1; Length 867;
 Best Local Similarity 94.3%; Pred. No. 3.5e-15;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTVMQIKOLQARIILAVERYL 35
 Db 564 NNLRAIEAQOHLQLTVMQIKOLQARIILAVERYL 598

RESULT 28
 ENV_HV1C4 STANDARD; PRT; 868 AA.
 ID ENV_HV1C4 STANDARD; PRT; 868 AA.
 AC P05879;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041461; Pubmed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
 RA Andersen P.R., Devare S.G.;
 RT "Molecular cloning and primary nucleotide sequence analysis of a
 RT distinct human immunodeficiency virus isolate reveal significant
 RT divergence in its genomic sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RL [2]
 RN SEQUENCE OF 34-43.
 RX MEDLINE=90253924; Pubmed=2187500;
 RA Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Iusso P.,
 RA Devico A.B., Copeland T., Oroszian S., Gallo R.C., Sarradharan M.G.;
 RT "Characterization of the secreted, native gp120 and gp160 of the human
 RT immunodeficiency virus type 1";
 RT AIDS Res. Hum. Retroviruses 6:371-380(1990).
 RL AIDS Res. Hum. Retroviruses 6:371-380(1990).
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 CC EMBL; M13137; AAA44311.1; .
 DR PIR; C25523; VCLJH4.
 DR HIV; M13137; ENVSDDC45.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR007777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 RT SIGNAL.
 FT CHAIN 1 33
 FT CHAIN 34 522 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).
 FT CHAIN 523 868 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 55 75 BY SIMILARITY.
 FT DISULFID 120 216 BY SIMILARITY.
 FT DISULFID 127 207 BY SIMILARITY.
 FT DISULFID 132 163 BY SIMILARITY.
 FT DISULFID 229 258 BY SIMILARITY.
 FT DISULFID 239 250 BY SIMILARITY.
 FT DISULFID 307 341 BY SIMILARITY.
 FT DISULFID 387 456 BY SIMILARITY.
 FT DISULFID 394 429 BY SIMILARITY.

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 828 828 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 868 AA; 98698 MW; A11527FC52A6F0C8 CRC64;
 Query Match 93.6%; Score 160; DB 1; Length 868;
 Best Local Similarity 94.3%; Pred. No. 3.5e-15;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTVMQIKOLQARIILAVERYL 35
 Db 565 NNLRAIEAQOHLQLTVMQIKOLQARIILAVERYL 599

RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.
 ID ENV_HV1Z8 STANDARD; PRT; 863 AA.
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; Pubmed=3395517;
 RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Straal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1";
 RT AIDS Res. Hum. Retroviruses 4:165-173(1988).
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
 CC ZAIREAN MALE.
 CC -----
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CC -----
DR EMBL; J03653; AAA44684.1; -.
DR HIV; J03653; ENV5JY1.
DR Interpro: IPR000328; Env GP41.
DR Interpro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 30 518 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 452 BY SIMILARITY.
FT DISULFID 395 425 BY SIMILARITY.
FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FA1641 CRC64;

Query Match 90.6%; Score 155; DB 1; Length 863;
Best Local Similarity 88.6%; Pred. No. 1.8e-14;
Matches 31; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OS Chimpanzee immunodeficiency virus (SIVcpz) (CIV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huec T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52154; CAA36407.1; -.
CC PIR; S09990; VCLJST.
DR HIV; X52154; ENV5CPZ.
DR Interpro: IPR000328; Env GP41.
DR Interpro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 500 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 501 854 POTENTIAL.
FT DISULFID 517 517 POTENTIAL.
FT TRANSMEM 675 693 POTENTIAL.
FT TRANSMEM 805 821 POTENTIAL.
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FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D983 CRC64;

Query Match 89.5%; Score 153; DB 1; Length 854;
Best Local Similarity 82.9%; Pred. No. 3.5e-14;
Matches 29; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Search completed: June 2, 2004, 11:42:56
Job time : 6.70652 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 29.3886 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-149
Sequence: 1 NNLRAIEAQHLLQLTWQIKQLQARIILAVERYL 35

Scoring table: BLOSUP62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvtrius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	95.9	132	15	090052
2	164	95.9	132	15	07SLZ2
3	164	95.9	139	15	07SLZ9
4	164	95.9	143	15	07SM06
5	164	95.9	144	15	07ZCD7
6	164	95.9	144	15	07ZCD6
7	164	95.9	153	15	07SM03
8	164	95.9	357	15	078119
9	164	95.9	588	15	0993A8
10	164	95.9	588	15	0993A7
11	164	95.9	589	15	0993B1
12	164	95.9	590	15	0993A9
13	164	95.9	616	15	0993B0
14	164	95.9	618	15	0993B2
15	164	95.9	724	15	09QKH4
16	164	95.9	727	15	09Q723

17	164	95.9	747	15	070607	070607 human immun
18	164	95.9	748	15	070606	070606 human immun
19	164	95.9	752	15	070604	070604 human immun
20	164	95.9	752	15	070605	070605 human immun
21	164	95.9	752	15	070608	070608 human immun
22	164	95.9	757	15	090722	090722 human immun
23	164	95.9	811	15	09DVL6	09DVL6 human immun
24	164	95.9	839	15	09QKH5	09QKH5 human immun
25	164	95.9	841	15	09QKH1	09QKH1 human immun
26	164	95.9	842	15	073341	073341 human immun
27	164	95.9	842	15	070895	070895 human immun
28	164	95.9	842	15	073340	073340 human immun
29	164	95.9	847	15	069996	069996 human immun
30	164	95.9	850	15	056564	056564 human immun
31	164	95.9	851	15	078243	078243 human immun
32	164	95.9	854	15	056566	056566 human immun
33	164	95.9	854	15	085582	085582 human immun
34	164	95.9	854	15	072502	072502 human immun
35	164	95.9	854	15	090178	090178 human immun
36	164	95.9	854	15	078705	078705 human immun
37	164	95.9	855	15	08AQV7	08AQV7 human immun
38	164	95.9	855	15	08ADT7	08ADT7 human immun
39	164	95.9	856	15	074090	074090 human immun
40	164	95.9	856	15	092877	092877 simian-huna
41	164	95.9	856	15	074599	074599 human immun
42	164	95.9	856	15	041772	041772 human immun
43	164	95.9	857	15	092822	092822 human immun
44	164	95.9	857	15	071013	071013 human immun
45	164	95.9	857	15	089654	089654 human immun
46	164	95.9	857	15	080847	080847 human immun
47	164	95.9	859	15	09QAC1	09QAC1 human immun
48	164	95.9	859	15	090202	090202 human immun
49	164	95.9	860	15	073312	073312 human immun
50	164	95.9	860	15	073310	073310 human immun
51	164	95.9	860	15	073311	073311 human immun
52	164	95.9	860	15	073309	073309 human immun
53	164	95.9	860	15	09E518	09E518 human immun
54	164	95.9	861	15	080848	080848 human immun
55	164	95.9	861	15	080849	080849 human immun
56	164	95.9	864	15	09YP39	09YP39 human immun
57	164	95.9	864	15	07ZJ08	07ZJ08 human immun
58	164	95.9	869	15	073302	073302 human immun
59	164	95.9	875	15	091U29	091U29 human immun
60	164	95.9	875	15	091U00	091U00 human immun
61	164	95.9	86	15	07ZC7	07ZC7 human immun
62	164	95.9	86	15	07ZC78	07ZC78 human immun
63	164	95.9	91	15	07ZCF4	07ZCF4 human immun
64	164	95.9	124	15	076270	076270 human immun
65	164	95.9	125	15	091WP9	091WP9 human immun
66	164	95.9	132	15	091W05	091W05 human immun
67	164	95.9	133	15	090020	090020 human immun
68	164	95.9	134	15	07ZC75	07ZC75 human immun
69	164	95.9	137	15	09DQM4	09DQM4 human immun
70	164	95.9	142	15	091WQ7	091WQ7 human immun
71	164	95.9	142	15	07ZCE7	07ZCE7 human immun
72	164	95.9	144	15	070207	070207 human immun
73	164	95.9	144	15	07ZCF1	07ZCF1 human immun
74	164	95.9	144	15	07ZCF0	07ZCF0 human immun
75	164	95.9	144	15	07ZCB8	07ZCB8 human immun
76	164	95.9	144	15	07ZCD0	07ZCD0 human immun
77	164	95.9	144	15	07ZCB9	07ZCB9 human immun
78	164	95.9	144	15	07ZCB8	07ZCB8 human immun
79	164	95.9	144	15	07ZCB6	07ZCB6 human immun
80	164	95.9	144	15	07ZCB5	07ZCB5 human immun
81	164	95.9	144	15	07ZCC2	07ZCC2 human immun
82	164	95.9	144	15	07ZCC1	07ZCC1 human immun
83	164	95.9	144	15	07ZCB3	07ZCB3 human immun
84	164	95.9	144	15	07ZCB3	07ZCB3 human immun
85	164	95.9	144	15	07ZCB2	07ZCB2 human immun
86	164	95.9	144	15	07ZCB1	07ZCB1 human immun
87	164	95.9	144	15	07ZCB0	07ZCB0 human immun
88	164	95.9	144	15	07ZCA4	07ZCA4 human immun
89	164	95.9	144	15	07ZC97	07ZC97 human immun

90 163 95.3 144 15 Q7ZC96 Q7ZC96 human immun
ALIGNMENTS

RESULT 1

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Q90052 ID 090052 PRELIMINARY; PRT; 132 AA.  
AC 090052;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxId=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=99ES-MOI496;  
RX MEDLINE=21332034; Pubmed=11429126;  
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,  
RA Garcia-Saiz A.;  
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea,";  
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).  
DR EMBL; AF331089; AK92300.1; -.  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0019031; C: viral envelope; IEA.  
DR GO: GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR00328; Env_GP41.  
DR Pfam; PF00517; GP41; 1.  
KM Transmembrane.  
FT NON_TER 1  
FT SEQUENCE 132 AA; 15708 MW; 51D9DB8AED574FAB CRC64;  
SQ  
Query Match 95.9%; Score 164; DB 15; Length 132;  
Best Local Similarity 97.1%; Pred. No. 6.8e-16;  
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35  
Db 10 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 44  
RESULT 2  
Q7SLZ2 ID Q7SLZ2 PRELIMINARY; PRT; 132 AA.  
AC Q7SLZ2;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxId=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GT970;  
RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
infection in Equatorial Guinea, 1996-1998,";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF530024; AAP87755.1; -.  
KM Envelope protein.  
FT NON_TER 1  
FT SEQUENCE 132 AA; 15717 MW; CA7F0709A8949B33 CRC64;  
SQ  
Query Match 95.9%; Score 164; DB 15; Length 132;  
Best Local Similarity 97.1%; Pred. No. 6.8e-16;
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Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35  
Db 11 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 45
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RESULT 3

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Q7SLZ9 ID Q7SLZ9 PRELIMINARY; PRT; 139 AA.  
AC Q7SLZ9;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxId=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GT966;  
RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
infection in Equatorial Guinea, 1996-1998,";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF530017; AAP87748.1; -.  
KM Envelope protein.  
FT NON_TER 1  
FT NON_TER 139  
FT SEQUENCE 139 AA; 16651 MW; 53F75C8EF664BA7A CRC64;  
SQ
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Query Match 95.9%; Score 164; DB 15; Length 139;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35  
Db 11 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 45
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RESULT 4

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DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxId=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GT1138;  
RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
infection in Equatorial Guinea, 1996-1998,";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF530010; AAP87741.1; -.  
KM Envelope protein.  
FT NON_TER 1  
FT NON_TER 143  
FT SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BE0 CRC64;  
SQ
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Query Match 95.9%; Score 164; DB 15; Length 143;
Best Local Similarity 97.1%; Pred. No. 7.4e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 11 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 45
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RESULT 5
Q7ZCD7
ID 07ZCD7 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLX53-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185384; AA065659.1; -.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Envelope protein..
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EBB CRC64;
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Query Match 95.9%; Score 164; DB 15; Length 144;
Best Local Similarity 97.1%; Pred. No. 7.5e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35
Db 24 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 58
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Query Match 95.9%; Score 164; DB 15; Length 144;
Best Local Similarity 97.1%; Pred. No. 7.5e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35
Db 24 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 58

RESULT 7
Q7SM03
ID 07SM03 PRELIMINARY; PRT; 153 AA.
AC Q7SM03;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GR598;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF530013; AAB87744.1; -.
KM Envelope protein..
FT NON_TER 1 1
FT NON_TER 153 153
SQ SEQUENCE 153 AA; 18136 MW; 014FA9B1FEFC035 CRC64;
```

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Query Match 95.9%; Score 164; DB 15; Length 153;
Best Local Similarity 97.1%; Pred. No. 7.9e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 35
Db 11 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYL 45
```

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RESULT 8
Q78119
ID 078119 PRELIMINARY; PRT; 357 AA.
AC Q78119;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid."
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL: X61356; CAA43624.1; -.
DR PIR: A53591; A53591.
DR PIR: S70422; S21996.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1 1
FT NON_TER 357 357
SQ SEQUENCE 357 AA; 41118 MW; FE4CA7E122ABBE6 CRC64;
```

Query Match 95.9%; Score 164; DB 15; Length 357;
 Best Local Similarity 97.1%; Pred. No. 1.9e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYL 35
 Db 54 NNLRAIEAQOHLQLTWQIKQARILAVERYL 88

RESULT 9

Q993A8 PRELIMINARY; PRT; 588 AA.
 AC Q993A8; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RA DCostra S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF21147; AAK20295.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coats protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240A8B CRC64;

Query Match 95.9%; Score 164; DB 15; Length 588;
 Best Local Similarity 97.1%; Pred. No. 3.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYL 35
 Db 496 NNLRAIEAQOHLQLTWQIKQARILAVERYL 530

RESULT 10

Q993A7 PRELIMINARY; PRT; 588 AA.
 AC Q993A7; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RA DCostra S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF21148; AAK20296.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.

OS Viruses; Retrovird viruses; Retroviridae; Lentivirus.

DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coats protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B5922FC6D CRC64;

Query Match 95.9%; Score 164; DB 15; Length 588;
 Best Local Similarity 97.1%; Pred. No. 3.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYL 35
 Db 496 NNLRAIEAQOHLQLTWQIKQARILAVERYL 530

RESULT 11

Q993B1 PRELIMINARY; PRT; 589 AA.
 AC Q993B1; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RA DCostra S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF21144; AAK20292.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coats protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 589;
 Best Local Similarity 97.1%; Pred. No. 3.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYL 35
 Db 496 NNLRAIEAQOHLQLTWQIKQARILAVERYL 530

RESULT 12

Q993A9 PRELIMINARY; PRT; 590 AA.
 AC Q993A9; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=wt2;
 RA Dcosta S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF321146; AAK20294.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;

Query Match 95.9%; Score 164; DB 15; Length 590;
 Best Local Similarity 97.1%; Pred. No. 3.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
 Db 497 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 531

RESULT 13
 Q993B0 PRELIMINARY; PRT; 616 AA.
 AC Q993B0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1H6;
 RA Dcosta S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF321145; AAK20293.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 616 AA; 69189 MW; 57A8E20F9A580A4F CRC64;

Query Match 95.9%; Score 164; DB 15; Length 616;
 Best Local Similarity 97.1%; Pred. No. 3.4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
 Db 497 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 531

RESULT 14
 Q993B2 PRELIMINARY; PRT; 618 AA.
 AC Q993B2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1B6;
 RA Dcosta S.S., Hurwitz J.L.;
 RT "Escape mutants to determine structure of gp120 of HIV-1.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF321143; AAK20291.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;

Query Match 95.9%; Score 164; DB 15; Length 618;
 Best Local Similarity 97.1%; Pred. No. 3.5e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
 Db 499 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 533

RESULT 15
 Q99KH4 PRELIMINARY; PRT; 724 AA.
 AC Q99KH4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22233V5;
 RX MEDLINE=99094949; PubMed=9878014;
 RA Van Dyke R.B., Korber B.T., Poppe E., Macken C., Widmayer S.M.,
 RA Bardeguez A., Hansen I.C., Wiznia A., Luzzatiga K., Viscarello R.R.,
 RA Wolinsky S., the Ariel Core Investigators;
 RT "The Ariel Project: A prospective cohort study of maternal-child
 RT transmission of human immunodeficiency virus type 1 in the era of
 RT maternal antiretroviral therapy.";
 RL J. Infect. Dis. 179:319-328(1999).
 DR EMBL; AF12564; AF13542.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 724 AA; 81330 MW; F579661356801958 CRC64;
 Query Match 95.9%; Score 164; DB 15; Length 724;
 Best Local Similarity 97.1%; Pred. No. 4.1e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 35
 Db 533 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 567
 RESULT 16
 090723 PRELIMINARY; PRT; 727 AA.
 AC 090723;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope polypeptide variant.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IIIBX;
 RX MEDLINE=9272698; PubMed=10339592;
 RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
 RA Chaiken I., Hoxie J.A., Doms R.W.;
 RT "Stable exposure of the coreceptor-binding site in a CD4-independent
 RT HIV-1 envelope protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IIIBX;
 RX MEDLINE=20027260; PubMed=10559349;
 RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
 RA Matthews T.J., Doms R.W., Hoxie J.A.;
 RT "Determinants of CD4 independence for a human immunodeficiency virus
 RT type 1 variant map outside regions required for coreceptor
 RT specificity."
 RL J. Virol. 73:10310-10319(1999).
 DR EMBL: AF189158; AAF25627.1; -.
 DR PIR: A53591; A53591.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 GN Interpro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 727 AA; 82201 MW; F90FD626D26B9E66 CRC64;
 Query Match 95.9%; Score 164; DB 15; Length 727;
 Best Local Similarity 97.1%; Pred. No. 4.1e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 35
 Db 548 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 582
 RESULT 17
 070607 PRELIMINARY; PRT; 747 AA.
 AC 070607;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RX MEDLINE=9517297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Laubenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12034; AAA76669.1; -.
 DR PIR: A53591; A53591.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON TER 747
 SQ SEQUENCE 747 AA; 84250 MW; 732B836A52245F14 CRC64;
 Query Match 95.9%; Score 164; DB 15; Length 747;
 Best Local Similarity 97.1%; Pred. No. 4.2e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 35
 Db 548 NNLRAIEAQOHLQTLTWQIKQARILAVERYL 582
 RESULT 18
 070606 PRELIMINARY; PRT; 748 AA.
 AC 070606;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RX MEDLINE=9517297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Laubenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12032; AAA76668.1; -.
 DR PIR: A53591; A53591.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 748 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 95.9%; Score 164; DB 15; Length 748;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 35
Db 549 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 583

RESULT 19
Q70604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 35
Db 553 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 587

RESULT 20
Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 35
Db 553 NNLRLAEAOQHLLQTLTWGKQIQAARILAVERYL 587

RESULT 21
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12035; AAA76670.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;
Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 22
090722 PRELIMINARY; PRT; 757 AA.
ID 090722
AC Q90722; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBX;
RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
HIV-1 envelope protein.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364 (1999).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=IIIBX;
RC MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
type 1 variant map outside regions required for coreceptor
specificity.";
RT J. Virol. 73:10310-10319 (1999).
DR EMBL: AF189159; AAF25628.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AFB8D263BD2E CRC64;

Query Match 95.9%; Score 164; DB 15; Length 757;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 548 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 582

RESULT 23
090726 PRELIMINARY; PRT; 811 AA.
ID 090726
AC Q90726; (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; PubMed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.,
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
group M genetic diversity in the Democratic Republic of Congo suggests
that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507 (2000).
DR EMBL: AF401037; CAC15045.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 811
FT NON_TER 811
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;
Query Match 95.9%; Score 164; DB 15; Length 811;
Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 557 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 591

RESULT 24
090725 PRELIMINARY; PRT; 839 AA.
ID 090725
AC Q90725; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22211V4;
RX MEDLINE=99094949; PubMed=9878014;
RA Van Dyke R.B., Kotber B.T., Popok E., Macken C., Widmayer S.M.,
Bardaguer A., Hansen I.C., Wiznia A., Luzzuriaga K., Viscarello R.R.,

RA Wolinsky S., the Ariel Core Investigators;
 RT "The Ariel Project: A prospective cohort study of maternal-child
 transmission of human immunodeficiency virus type 1 in the era of
 RT maternal antiretroviral therapy";
 RU J. Infect. Dis. 179:319-328(1999).
 DR EMBL: AF112563; AAF1341.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1
 FT 839 839
 SQ SEQUENCE 839 AA; 94391 MW; C046E34F0CF948C CRC64;

Query Match 95.9%; Score 164; DB 15; Length 839;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
 Db 537 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 571

RESULT 25
 ID 090KJ1 PRELIMINARY; PRT; 841 AA.
 AC 090KJ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22202V3.6;
 RX MEDLINE=99094949; PubMed=9878014;
 RA Van Dyke R.B., Korber B.T., Popek E., Macken C., Widmayer S.M.,
 RA Bardeguen A., Hansen I.C., Winkler A., Luzuriaga K., Viscarello R.R.,
 RA Wolinsky S., the Ariel Core Investigators;
 RT "The Ariel Project: A prospective cohort study of maternal-child
 transmission of human immunodeficiency virus type 1 in the era of
 RT maternal antiretroviral therapy";
 RU J. Infect. Dis. 179:319-328(1999).
 DR EMBL: AF112547; AAF13325.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 1
 FT 841 841
 SQ SEQUENCE 841 AA; 95389 MW; E9086659E7E1D447 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 841;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
 Db 538 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 572

RESULT 26
 ID 073341 PRELIMINARY; PRT; 842 AA.
 AC 073341;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
 RA Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization";
 RU AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL: U39236; AAB37173.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1E991 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
 Db 539 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 573

RESULT 27
 ID 070895 PRELIMINARY; PRT; 842 AA.
 AC 070895;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
 DE Envelope gp160.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=93br029;
 RX MEDLINE=98285725; PubMed=9621027;
 RA Gao F., Robertson D.L., Carruthers C.D., Morrison S.G., Jian B.,
 RA Chen Y., Barre-Sinoussi F., Girard M., Srinivasan A., Abimiku A.G.,
 RA Shaw G.M., Sharp P.M., Hahn B.H.;
 RT "A comprehensive panel of near-full-length clones and reference
 RT sequences for non-subtype B isolates of human immunodeficiency virus
 RT type 1";
 RU J. Virol. 72:5680-5698(1998).
 DR EMBL: AF005495; AAD03179.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
 Db 538 NNLRAIEAQOHLQLTWQIKOLQARILAVERYL 572

DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94810 MW; F82041B1D93DCAD CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 35
 Db 539 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 573

RESULT 28
 Q73340 PRELIMINARY; PRT; 842 AA.
 AC Q73340; (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranbar S., Holmes H.,
 Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization";
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 RU EMBL, U39235; AAB37172.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 607BAF2A7B791EB CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 35
 Db 539 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 573

RESULT 29
 Q69996 PRELIMINARY; PRT; 847 AA.
 AC Q69996; (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
 RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., Shaw G.M.,
 RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization";
 RL J. Virol. 70:1651-1657(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA NIAID/NIH DAIDS Variation Program;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA McEvilly M.M.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08445; AAB04071.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 847 AA; 95602 MW; FCBCEA7AF446FB20 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 847;
 Best Local Similarity 97.1%; Pred. No. 4.8e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 35
 Db 544 NNLRAIEAOQHLLQTLTWQIKOLQARIIVAYRYL 578

RESULT 30
 O56564 PRELIMINARY; PRT; 850 AA.
 AC O56564; (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PIH155;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Ataman-Onal Y., Coliflier C., Giraud A., Babic-Ercceg A., Biron F.,
 RA Verrier B.;
 RT "Comparative primary HIV type 1 infection";
 RT AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 RU EMBL, AF041130; AAC02521.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 850 AA; 96294 MW; F3652F9F6361BA8 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 850;
Best Local Similarity 97.1%; Pred. No. 4.8e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLRAIEAOQHLLQLTWQIKQLQARI LAVERYL 35
Db 547 NNLRLRAIEAOQHLLQLTWQIKQLQARI LAVERYL 581

Search completed: June 2, 2004, 11:48:20
Job time : 30.3866 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 12.9348 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-149
Perfect score: 171
Sequence: 1 NNILRAIEAQHLLQLTWQIKQLQARILAVERYL 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	38 4	US-08-973-952-82	Sequence 82, Appl
2	164	95.9	35 4	US-09-515-965A-1720	Sequence 1720, Ap
3	164	95.9	36 4	US-09-515-965A-1721	Sequence 1721, Ap
4	164	95.9	37 4	US-09-515-965A-1722	Sequence 1722, Ap
5	164	95.9	38 1	US-08-374-666-1	Sequence 1, Appli
6	164	95.9	38 3	US-08-486-099-89	Sequence 89, Appl
7	164	95.9	38 3	US-08-360-107A-99	Sequence 99, Appl
8	164	95.9	38 3	US-08-360-107A-132	Sequence 132, App
9	164	95.9	38 3	US-08-484-223B-89	Sequence 89, Appl
10	164	95.9	38 3	US-08-919-597-89	Sequence 89, Appl
11	164	95.9	38 3	US-08-475-668A-89	Sequence 89, Appl
12	164	95.9	38 3	US-08-485-551A-89	Sequence 89, Appl
13	164	95.9	38 3	US-08-471-913A-89	Sequence 89, Appl
14	164	95.9	38 3	US-08-485-264A-89	Sequence 89, Appl
15	164	95.9	38 3	US-09-082-279B-16	Sequence 16, Appl
16	164	95.9	38 3	US-09-082-279B-507	Sequence 507, App
17	164	95.9	38 3	US-09-082-279B-604	Sequence 604, App
18	164	95.9	38 3	US-09-082-279B-661	Sequence 661, App
19	164	95.9	38 3	US-09-082-279B-662	Sequence 662, App
20	164	95.9	38 3	US-09-082-279B-663	Sequence 663, App
21	164	95.9	38 4	US-08-474-349A-89	Sequence 89, Appl
22	164	95.9	38 4	US-08-474-349A-441	Sequence 441, App
23	164	95.9	38 4	US-09-315-304B-16	Sequence 16, Appl
24	164	95.9	38 4	US-09-315-304B-507	Sequence 507, App
25	164	95.9	38 4	US-09-315-304B-604	Sequence 604, App
26	164	95.9	38 4	US-09-315-304B-661	Sequence 661, App
27	164	95.9	38 4	US-09-315-304B-662	Sequence 662, App

28	164	95.9	38 4	US-09-315-304B-663	Sequence 663, App
29	164	95.9	38 4	US-08-255-208A-25	Sequence 25, Appl
30	164	95.9	38 4	US-08-470-896-89	Sequence 89, Appl
31	164	95.9	38 4	US-08-485-546A-89	Sequence 89, Appl
32	164	95.9	38 4	US-09-796-202-11	Sequence 11, Appl
33	164	95.9	38 4	US-09-834-784-16	Sequence 16, Appl
34	164	95.9	38 4	US-09-834-784-507	Sequence 507, App
35	164	95.9	38 4	US-09-834-784-604	Sequence 604, App
36	164	95.9	38 4	US-09-834-784-661	Sequence 661, App
37	164	95.9	38 4	US-09-834-784-662	Sequence 662, App
38	164	95.9	38 4	US-09-834-784-663	Sequence 663, App
39	164	95.9	38 4	US-08-464-003-1	Sequence 1, Appli
40	164	95.9	38 4	US-09-779-451-2	Sequence 2, Appli
41	164	95.9	38 4	US-09-515-965A-16	Sequence 16, Appl
42	164	95.9	38 4	US-09-515-965A-507	Sequence 507, App
43	164	95.9	38 4	US-09-515-965A-604	Sequence 604, App
44	164	95.9	38 4	US-09-515-965A-661	Sequence 661, App
45	164	95.9	38 4	US-09-515-965A-662	Sequence 662, App
46	164	95.9	38 4	US-09-515-965A-663	Sequence 663, App
47	164	95.9	38 4	US-09-350-641C-16	Sequence 16, Appl
48	164	95.9	38 4	US-09-350-641C-507	Sequence 507, App
49	164	95.9	38 4	US-09-350-641C-604	Sequence 604, App
50	164	95.9	38 4	US-09-350-641C-661	Sequence 661, App
51	164	95.9	38 4	US-09-350-641C-662	Sequence 662, App
52	164	95.9	38 4	US-09-350-641C-663	Sequence 663, App
53	164	95.9	41 1	US-08-073-028-8	Sequence 8, Appli
54	164	95.9	41 1	US-08-374-666-3	Sequence 9, Appli
55	164	95.9	41 1	US-08-374-666-9	Sequence 8, Appli
56	164	95.9	41 3	US-08-486-099-8	Sequence 8, Appli
57	164	95.9	41 3	US-08-360-107A-8	Sequence 8, Appli
58	164	95.9	41 3	US-08-484-223B-242	Sequence 242, App
59	164	95.9	41 3	US-08-484-223B-243	Sequence 243, App
60	164	95.9	41 3	US-08-484-223B-243	Sequence 8, Appli
61	164	95.9	41 3	US-08-919-597-8	Sequence 8, Appli
62	164	95.9	41 3	US-08-475-668A-8	Sequence 8, Appli
63	164	95.9	41 3	US-08-485-551A-8	Sequence 8, Appli
64	164	95.9	41 3	US-08-471-913A-8	Sequence 8, Appli
65	164	95.9	41 3	US-08-554-616-8	Sequence 8, Appli
66	164	95.9	41 3	US-08-485-264A-8	Sequence 8, Appli
67	164	95.9	41 3	US-09-082-279B-496	Sequence 496, App
68	164	95.9	41 3	US-09-082-279B-601	Sequence 601, App
69	164	95.9	41 3	US-09-082-279B-633	Sequence 633, App
70	164	95.9	41 3	US-09-082-279B-1163	Sequence 1163, App
71	164	95.9	41 4	US-08-474-349A-8	Sequence 8, Appli
72	164	95.9	41 4	US-09-315-304B-601	Sequence 601, App
73	164	95.9	41 4	US-09-315-304B-633	Sequence 633, App
74	164	95.9	41 4	US-09-315-304B-1163	Sequence 1163, App
75	164	95.9	41 4	US-08-255-208A-8	Sequence 8, Appli
76	164	95.9	41 4	US-08-973-952-8	Sequence 8, Appli
77	164	95.9	41 4	US-08-470-896-8	Sequence 8, Appli
78	164	95.9	41 4	US-08-485-546A-8	Sequence 8, Appli
79	164	95.9	41 4	US-08-834-784-496	Sequence 496, App
80	164	95.9	41 4	US-08-834-784-601	Sequence 601, App
81	164	95.9	41 4	US-08-834-784-633	Sequence 633, App
82	164	95.9	41 4	US-09-834-784-633	Sequence 633, App
83	164	95.9	41 4	US-09-834-784-1163	Sequence 1163, App
84	164	95.9	41 4	US-08-464-003-3	Sequence 3, Appli
85	164	95.9	41 4	US-08-464-003-9	Sequence 9, Appli
86	164	95.9	41 4	US-09-515-965A-496	Sequence 496, App
87	164	95.9	41 4	US-09-515-965A-601	Sequence 601, App
88	164	95.9	41 4	US-09-515-965A-633	Sequence 633, App
89	164	95.9	41 4	US-09-515-965A-1163	Sequence 1163, App
90	164	95.9	41 4	US-09-350-641C-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6473491
; GENERAL INFORMATION:

```
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORIAL THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ. ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82
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Query Match 100.0%; Score 171; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
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```
RESULT 2
US-09-515-965A-1720
Sequence 1720, Application US/09515965A
```

```
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1720
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1720
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Query Match 95.9%; Score 164; DB 4; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
```

```
RESULT 3
```

```
US-09-515-965A-1721
Sequence 1721, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
```

```
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1721
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1721
```

```
Query Match 95.9%; Score 164; DB 4; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
```

```
RESULT 4
US-09-515-965A-1722
Sequence 1722, Application US/09515965A
```

```
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1722
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1722
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Query Match 95.9%; Score 164; DB 4; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYL 35
```

```
RESULT 5
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```
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
```

APPLICANT: Matthews, Thomas J.
CURRENT APPLICATION DATA:
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CORRESPONDENCE ADDRESSES:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 95.9%; Score 164; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQIQAIIAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQIQAIIAVERYL 35

RESULT 6
US-08-486-099-89
Sequence 89, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CORRESPONDENCE ADDRESSES:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQIQAIIAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQIQAIIAVERYL 35

RESULT 7
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35
DB 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35

RESULT 8
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35
DB 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35

RESULT 9
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35
DB 1 NNLRLAEAOQHLLQLTWQIKOLQARILAVERYL 35

RESULT 10
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYL 35

RESULT 11
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYL 35

RESULT 12
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35

RESULT 13
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35

RESULT 14
US-08-485-264A-89

Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35

RESULT 15
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guttridge, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Arner, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0

```
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16
```

```
Query Match          95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
```

```
RESULT 16
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507
```

```
Query Match          95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
```

```
RESULT 17
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

```
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604
```

```
Query Match          95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
```

```
RESULT 18
US-09-082-279B-661
Sequence 661, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-661
```

```
Query Match          95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB      2 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 36
```

```
RESULT 19
US-09-082-279B-662
Sequence 662, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 662
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-662
```

```
Query Match          95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
```

	Matches	34, Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	1	NNLRATEAQOHLQLTWTWQIKQLQARILAVERYL	35			
Db	3	NNLRATEAQOHLQLTWTWGIKQLQARILAVERYL	37			

1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYL 35
 |||||
 3 NNLRAIEAQHLLQLTWGIKQLQARILAVERYL 37

```

RESULT 20
US-09-082-279B-663
Sequence 663, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Mernitka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1515
SOFTWARE: FaalSeq for Windows Version 3.0
SEQ ID NO 663
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-663

```

Query Match	95.9%	Score 164;	DB 3;	Length 38;
Best Local Similarity	97.1%	Pred. No. 2.4e-17;		
Matches 34;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

[illegible]

RESULT 21
 US-08-474-349A-89
 Sequence 89, Application US/08474349A
 Patent No. 633395
 GENERAL INFORMATION:
 APPLICANT: Bolognesi, Dani P.
 APPLICANT: Mathews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Peteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
 TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
 NUMBER OF INVENTION: 517
 NUMBER OF SEQUENCES: 517
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,349A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION:

```

? ATTORNEY/AGENT INFORMATION:
? NAME: Cozzuzi, Laura A.
? REGISTRATION NUMBER: 30,742
? REFERENCE/DOCKET NUMBER: 7872-0244
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 790-9090
? TELEFAX: (212) 669-9741/8864
? TELEEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 89:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 38 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: unknown
? MOLECULE TYPE: peptide
US-08-474-342A-89

```

Query Match	95.9%;	Score 164;	DB 4;	Length 38;
Best Local Similarity	97.1%;	Pred. No. 2.4e-17;		
Matches 34;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Dy 1 NNLLRAIEAQGHLLQLTWGIKQIARILAVERYL 35
Db 1 NNLLRAIEAQGHLLQLTWGIIKQIARILAVERYL 35	

RESULT 22
 US-08-474-349A-441
 Sequence 441, Application US/08474349A
 Patent No. 633395
 GENERAL INFORMATION:
 APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Petteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
 TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
 TITLE OF INVENTION: VIRUS TRANSMISSION
 NUMBER OF SEQUENCES: 517
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474.349A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-024
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 441:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-08-474-349A-441

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
Db 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35

RESULT 23

US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 16

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-16

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;Qy 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
Db 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35

RESULT 24
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 507

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-507

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
Db 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35

RESULT 25

US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 604

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-604

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;Qy 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
Db 1 NNLLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35

RESULT 26
US-09-315-304B-661
Sequence 661, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 661

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-661

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 35
Db 2 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 36

RESULT 27
US-09-315-304B-662
; Sequence 662, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 662
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-662

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 35
Db 3 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 37

RESULT 28
US-09-315-304B-663
; Sequence 663, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 663
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-663

Query Match 95.9%; Score 164; DB 4; Length 38;

Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 35
Db 4 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 38

RESULT 29
US-08-255-208A-25
; Sequence 25, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr, Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2,4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGKIQOLQARILAVERYL 35

RESULT 30
US-08-470-896-89
; Sequence 89, Application US/08470896
; Patent No. 6475055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
DB 1 NNLRLRAIEAQOHLQLTWQIKQLQARILAVERYL 35

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 32.2418 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-149
Perfect score: 171
Sequence: 1 NMLRAIEAQHLLQLTWQIKQIARILAVERYL 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 28138677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	38	14	US-10-252-136-82 Sequence 82, Appl
2	164	95.9	35	15	US-10-005-305-128 Sequence 128, App
3	164	95.9	36	15	US-10-005-305-129 Sequence 129, App
4	164	95.9	37	15	US-10-005-305-130 Sequence 130, App
5	164	95.9	38	9	US-09-796-202-11 Sequence 11, Appl
6	164	95.9	38	9	US-09-779-451-2 Sequence 2, Appl
7	164	95.9	38	9	US-09-912-824-2 Sequence 2, Appl
8	164	95.9	38	10	US-09-493-346-2 Sequence 2, Appl
9	164	95.9	38	12	US-10-267-682-89 Sequence 89, Appl
10	164	95.9	38	12	US-10-267-748-89 Sequence 89, Appl
11	164	95.9	38	12	US-09-809-060-6 Sequence 6, Appl
12	164	95.9	38	12	US-09-809-060-7 Sequence 7, Appl
13	164	95.9	38	12	US-10-663-589-3 Sequence 3, Appl
14	164	95.9	38	12	US-10-681-879-2 Sequence 2, Appl
15	164	95.9	38	12	US-09-828-615-2 Sequence 2, Appl

16	164	95.9	38	14	US-10-116-797-2 Sequence 2, Appl
17	164	95.9	38	14	US-10-323-314-11 Sequence 11, Appl
18	164	95.9	38	14	US-10-414-192-11 Sequence 1, Appl
19	164	95.9	38	14	US-10-351-641-16 Sequence 16, Appl
20	164	95.9	38	14	US-10-351-641-507 Sequence 507, App
21	164	95.9	38	14	US-10-351-641-604 Sequence 604, App
22	164	95.9	38	14	US-10-351-641-661 Sequence 661, App
23	164	95.9	38	14	US-10-351-641-662 Sequence 662, App
24	164	95.9	38	14	US-10-351-641-663 Sequence 663, App
25	164	95.9	38	15	US-10-005-305-165 Sequence 165, App
26	164	95.9	38	15	US-10-005-305-202 Sequence 202, App
27	164	95.9	38	15	US-10-005-305-203 Sequence 203, App
28	164	95.9	38	15	US-10-420-194-1234 Sequence 1234, Ap
29	164	95.9	38	16	US-10-664-021-2 Sequence 2, Appl
30	164	95.9	38	16	US-10-671-316-2 Sequence 8, Appl
31	164	95.9	41	12	US-10-267-682-8 Sequence 8, Appl
32	164	95.9	41	12	US-10-267-748-8 Sequence 8, Appl
33	164	95.9	41	12	US-10-663-589-30 Sequence 30, Appl
34	164	95.9	41	12	US-10-663-589-33 Sequence 33, Appl
35	164	95.9	41	12	US-10-663-589-35 Sequence 35, Appl
36	164	95.9	41	14	US-10-252-136-8 Sequence 8, Appl
37	164	95.9	41	14	US-10-414-192-3 Sequence 3, Appl
38	164	95.9	41	14	US-10-414-192-9 Sequence 9, Appl
39	164	95.9	41	14	US-10-351-641-466 Sequence 466, App
40	164	95.9	41	14	US-10-351-641-601 Sequence 601, App
41	164	95.9	41	14	US-10-351-641-633 Sequence 633, App
42	164	95.9	41	14	US-10-351-641-1163 Sequence 1163, Ap
43	164	95.9	41	16	US-10-664-021-27 Sequence 27, Appl
44	164	95.9	41	12	US-10-663-589-36 Sequence 36, Appl
45	164	95.9	44	14	US-10-671-316-27 Sequence 27, Appl
46	164	95.9	44	14	US-10-671-316-26 Sequence 26, Appl
47	164	95.9	44	14	US-10-414-192-10 Sequence 10, Appl
48	164	95.9	45	9	US-09-779-451-9 Sequence 9, Appl
49	164	95.9	45	12	US-09-809-060-50 Sequence 50, Appl
50	164	95.9	45	12	US-10-663-589-29 Sequence 29, Appl
51	164	95.9	45	14	US-10-351-641-1164 Sequence 1164, Ap
52	164	95.9	45	16	US-10-664-021-26 Sequence 26, Appl
53	164	95.9	48	14	US-10-671-316-26 Sequence 26, Appl
54	164	95.9	48	14	US-10-263-103-26 Sequence 26, Appl
55	164	95.9	49	9	US-09-796-202-3 Sequence 3, Appl
56	164	95.9	49	12	US-10-663-589-26 Sequence 26, Appl
57	164	95.9	49	14	US-10-323-314-3 Sequence 23, Appl
58	164	95.9	49	16	US-10-664-021-23 Sequence 23, Appl
59	164	95.9	51	12	US-10-671-316-23 Sequence 23, Appl
60	164	95.9	51	12	US-10-663-589-27 Sequence 27, Appl
61	164	95.9	51	14	US-10-351-641-745 Sequence 745, App
62	164	95.9	51	16	US-10-664-021-24 Sequence 24, Appl
63	164	95.9	52	14	US-10-671-316-24 Sequence 24, Appl
64	164	95.9	53	14	US-10-351-641-1119 Sequence 1119, Ap
65	164	95.9	53	14	US-10-351-641-955 Sequence 955, App
66	164	95.9	53	14	US-10-351-641-1062 Sequence 1062, Ap
67	164	95.9	55	9	US-09-779-451-1 Sequence 1, Appl
68	164	95.9	55	12	US-09-809-060-14 Sequence 14, Appl
69	164	95.9	57	15	US-10-438-691-1 Sequence 1, Appl
70	164	95.9	59	16	US-10-664-021-1 Sequence 1, Appl
71	164	95.9	59	16	US-10-671-316-1 Sequence 1, Appl
72	164	95.9	60	12	US-10-663-589-1 Sequence 1, Appl
73	164	95.9	63	12	US-10-267-748-201 Sequence 201, App
74	164	95.9	63	12	US-10-267-682-201 Sequence 201, App
75	164	95.9	63	14	US-10-252-136-54 Sequence 54, Appl
76	164	95.9	101	14	US-10-263-103-31 Sequence 31, Appl
77	164	95.9	103	14	US-10-263-103-29 Sequence 29, Appl
78	164	95.9	103	14	US-10-263-103-32 Sequence 32, Appl
79	164	95.9	103	15	US-10-438-691-3 Sequence 3, Appl
80	164	95.9	105	14	US-10-263-103-28 Sequence 28, Appl
81	164	95.9	105	14	US-10-263-103-30 Sequence 30, Appl
82	164	95.9	108	14	US-10-263-103-33 Sequence 33, Appl
83	164	95.9	113	15	US-10-438-691-4 Sequence 4, Appl
84	164	95.9	177	14	US-10-040-349B-2 Sequence 2, Appl
85	164	95.9	198	9	US-09-854-816-88 Sequence 88, Appl
86	164	95.9	198	9	US-09-854-816-89 Sequence 89, Appl
87	164	95.9	200	14	US-10-263-103-25 Sequence 25, Appl
88	164	95.9	200	15	US-10-438-691-8 Sequence 8, Appl
89	164	95.9	232	14	US-10-059-271-81 Sequence 81, Appl

89 164 95.9 254 14 US-10-059-271-82
90 164 95.9 256 14 US-10-059-271-97

ALIGNMENTS

RESULT 1

US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 171; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 6, 2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35

RESULT 2

US-10-005-305-128
; Sequence 128, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-128

Query Match 95.9%; Score 164; DB 15; Length 35;
Best Local Similarity 97.1%; Pred. No. 5, 5e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35

RESULT 3

US-10-005-305-129
; Sequence 129, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-129

Query Match 95.9%; Score 164; DB 15; Length 36;
Best Local Similarity 97.1%; Pred. No. 5, 7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35

RESULT 4

US-10-005-305-130
; Sequence 130, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-130

Query Match 95.9%; Score 164; DB 15; Length 37;
Best Local Similarity 97.1%; Pred. No. 5, 8e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYL 35

RESULT 5
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 95.9%; Score 164; DB 9; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35

RESULT 6
US-09-779-451-2
; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 95.9%; Score 164; DB 9; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35

RESULT 7
US-09-912-824-2
; Sequence 2, Application US/09912824
; Patent No. US20020106374A1
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF HIV-1 INFECTION
; FILE REFERENCE: 2048/62942-B

; CURRENT APPLICATION NUMBER: US/09/912,824
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 Peptide
US-09-912-824-2

Query Match 95.9%; Score 164; DB 9; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35

RESULT 8
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 95.9%; Score 164; DB 10; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWGKIKQLQARILAVERYL 35

RESULT 9
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matchnews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petreway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIGKQLQARILAVERYL 35

RESULT 10
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Peteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIGKQLQARILAVERYL 35

RESULT 11
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIGKQLQARILAVERYL 35

RESULT 12
US-09-809-060-7
Sequence 7, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001

;; CURRENT APPLICATION NUMBER: US/09/809,060
;; CURRENT FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: US 60/189,981
;; PRIOR FILING DATE: 2000-03-17
;; NUMBER OF SEQ ID NOS: 87
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 7
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 13
US-10-663-589-3
;; Sequence 3, Application US/10663589
;; Publication No. US200400637A1
;; GENERAL INFORMATION:
;; APPLICANT: Timmers, Inc.
;; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
;; FILE REFERENCE: TRM-003
;; CURRENT APPLICATION NUMBER: US/10/663,589
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR APPLICATION NUMBER: US 60/414,441
;; PRIOR FILING DATE: 2002-09-27
;; NUMBER OF SEQ ID NOS: 95
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 3
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 14
US-10-681-879-2
;; Sequence 2, Application US/10681879
;; Publication No. US20040062767A1
;; GENERAL INFORMATION:
;; APPLICANT: Olson, William C
;; APPLICANT: Maddon, Paul J
;; TITLE OF INVENTION: Compositions and Methods for inhibition of HIV-1
;; FILE REFERENCE: 61009
;; CURRENT APPLICATION NUMBER: US/10/681,879
;; CURRENT FILING DATE: 2003-10-09
;; PRIOR APPLICATION NUMBER: US/09/493,346
;; PRIOR FILING DATE: 2000-01-28
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 15
US-09-828-615-2
;; Sequence 2, Application US/09828615
;; Publication No. US20020146415A1
;; GENERAL INFORMATION:
;; APPLICANT: Olsen, William C.
;; APPLICANT: Maddon, Paul J.
;; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
;; FILE REFERENCE: 64672
;; CURRENT APPLICATION NUMBER: US/09/828,615
;; CURRENT FILING DATE: 2001-04-06
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 16
US-10-116-797-2
;; Sequence 2, Application US/10116797
;; Publication No. US2003004411A1
;; GENERAL INFORMATION:
;; APPLICANT: Olsen, William C.
;; APPLICANT: Maddon, Paul J.
;; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
;; FILE REFERENCE: 64672-A
;; CURRENT APPLICATION NUMBER: US/10/116,797
;; CURRENT FILING DATE: 2002-10-15
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 17
US-10-323-314-11
;; Sequence 11, Application US/10323314
;; Publication No. US20030139571A1

GENERAL INFORMATION:
APPLICANT: Diagic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/NAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35

RESULT 18
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
Matthews, Thomas J.
Bolognesi, Dani P.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 95.9%; Score 164; DB 14; Length 38;

Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35

RESULT 19
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Mertuka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-100

CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35
DB 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYL 35

RESULT 20
US-10-351-641-507
Sequence 507, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Mertuka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35

RESULT 21
US-10-351-641-604

Sequence 604, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35

RESULT 22
US-10-351-641-661

Sequence 661, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304

PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-661

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
DB 2 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 36

RESULT 23
US-10-351-641-662

Sequence 662, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 662
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-662

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 35
DB 3 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYL 37

RESULT 24
US-10-351-641-663

Sequence 663, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

;; TITLE OF INVENTION: PROPERTIES
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 663
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-663

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB 4 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 38

RESULT 25
US-10-005-305-165
;; Sequence 165, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 165
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 26
US-10-005-305-202
;; Sequence 202, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS

;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 202
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 27
US-10-005-305-203
;; Sequence 203, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 203
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35
DB 1 NNLRRAIEAQOHLQLTWGIKQLQARILAVERYL 35

RESULT 28
US-10-420-194-1234
;; Sequence 1234, Application US/10420194
;; Publication No. US20040006035A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: McSwigen, Jim
;; APPLICANT: Blatc, Larry
;; APPLICANT: Macejak, Dennis

```

TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
FILE REFERENCE: MEMB02-305-A (400/011)
CURRENT FILING DATE: 2003-04-22
PRIORITY APPLICATION NUMBER: US/10/420,194
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US 60/398,036
PRIORITY FILING DATE: 2002-07-23
PRIORITY APPLICATION NUMBER: US 60/374,722
PRIORITY FILING DATE: 2002-04-22
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: US 60/386,782
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: US 60/406,784
PRIORITY FILING DATE: 2002-08-29
PRIORITY APPLICATION NUMBER: US 60/408,378
PRIORITY FILING DATE: 2002-09-05
PRIORITY APPLICATION NUMBER: US 60/409,293
PRIORITY FILING DATE: 2002-09-09
PRIORITY APPLICATION NUMBER: US 60/440,129
PRIORITY FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match          95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  NNLRLAIEAQOHLQLTWQIKQLQARILAVERYL 35
          |||||
DB      1  NNLRLAIEAQOHLQLTWQIKQLQARILAVERYL 35

RESULT 29
US-10-664-021-2
; Sequence 2, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
; TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
; FILE REFERENCE: TRM-001
; CURRENT APPLICATION NUMBER: US/10/664,021
; PRIORITY APPLICATION NUMBER: US 60/414,514
; PRIORITY FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-664-021-2
Query Match          95.9%; Score 164; DB 16; Length 38;

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Qy      1 NNLRAIEAQOHLQLTWQIQOLQARILAVERYL 35
      |||||
Db      1 NNLRAIEAQOHLQLTWQIGIKQLQARILAVERYL 35
      |||||

Best Local Similarity 97.1%; Pred.No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 30
; Sequence 2, Application US/10671316
; Publication No. US20040091855X1
; GENERAL INFORMATION:
; APPLICANT: Trimeix, Inc.
; TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HR1
; FILE REFERENCE: TRM-002
; CURRENT APPLICATION NUMBER: US/10/671,316
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,515
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match          95.9%; Score 164; DB 16; Length 38;
Best Local Similarity 97.1%; Pred.No. 6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NNLRAIEAQOHLQLTWQIQOLQARILAVERYL 35
      |||||
Db      1 NNLRAIEAQOHLQLTWQIGIKQLQARILAVERYL 35
      |||||

Search completed: June 2, 2004, 12:29:25
Job time : 33.2418 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 46.3505 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-179
Sequence: 1 NLRA1EAQOHLQLTWQIKQLQARLAVERYLKDQ 37

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	100.0	37	3	AAB14739
2	181	100.0	37	4	AAB55004
3	181	100.0	38	2	AAB98408
4	181	100.0	38	4	AAB54785
5	181	100.0	38	4	AAB55005
6	181	100.0	38	4	AAB54970
7	181	100.0	38	4	AAB92244
8	181	100.0	38	4	AAB14011
9	181	100.0	38	5	AA018771
10	176	97.2	37	3	AAB14705
11	176	97.2	37	4	AAB54969
12	175	96.7	36	3	AAB14738
13	175	96.7	36	4	AAB55003
14	174	96.1	37	3	AAB52785
15	174	96.1	38	2	AAR55635
16	174	96.1	38	2	AAR55636
17	174	96.1	38	2	AAW47216
18	174	96.1	38	2	AAW27614
19	174	96.1	38	3	AAV88666
20	174	96.1	38	3	AAV88730
21	174	96.1	38	3	AAV88731
22	174	96.1	38	3	AAV89145
23	174	96.1	38	3	AAV89146
24	174	96.1	38	3	AAV89243
25	174	96.1	38	3	AAB14530

26	174	96.1	38	3	AAB52824
27	174	96.1	38	3	AAB52786
28	174	96.1	38	3	AAB52823
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31	174	96.1	38	4	AAV877021
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34	174	96.1	38	4	AAV877596
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41	174	96.1	38	4	AAV8770184
42	174	96.1	38	4	AAV8770184
43	174	96.1	38	4	AAV8770184
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62	174	96.1	38	4	AAV8770184
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64	174	96.1	38	4	AAV8770184
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66	174	96.1	38	4	AAV8770184
67	174	96.1	38	4	AAV8770184
68	174	96.1	38	4	AAV8770184
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84	174	96.1	38	4	AAV8770184
85	174	96.1	38	4	AAV8770184
86	174	96.1	38	4	AAV8770184
87	174	96.1	38	4	AAV8770184
88	174	96.1	38	4	AAV8770184
89	174	96.1	38	4	AAV8770184
90	174	96.1	38	4	AAV8770184

ALIGNMENTS

RESULT 1
ID AAB14739 standard; peptide: 37 AA.

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AAB14739;
12-SEP-2003 (revised)
24-NOV-2000 (first entry)
HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil,
core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
humoral response; broad spectrum vaccine; anti-HIV;
envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
isolate LAI.
Human immunodeficiency virus 1.
MO200040616-A1.
13-JUL-2000.
10-JAN-2000; 200OMO-US000456.
08-JAN-1999; 99US-0115404P.
07-JAN-2000; 2000US-00480336.
(WILD/) WILD C T.
(WEIS/) WEISS C D.
Wild CT, Weiss CD;
WPI; 2000-465959/40.
Raising neutralizing antibody response to human immunodeficiency virus,
comprises administering a polypeptide capable of forming a stable coiled-
coil solution structure.
Disclosure; Page 38; 97pp; English.
Sequences AAB14672-B14739 represent peptides derived from the N-helical
domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
isolate LAI. The invention relates to raising a neutralising antibody
response to a broad spectrum of HIV (human immunodeficiency virus)
strains and isolates, comprising the administration of a peptide which
corresponds to or mimics highly conserved portions of gp41 which are
important in mediating the process of viral entry into host cells. Such
peptides can correspond to or mimic the coiled coil solution structure of
the N-helical domain (the heptad repeat region), or can correspond or
mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
helical segment), or the gp41 core 6-helix bundle, which is formed by the
interaction of the N- and C-helical domains of three gp41 proteins. The
peptides can be administered either singly or as a combination
(particularly a combination of N-helical and C-helical peptides), and can
be multimerised. For example, N- and C-helical domain peptides can be
alternately linked together to form a peptide which mimics the core 6-
helix bundle. Administration of the peptide(s) generates a humoral
response, with the production of antibodies against gp41 structures
involved in viral entry. As these portions of gp41 are well conserved,
such antibodies may be effective against a broad range of HIV strains and
isolates. The peptide compositions may be administered as a prophylactic
or therapeutic vaccine to generate antibodies which reduce or inhibit the
ability of HIV to infect uninfected cells. A composition comprising
polyclonal or monoclonal antibodies can be administered to reduce HIV
infection of uninfected cells. Antibodies raised against entry-relevant
gp41 structures may also be used therapeutically and as tools to further
elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
standardise OS field)

Sequence 37 AA;

QY 1 NLRAIEAQHLLQTWQIKQLAARILAVERYLKDQ 37
Dd 1 NLRATAEAOHLLOLTWGIKQLCARLALAVERYLKDQ 37

RESULT 2

ID AAB55004 standard; peptide; 37 AA.

AC AAB55004 ;

DT 11-SEP-2003 (revised)

DI 05-MAR-2001 (LIBC entry)

DE Anti-HIV peptide DPlO/ amino truncation peptide #34: XX

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW anti-fusogenic: mobile blood measles virus: MeV: STV:

human immunodeficiency virus; human parainfluenza virus; HPIV; KSV; simian immunodeficiency virus; human parainfluenza virus; HPIV; KSV; human respiratory syncytial virus; human immunodeficiency virus; HTV

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PR 10-SEP-1999; 99US-0153406P.

PA (CONJ -) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

WPI: 2001-007496/01

XX A modified peptide and a reactive group which is reactive with amino
PT

PT groups, hydroxyl groups, or chiol groups on blood components to form stable covalent bonds useful for treatment of viral infections. e.g.

PT human immunodeficiency virus.

PS Disclosure; Page 139; 211pp; English.

CC The present invention describes a modified anti-viral peptide (I)

CC group which is reactive with amino groups, hydroxyl groups, or thiol

CC viral and anti-fusogenic activities. (I) inhibits viral infection of

CC the level of membrane fusion events between two or more entities, e.g.,

CC occurs in the absence of the peptide. (I) is useful in the treatment of

CC MeV, and SIV. (I) may be administered prophylactically to previously

CC been subjected to a high risk of exposure to a virus. By bonding of long-

blood cells and platelets the activity is extended for days to weeks.

CC This is due to improved stability in vivo and a reduced susceptibility to
CC penicillinase or protease degradation. This minimises the need for more

CC frequent, or even continual, administration of the peptides. AAB54/84 co
CC AAB55431 represent peptides used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XY

Sequence 37 AA;

Query Match	Score	ID	Length
100.0%	181	DB 4	37
100.0%	3	18-16	

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLRLAIEAQHLLQLTWQIKOLQARILAEVERYLKDQ 37

Db 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 37

RESULT 3

AAR98408 AAR98408 standard; peptide; 38 AA.

AC AAR98408;

DT 16-OCT-2003 (revised)

DT 17-FEB-1997 (first entry)

DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;

KM ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;

KM influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX MO9619495-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-US016733.

XX 20-DEC-1994; 94US-00360107.

XX 06-JUN-1995; 95US-00470896.

XX (UYDU-) UNIV DUKE.

XX (TRIM-) TRIMERIS INC.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;

XX Peteway SR, Langlois AJ;

XX WPI; 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an

XX isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence

XX search motif.

XX Disclosure; Page 30; 471pp; English.

XX The sequences given in AAR98398-408 represent peptides which exhibit

XX antifusogenic activity, antiviral capability and/or the ability to

XX modulate intracellular processes involving coiled-coil peptide

XX structures. These peptides are recognised by the ALLMOT15, 107x178x4 and

XX PLZIP search motifs. These peptides may be used to inhibit the

XX transmission of a virus, pref. HIV, influenza virus, or hepatitis B

XX virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 38 AA;

XX Query Match 100.0%; Score 181; DB 2; Length 38;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-16;

XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 37

2 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 38

RESULT 4

AAB54785 AAB54785 standard; peptide; 38 AA.

AC AAB54785;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.

XX Long laesting fusion peptide inhibitor; viral infection; antiviral;

KM antifusogenic; mobile blood component; measles virus; MeV; SIV;

KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

XX human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus 1.

XX WO200069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000MO-US013651.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX (CONU-) CONNUCHEM INC.

XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino

XX groups, hydroxyl groups, or thiol groups on blood components to form

XX stable covalent bonds useful for treatment of viral infections, e.g.

XX human immunodeficiency virus.

XX Claim 6; Page 173; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)

XX comprising a peptide that exhibits anti-viral activity and a reactive

XX group which is reactive with amino groups, hydroxyl groups, or thiol

XX groups on blood components to form stable covalent bonds. (I) has anti-

XX viral and anti-fusogenic activities. (I) inhibits viral infection of

XX cells by inhibiting cell-cell fusion or free virus infection or to reduce

XX the level of membrane fusion events between two or more entities, e.g.,

XX virus-cell or cell-cell, relative to the level of membrane fusion that

XX occurs in the absence of the peptide. (I) is useful in the treatment of

XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,

XX MeV, and SIV. (I) may be administered prophylactically to previously

XX uninfected individuals. This is useful in cases where an individual has

XX been subjected to a high risk of exposure to a virus. By bonding of long-

XX lived components of the blood, such as immunoglobulin, serum albumin, red

XX blood cells and platelets the activity is extended for days to weeks.

XX This is due to improved stability in vivo and a reduced susceptibility to

XX peptidase or protease degradation. This minimises the need for more

XX frequent, or even continual, administration of the peptide. AAB54784 to

XX AAB5431 represent peptides used in the exemplification of the present

XX invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

XX Query Match 100.0%; Score 181; DB 4; Length 38;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-16;

XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 37

2 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 38

RESULT 5

AAB55005 AAB55005 standard; peptide; 38 AA.

AC AAB55005;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 amino truncation peptide #35.

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antifeugenic; mobile blood component; measles virus; MeV; STV;
KM smian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
OS Human immunodeficiency virus 1.
XX
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Disclosure; Page 139; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and STV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 181; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLRRAIEAQOHLQLTWQWIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQOHLQLTWQWIKQLQARILAVERYLKQ 38
RESULT 6
AAB54970
ID AAB54970 standard; peptide; 38 AA.
XX
XX AAB54970;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #35.
DE
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;

KW antifeugenic; mobile blood component; measles virus; MeV; STV;
KM human immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
OS Human immunodeficiency virus 1.
XX
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and STV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 181; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLRRAIEAQOHLQLTWQWIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQOHLQLTWQWIKQLQARILAVERYLKQ 38
RESULT 7
AAB92244
ID AAB92244 standard; peptide; 38 AA.
XX
XX AAB92244;
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Virus related peptide SEQ ID NO:1420.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

```

XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013576.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K,
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity.
XX
XX Disclosure; Page 662; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidease stabilized therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity in
XX vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention
XX
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 181; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLRAIEAOQHLLQLTWMOIKQLQARI LAVERYLKDD 37
Db 2 NLRAIEAOQHLLQLTWMOIKQLQARI LAVERYLKDD 38
RESULT 8
AAU14011
ID AAU14011 standard; peptide; 38 AA.
XX
XX AAU14011;
XX
XX 11-SEP-2003 (revised)
XX 21-NOV-2001 (first entry)
XX
XX DP107 peptide from HIV-1 transmembrane protein gp41.
XX
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX antitubercogenic; antiviral; HIV transmission.
XX
XX Human immunodeficiency virus 1; isolate LAI.
XX
XX Key Location/Qualifiers
XX Misc-difference 1..35 Amino acids 1-35 can be optionally and serially
FT /note="

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FT deleted from the N-terminus"
FT Misc-difference 4..38
FT /note="Amino acids 4-38 can be optionally and serially
FT deleted from the C-terminus"
XX
XX WO200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX Identifying a compound that inhibits the formation of or disrupts a
XX DP107/DP178 complex, especially compounds with antitubercogenic, antiviral
XX or intracellular modulatory activity, by detecting the formation of a
XX DP107/DP178 complex.
XX
XX Disclosure; Page 33; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
XX activity. The peptides of the invention (AAU2559-AAU14009) comprise
XX DP178-like and DP107-like peptides. The DP178 peptide corresponds to
XX amino acids 639-673 of the transmembrane protein gp41 from human
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
XX also relates to a method of identifying compounds that inhibit the
XX formation of or disrupts a DP107/DP178 complex. The method comprises
XX detecting the formation of a DP107/DP178 complex, both in the presence or
XX absence of a test compound, in a reaction mixture containing DP107 and
XX DP178 peptides. The method is useful for identifying compounds, including
XX small molecule compounds, which may themselves exhibit antitubercogenic,
XX antiviral or intracellular modulatory activity. The DP178-like/DP107-like
XX peptides are useful to inhibit human and non-human retroviral,
XX particularly HIV, transmission to uninfected cells. The present sequence
XX represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 181; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLRAIEAOQHLLQLTWMOIKQLQARI LAVERYLKDD 37
Db 2 NLRAIEAOQHLLQLTWMOIKQLQARI LAVERYLKDD 38
RESULT 9
AAO18771
ID AAO18771 standard; peptide; 38 AA.
XX
XX AAO18771;
XX
XX 29-OCT-2002 (first entry)
XX
XX HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
XX
XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
XX gp41.
XX
XX Human immunodeficiency virus.
XX
XX WO200256902-A2.
XX
XX 25-JUL-2002.
FT

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XX 17-DEC-2001; 2001WO-US048802.
XX
XX 19-DEC-2000; 2000US-0256657P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Baroudy BM;
XX WPI; 2002-636513/68.
XX
XX Treatment of HIV infection in an individual involves administration of a
PT combination of chemokine co-receptor five antagonist and a specified HIV
PT envelope polypeptide.
XX
XX Disclosure; Page 34; 52pp; English.
XX
XX The present invention relates to a method of treating an HIV infection in
CC an individual, which involves administering in combination a chemokine co-
CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
CC derivative. Other viral infections can also be treated using the method.
CC The present sequence is a peptide derived from HIV and useful in the
CC method of the invention
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 181; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2,2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLRRAIEAQOHLQLTWTWQIKQLQARILAVERYIKDQ 37
Db 2 NLRRAIEAQOHLQLTWTWQIKQLQARILAVERYIKDQ 38
RESULT 10
AAB14705
ID AAB14705 standard; peptide; 37 AA.
XX
XX AAB14705;
AC
XX
XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200040616-A1.
PN
XX
XX 13-JUL-2000.
PD
XX
XX 10-JAN-2000; 2000WO-US000456.
PF
XX
XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
XX WILD CT, Weiss CD;
PI
XX
XX WPI; 2000-465959/40.
DR
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.

XX Disclosure; Page 36; 97pp; English.
PS
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralising antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
XX Sequence 37 AA;
SQ
Query Match 97.2%; Score 176; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.5e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLRRAIEAQOHLQLTWTWQIKQLQARILAVERYIKD 36
Db 2 NLRRAIEAQOHLQLTWTWQIKQLQARILAVERYIKD 37
RESULT 11
AAB54969
ID AAB54969 standard; peptide; 37 AA.
XX
XX AAB54969;
AC
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #34.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antitumorigenic; mobile blood component; measles virus; MeV; SiV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200069902-A1.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US013651.
PF
XX
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONU-) CONUCHEM INC.
PA
XX
XX Bridon DP, Dufresne RP, Boudjelal N, Robitaille M, Milner PG;
PI

XX WPI; 2001-007496/01.

DR A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

XX Disclosure; Page 137; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to prevent
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB54931 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 37 AA;

Query Match 97.2%; Score 176; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.5e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYIKD 36
1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYIKD 37

DB AAB14738 standard; peptide; 36 AA.

XX AAB14738;

DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)

DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #67.

XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX isolate LAI.

OS Human immunodeficiency virus 1.

XX WO2000040616-A1.

XX 13-JUL-2000.

XX 10-JAN-2000; 2000WO-US000456.

XX 08-JAN-1999; 99US-0115404P.

XX 07-JAN-2000; 2000US-00480336.

XX (WILD/) WILD C T.
XX (WEIS/) WEISS C D.

PI Wild CT, Weiss CD;

XX WPI; 2000-465959/40.

DR Raising neutralizing antibody response to human immunodeficiency virus,
XX comprising administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.

XX Disclosure; Page 38; 97pp; English.

XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralising antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond to
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)

XX Sequence 36 AA;

Query Match 96.7%; Score 175; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRAIEAOQHLLQLTWQIKQLQARILAVERYIKDQ 37
1 LRAIEAOQHLLQLTWQIKQLQARILAVERYIKDQ 36

DB AAB55003 standard; peptide; 36 AA.

XX AAB55003;

DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 amino truncation peptide #33.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.

XX WO2000069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013651.

XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 139; 211pp; English.
XX
CC The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 36 AA;
Query Match 96.7%; Score 175; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LRAIAEQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 1 LRAIAEQOHLQLTWQIKQLQARILAVERYLKDQ 36
RESULT 14
AAB52785
ID AAB52785 standard; peptide; 37 AA.
XX
AC AAB52785;
XX
DT 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
DE T21/DP107 peptide fragment #67.
XX
KW Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KW chemottractant.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200066622-A1.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012371.
XX
PR 05-MAY-1999; 99US-0132686P.
XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
DR WPI; 2000-656493/63.
XX
PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
PS Claim 12; Page 29; 148pp; English.
XX
CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 37 AA;
Query Match 96.1%; Score 174; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 37
Db 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 37
RESULT 15
AAR55635
ID AAR55635 standard; peptide; 38 AA.
XX
AC AAR55635;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
DE DP-139 - DP-107 analogue.
XX
KW Leucine zipper; HIV-1; human immunodeficiency virus;
KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KW antiviral; gp41.
XX
OS Synthetic.
XX
PN WO9402505-A1.
XX
PD 03-FEB-1994.
XX
PF 19-JUL-1993; 93WO-US006769.
XX
PR 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Wild CT, Matthews TJ, Bolognesi DP;
XX WPI; 1994-048790/06.
XX
PT New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.
XX
PS Disclosure; Page 25; 38pp; English.
XX
CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 XX

XX Sequence 38 AA;

Query Match 96.1%; Score 174; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLIRAIQAQHLQLTWTWQIKQLQARILAVERYLKQ 37
 Db 2 NLIRAIQAQHLQLTWTWQIKQLQARILAVERYLKQ 38

RESULT 16

AAR55636 standard; peptide; 38 AA.

XX AAR55636;

XX 25-MAR-2003 (revised)

XX 25-JUL-1994 (first entry)

XX DP-140 - DP-107 analogue.

XX Leucine zipper; HIV-1; human immunodeficiency virus;

XX transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

XX antiviral; gp41.

XX Synthetic.

XX MO9402505-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93MO-US006769.

XX 20-JUL-1992; 92US-00916540.

XX 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

XX Wild CT, Mathews TJ, Bolognesi DP;

XX WPI; 1994-048790/06.

XX New peptides corresponding to HIV transmembrane protein - used for

XX inhibiting infection of cells by an enveloped virus, partic. for

XX inhibiting HIV-induced cell fusion.

XX Disclosure; Page 25; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

XX of forming a heterodimer with DP-107; or a multimer of these peptides can

XX be contacted with an HIV-infected cell to inhibit HIV- induced cell

XX fusion. DP-107 is based on a highly conserved region in the transmembrane

XX protein (TM) of HIV-1 (gp41) which was predicted to form an extended

XX amphipathic alpha-helix with structural analogues in the TM proteins of

XX several fusogenic viruses. Other peptides studied and DP-107 analogues

XX are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to

XX correct PN field.)

XX Sequence 38 AA;

Query Match 96.1%; Score 174; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1.8e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLIRAIQAQHLQLTWTWQIKQLQARILAVERYLKQ 37
 Db 2 NLIRAIQAQHLQLTWTWQIKQLQARILAVERYLKQ 38

RESULT 17

AAR47216 standard; peptide; 38 AA.

XX AAR47216;

XX 25-MAR-2003 (revised)

XX 25-JUL-1994 (first entry)

XX DP-107 - HIV-1 TM protein (558-595).

XX Leucine zipper; HIV-1; human immunodeficiency virus;

XX transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

XX antiviral; gp41.

XX Synthetic.

XX MO9402505-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93MO-US006769.

XX 20-JUL-1992; 92US-00916540.

XX 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

XX Wild CT, Mathews TJ, Bolognesi DP;

XX WPI; 1994-048790/06.

XX New peptides corresponding to HIV transmembrane protein - used for

XX inhibiting infection of cells by an enveloped virus, partic. for

XX inhibiting HIV-induced cell fusion.

XX Claim 1; Page 27; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

XX of forming a heterodimer with DP-107; or a multimer of these peptides can

XX be contacted with an HIV-infected cell to inhibit HIV- induced cell

XX fusion. DP-107 is based on a highly conserved region in the transmembrane

XX protein (TM) of HIV-1 (gp41) which was predicted to form an extended

XX amphipathic alpha-helix with structural analogues in the TM proteins of

XX several fusogenic viruses. Other peptides studied and DP-107 analogues

XX are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to

XX correct PN field.)

XX Sequence 38 AA;

Query Match 96.1%; Score 174; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1.8e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 18

AAW27614 standard; peptide; 38 AA.

```

XX AA27614;
AC 25-MAR-2003 (revised)
DT 22-DEC-1997 (first entry)
XX
DE Human immunodeficiency virus gp41 derived peptide DP-107.
XX
KW Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
KM inhibition; induction; cell fusion; transmission; type 1.
XX
OS Human immunodeficiency virus.
XX
PN US5656480-A.
XX
PD 12-AUG-1997.
XX
PF 27-JAN-1995; 95US-00374666.
XX
PR 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
PR 19-JUL-1993; 93WO-US006769.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Bolognesi DP, Wild CT, Matthews TJ;
XX
DR WPI; 1997-414595/38.
XX
PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
XX
PT syncytia formation and transmission.
XX
PS Claim 1; Col 13-14; 18pp; English.
XX
CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein
CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
CC cell fusion in a culture and cell free HIV transmission in a culture to a
CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
CC MAR-2003 to correct PF field.)
XX
SQ Sequence 38 AA;
QY
Db 1 NLRRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 37
2 NLRRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 38

RESULT 19
AAV88666
ID AAV88666 standard; peptide; 38 AA.
XX
AC AAV88666;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 21.
XX
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO95959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1999; 99WO-US011219.

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XX 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX
PT comprises enhancer sequence.
XX
PS Disclosure; Page 21; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
XX
CC sequence linked to core polypeptides. The enhancer polypeptides are
XX
CC derived from various retroviral envelope (gp41) protein sequences,
XX
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX
CC pharmacokinetic properties such as increasing the half-life of any core
XX
CC polypeptide that they are linked to. The core polypeptides are any
XX
CC polypeptide that may be introduced into a living system and that can
XX
CC function as a pharmacologically useful peptide for the treatment or
XX
CC prevention of a disease. The core polypeptides are bioactive peptides
XX
CC selected from a growth factor, cytokine, differentiation factor,
XX
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX
CC factor. The peptides of the invention can be used for inhibiting viral
XX
CC infection and can be used in anti-viral and anti-fusogenic treatments.
XX
CC Sequences AAV88651-Y90055 represent core polypeptide fragments that can
XX
CC be used in the invention. Some sequences among those indicated also
XX
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
QY
Db 1 NLRRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 37
2 NLRRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 38

RESULT 20
AAV88730
ID AAV88730 standard; peptide; 38 AA.
XX
AC AAV88730;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 85.
XX
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO95959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.

```


PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 22; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA:
Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
2 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 38
Db
RESULT 21
AAY86731
ID AAY86731 standard; peptide; 38 AA.
XX
AC AAY86731;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 86.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO95959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA:
Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
2 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 38
Db
RESULT 22
AAY89145
ID AAY89145 standard; peptide; 38 AA.
XX
AC AAY89145;
XX
DT 23-MAY-2000 (first entry)
XX
XX
DE Core polypeptide fragment T No. 583.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO95959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 30; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA:

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 37
DB 2 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 38

RESULT 23

AA89146
ID AAY89146 standard; peptide; 38 AA.

AC AAY89146;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 583.

KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PS (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

PS Disclosure; Page 30; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA:

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 37
DB 2 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 38

RESULT 24

AA89243
ID AAY89243 standard; peptide; 38 AA.

AC AAY89243;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 681.

KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PS (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

PS Disclosure; Page 32; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA:

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 37
DB 2 NLRAIEAOQHLLQLTWQIKQLQARILAVERYLKQD 38

RESULT 25

AA814530
ID AAB14530 standard; peptide; 38 AA.

XX AAB14530;
 XX
 XX 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 DE HIV-1 isolate LA1 gp41 N-helical domain residues 558-595 (peptide P-17).
 XX
 XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX WO200040616-A1.
 PN
 XX 13-JUL-2000.
 PD
 XX 10-JAN-2000; 2000WO-US000456.
 PF
 XX 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 PR
 XX (WIJD/) WEID C T.
 PA (WEIS/) WEISS C D.
 XX
 PI Wild CT, Weiss CD;
 XX
 XX WPI, 2000-465959/40.
 DR
 XX
 FT Raising neutralizing antibody response to human immunodeficiency virus,
 FT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 PT
 PS Claim 5; Page 56; 97pp; English.
 PS
 XX Sequences AAB14529-B14531 and AAB14537-B14566 represent specifically
 XX claimed peptides derived from the N-helical domain of the gp41 envelope
 CC glycoprotein from a variety of HIV-1 isolates. The invention relates to
 CC raising a neutralising antibody response to a broad spectrum of HIV
 CC (human immunodeficiency virus) strains and isolates, comprising the
 CC administration of a peptide which corresponds to or mimics highly
 CC conserved portions of a peptide which are important in mediating the process
 CC of viral entry into host cells. Such peptides can correspond to or mimic
 CC the coiled coil solution structure of the N-helical domain (the heptad
 CC repeat region), or can correspond or mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41
 CC core 6-helix bundle, which is formed by the interaction of the N- and C-
 CC helical domains of three gp41 proteins. The peptides can be administered
 CC either singly or as a combination (particularly a combination of N-
 CC helical and C-helical peptides), and can be multimerised. For example, N-
 CC and C-helical domain peptides can be alternately linked together to form
 CC a peptide which mimics the core 6-helix bundle. Administration of the
 CC peptide(s) generates a humoral response, with the production of
 CC antibodies against gp41 structures involved in viral entry. As these
 CC portions of gp41 are well conserved, such antibodies may be effective
 CC against a broad range of HIV strains and isolates. The peptide
 CC compositions may be administered as a prophylactic or therapeutic vaccine
 CC to generate antibodies which reduce or inhibit the ability of HIV to
 CC infect uninfected cells. A composition comprising polyclonal or
 CC monoclonal antibodies can be administered to reduce HIV infection of
 CC uninfected cells. Antibodies raised against entry-relevant gp41
 CC structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX Sequence 38 AA:
 XQ

OY		1	NLRAIEAQOHLLQLTWGIKQLQARILAAVERYLKDQ	37
Dd		2	NLRAIEAQOHLLQLTWGIKQLQARILAAVERYLKDQ	38
<hr/>				
RESULT 26				
ID	AAB52824	standard; peptide: 38 AA.		
XX				
AC	AAB52824;			
XX				
DT	12-SEP-2003	(revised)		
DT	23-FEB-2001	(first entry)		
XX		T21/DPI07 peptide fragment #101.		
DE				
KM		Antiinflammatory; T21/DPI07; gp41 ectodomain; HIV-1 fusion;		
XX		formyl peptide receptor family; FPR; inflammatory response up-regulation;		
KM		chemoattractant.		
XX				
OS		Human immunodeficiency virus 1.		
PN		WO20066622-A1.		
PD		09-NOV-2000.		
XX				
Pf	05-MAY-2000;	2000WO-USO12371.		
XX				
PR	05-MAY-1999;	99US-0132686P.		
XX		(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PA				
XX				
PI		Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;		
XX				
DR		WPI, 2000-656493/63.		
XX				
PT		Administration of peptide agents with a sequence corresponding to a		
PT		partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor antagonist		
PP		is used to modulate inflammation.		
XX				
PS		Disclosure; Page 28; 148pp: English.		
XX				
CC		The present sequence is a peptide fragment of T21/DPI07. T21/DPI07 is a		
CC		helical segment of the ectodomain of HIV-1 protein gp41. T21/DPI07 is		
CC		located in the amino terminus of the gp41 ectodomain. gp41 plays a		
CC		critical role in the fusion of HIV-1 and host cell membranes. T21/DPI07		
CC		interacts with members of the formyl peptide receptor (FPR) family and		
CC		thereby up-regulates an inflammatory response, and acts as a potent		
CC		chemoattractant and activator of human peripheral blood phagocytes (but		
CC		not T cells). The present peptide can be used to modulate an inflammatory		
CC		response in a subject. (Updated on 12-SEP-2003 to standardise OS field)		
XX				
SQ		Sequence 38 AA:		
	Query Match	96.1%; Score 174; DB 3; Length 38;		
	Best Local Similarity	97.3%; Pred. No. 1.8e-15;		
	Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
OY		1 NLRAIEAQOHLLQLTWGIKQLQARILAAVERYLKDQ	37	
Dd		2 NLRAIEAQOHLLQLTWGIKQLQARILAAVERYLKDQ	38	
<hr/>				
RESULT 27				
ID	AAB52786	standard; peptide: 38 AA.		
XX				
AC	AAB52786;			
XX				
DT	12-SEP-2003	(revised)		
DT	23-FEB-2001	(first entry)		
XX		T21/DPI07 peptide fragment #68.		

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200066622-A1.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012371.
XX
PR 05-MAY-1999; 99US-0132686P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
DR WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
PS Claim 12; Page 29; 148pp; English.
XX
CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
XX
Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
XX
RESULT 28
AAB52823
ID AAB52823 standard; peptide; 38 AA.
XX
AC AAB52823;
XX
DT 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #100.
DE
XX
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200066622-A1.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012371.
XX
PR 05-MAY-1999; 99US-0132686P.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
PS Claim 15; Page 42; 148pp; English.
XX
CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
XX
Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
XX
RESULT 29
AAG63858
ID AAG63858 standard; peptide; 38 AA.
XX
AC AAG63858;
XX
DT 11-SEP-2003 (revised)
DT 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of a HIV-1 gp41 peptide fragment.
DE
XX
XX HIV-1; isolate LAI; gp41; viral entry; envelope protein; glycoprotein;
KM viral infection; antiviral.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200159457-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004030.
XX
PR 10-FEB-2000; 2000US-0181543P.
PR 28-SEP-2000; 2000US-0235901P.
XX
PA (PANAN-) PANACOS PHARM INC.
XX
PI Wild CT, Allaway GP;
XX
DR WPI; 2001-522493/57.
XX
XX Screening for inhibitors of viral entry structure formation by
PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.
XX
PS Disclosure; Page 23; 68pp; English.
XX
CC The present sequence represents a fragment of a Human immunodeficiency
virus type 1 (HIV-1) isolate LAI gp41 protein. The peptide is used to

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.0543 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336A-179
Perfect score: 181
Sequence: 1 NLLRAIEAQOHLQLTWTWQIKQLQARIYAVERYLKQD 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	96.1	357	2 S21996	envelope protein g
2	174	96.1	851	2 S33985	env polypotein -
3	174	96.1	853	2 S54384	envelope polypote
4	174	96.1	854	2 S13288	env protein - huma
5	174	96.1	855	1 VCLJZR	env polypotein pr
6	174	96.1	856	1 VCLJH3	env polypotein pr
7	174	96.1	856	1 VCLJVL	env polypotein pr
8	174	96.1	861	1 VCLJIV	env polypotein pr
9	173	95.6	357	2 S22006	envelope protein g
10	173	95.6	357	2 S21994	envelope protein g
11	173	95.6	357	2 S22004	envelope protein g
12	173	95.6	358	2 S22002	envelope protein g
13	173	95.6	358	2 S22000	envelope protein g
14	173	95.6	358	2 S70417	envelope protein g
15	171	94.5	357	2 S21990	envelope protein g
16	171	94.5	357	2 S21992	envelope protein g
17	171	94.5	859	1 VCLJMN	env polypotein pr
18	170	93.9	443	2 C41621	env polypotein pr
19	170	93.9	445	2 A41621	env polypotein M
20	170	93.9	454	2 B41621	env polypotein D
21	170	93.9	729	1 VCLJUX	env polypotein pr
22	170	93.9	843	1 H44001	env polypotein pr
23	170	93.9	846	1 VCLJND	env polypotein pr
24	170	93.9	852	2 T12016	envelope glycoprot
25	170	93.9	855	1 VCLJN2	env polypotein pr
26	170	93.9	856	1 VCLJ3W	env polypotein pr
27	170	93.9	856	1 A44953	env polypotein pr
28	170	93.9	861	1 VCLJJB	env polypotein pr
29	170	93.9	861	1 VCLJSC	env polypotein pr

30	170	93.9	868	1 VCLJH4	env polypotein -
31	169	93.4	859	2 T01672	envelope polypote
32	166	91.7	358	2 S21998	envelope protein g
33	162	89.5	852	1 VCLJBR	env polypotein -
34	159	87.8	854	1 VCLJST	env polypotein pr
35	156	86.2	847	2 T09448	envelope glycoprot
36	156	86.2	847	2 S13289	env protein - huma
37	156	69.6	104	2 S52930	GP41 ENV protein -
38	125	69.1	864	1 VCLJG4	env polypotein -
39	125	69.1	877	2 C46356	env polypotein -
40	123	68.0	877	2 S49197	envelope protein p
41	120	68.3	732	2 S46352	env polypotein -
42	115	63.5	366	2 B41565	env polypotein -
43	115	63.5	863	2 A53034	gag polypotein -
44	113	62.4	712	1 VCLJH4	env polypotein pr
45	113	62.4	851	2 S12159	env protein - huma
46	113	62.4	852	1 VCLJG3	env polypotein pr
47	113	62.4	859	1 VCLJST	env polypotein pr
48	112	61.9	869	2 S53098	envelope polypote
49	112	61.9	859	1 VCLJCT	env polypotein pr
50	111	61.3	855	2 A45713	Env transmembrane
51	111	61.3	858	1 VCLJG2	env polypotein pr
52	111	61.3	881	2 S03068	env protein - huma
53	111	61.3	885	2 S04322	env polypotein -
54	111	61.3	886	2 T11555	env protein - sim1
55	110	60.8	881	1 VCLJG3	env polypotein -
56	109	60.2	859	2 S24571	env protein - huma
57	109	60.2	869	2 A47665	env protein gpi20 (
58	108	59.7	880	1 VCLJH2	env polypotein pr
59	107	59.1	151	2 S30458	env protein - huma
60	107	59.1	786	2 S28084	env polypotein -
61	107	59.1	889	1 VCLJG5	env polypotein -
62	106	58.6	887	2 T11566	envelope glycoprot
63	105	58.0	151	2 S30448	env protein - huma
64	105	58.0	151	2 S30453	env protein - huma
65	105	58.0	151	2 S30452	env protein - huma
66	105	58.0	151	2 S30450	env protein - huma
67	105	58.0	151	2 S30451	env protein - huma
68	103	56.9	151	2 S30459	env protein - huma
69	103	56.9	151	2 S30457	env protein - huma
70	103	56.9	151	2 S30456	env protein - huma
71	103	56.9	151	2 S30455	env protein - huma
72	103	56.9	151	2 S30454	env protein - huma
73	91	50.3	68	2 S60695	env protein - huma
74	91	50.3	68	2 S60693	env protein - huma
75	91	50.3	68	2 S60696	env protein - huma
76	91	50.3	68	2 S60705	gag protein - huma
77	91	50.3	68	2 S60707	env protein - huma
78	91	50.3	68	2 S60694	env protein - huma
79	91	50.3	68	2 S60687	env protein - huma
80	91	50.3	69	2 S60706	env protein - huma
81	89	49.2	68	2 S60692	env protein - huma
82	83	45.9	68	2 S60688	env protein - huma
83	80	44.2	69	2 S60690	env protein - huma
84	80	44.2	69	2 S60689	env protein - huma
85	80	44.2	69	2 S60691	env protein - huma
86	76	42.0	284	2 S60525	envelope polypote
87	76	42.0	297	2 S60538	envelope polypote
88	75	41.4	372	2 S46344	env polypotein -
89	75	41.4	375	2 S46345	env polypotein -
90	72	39.8	294	2 S60545	envelope polypote

ALIGNMENTS

RESULT 1
S21996
envelope protein gpi20/gp41 - human immunodeficiency virus type 1 (patient 27L)
C;Species: human immunodeficiency virus type 1; HIV-1
C;Date: 20-Feb-1995 #sequence_rev195 #text_change 26-Aug-1999
C;Accession: S70422; S21996
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:g1067129
A/Experimental source: patient 27L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.1%; Score 174; DB 2; Length 357;
Best Local Similarity 97.3%; Pred. No. 2, 6e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 55 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 91

RESULT 2

S33985
env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C/Accession: S33985
R/Carlini, F.
Submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33985
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-851 <CAR>
A/Cross-references: EMBL:Z15130; NID:960192; PIDN:CAA77628.1; PID:g60159
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.1%; Score 174; DB 2; Length 851;
Best Local Similarity 97.3%; Pred. No. 2, 6e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 549 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 585

RESULT 3

S54384
envelope polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1988
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <TR>
A/Cross-references: EMBL:M22639; NID:9329377; PIDN:AAA45370.1; PID:g329385
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 96.1%; Score 174; DB 2; Length 853;
Best Local Similarity 97.3%; Pred. No. 2, 6e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 551 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 587

RESULT 4

S13288
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C/Accession: S13288
R/O'Brien, W.A.; Koyangi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; MUID:91043044; PMID:2172833
A/Accession: S13288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OR>
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.1%; Score 174; DB 2; Length 854;
Best Local Similarity 97.3%; Pred. No. 2, 7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 552 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 588

RESULT 5

VCLZNR
env polyprotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cui
Gene 52, 71-82, 1987
A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleic
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <SRI>
A/Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:g329403
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <TM>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 96.1%; Score 174; DB 1; Length 855;
Best Local Similarity 97.3%; Pred. No. 2, 7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 553 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 589

RESULT 6

VCLTH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03973
R/Retner, U.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar
Nberg, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93553; MUID:85111123; PMID:2578615
A/Accession: A03973
A/Molecule type: DNA

A/Residues: 1-856 <RAT>
A/Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C/Genetics:
A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.1%; Score 174; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 2,7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 37
DB 554 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 590

RESULT 7
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03974
R/Mueering, W.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A/Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A/Reference number: A93355; MUID:5511157; PMID:2982104
A/Accession: A03974
A/Molecule type: DNA
A/Residues: 1-856 <MUE>
A/Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C/Genetics:
A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.1%; Score 174; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 2,7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 37
DB 554 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 590

RESULT 8
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03975
R/Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A/Title: Nucleotide sequence of the AIDS virus, LAV.
A/Reference number: A90866; MUID:85099333; PMID:2981635
A/Accession: A03975
A/Molecule type: DNA
A/Residues: 1-861 <NAL>
A/Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C/Genetics:

A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/1-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F:/616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.1%; Score 174; DB 1; Length 861;
Best Local Similarity 97.3%; Pred. No. 2,7e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 37
DB 559 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 595

RESULT 9
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C/Accession: S70420; S22006
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
Aids Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70420
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A/Experimental source: patient L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 357;
Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 37
DB 55 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKQD 91

RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 27B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21994; S70421
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S21994
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
Aids Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70421
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-140,'X',142-312,'X',314-357 <ST2>
A/Cross-references: EMBL:X61355; NID:g60179
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 357;

Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
|||
55 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 91

RESULT 11

S22004

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 48
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43616.1; PID:g60189
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined

A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:g60188
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 357;
Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
|||
55 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 91

RESULT 12

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined

A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:g60186
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 358;
Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
|||
56 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 92

RESULT 13

S22000

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 358;
Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
|||
56 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 92

RESULT 14

S70417

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined

A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.6%; Score 173; DB 2; Length 358;
Best Local Similarity 94.6%; Pred. No. 1,4e-15;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
|||
56 NLRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 92

RESULT 15

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990
A/Accession: S21990
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R,Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1176940
A/Accession: S70423
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332, 'X', 334-357 <STE2>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA3626.1; PID:G60176
C/Superfamily: type E retrovirus env polypeptide

Query Match 94.5%; Score 171; DB 2; Length 357;
Best Local Similarity 91.9%; Pred. No. 2.6e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 37
DB 55 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 91

RESULT 16
S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C/Accession: S70424; S21992
R,Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1176940
A/Accession: S70424
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61358; NID:G60177; PIDN:CAA3628.1; PID:G60178
A/Experimental source: patient 22
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polypeptide

Query Match 94.5%; Score 171; DB 2; Length 357;
Best Local Similarity 91.9%; Pred. No. 2.6e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 37
DB 55 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 91

RESULT 17
VCLMN
env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)
N/Alternate names: coat polypeptide
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C/Accession: A28922
R,Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, G.
Virology 164, 531-536, 1988
A/Title: Envelope sequences of two new United States HIV-1 isolates.
A/Reference number: A28922; MUID:88219542; PMID:3369091
A/Accession: A28922
A/Molecule type: DNA
A/Residues: 1-859 <GUR>
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypeptide
C/Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protein
F/1-29/Domain: signal sequence #status predicted <IG>
F/30-859/Product: env polypeptide #status predicted <BPP>
F/87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.5%; Score 171; DB 1; Length 859;
Best Local Similarity 91.9%; Pred. No. 6.7e-15;

Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 37
DB 558 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 594

RESULT 18
C41621
env polypeptide P - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polypeptide
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: C41621
R,Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; MUID:92107924; PMID:1763038
A/Accession: C41621
A/Molecule type: DNA
A/Residues: 1-443 <BUR>
A/Cross-references: GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:G555015
A/Note: this virus was isolated from the mother's sexual partner
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypeptide
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F/1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F/252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F/424-443/Domain: transmembrane #status predicted <TMN>
F/9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: cat

Query Match 93.9%; Score 170; DB 2; Length 443;
Best Local Similarity 91.9%; Pred. No. 4.5e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 37
DB 294 NLRRAIEAOQHMLQLTWVGIKQLQARVLAVERYLKQ 330

RESULT 19
A41621
env polypeptide M - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polypeptide
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: A41621
R,Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; MUID:92107924; PMID:1763038
A/Accession: A41621
A/Molecule type: DNA
A/Residues: 1-445 <BUR>
A/Cross-references: GB:M77228; NID:G328627; PIDN:AAB03790.1; PID:G555013
A/Note: this virus was isolated from the mother
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypeptide
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F/1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F/254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F/426-445/Domain: transmembrane #status predicted <TMN>
F/9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 93.9%; Score 170; DB 2; Length 445;
Best Local Similarity 91.9%; Pred. No. 4.5e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 37
      |||||:|||||:|||||:|||||:|||||:|||||:
Db      296 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 332

RESULT 20
B41621
env polyprotein D - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C/Accession: B41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:11763038
A:Accession: B41621
A:Molecule type: DNA
A:Residues: 1-454 <BUR>
A:Cross-references: GB:M77279
A>Note: this virus was isolated from the daughter
C/Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-263/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:454-554/Domain: transmembrane #status predicted <TM>
F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo
Query Match      93.9%; Score 170; DB 2; Length 454;
Best Local Similarity 91.9%; Pred. No. 4,6e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 37
      |||||:|||||:|||||:|||||:|||||:|||||:
Db      305 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 341

RESULT 21
VCLJXK
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C/Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A>Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C/Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-333/Domain: signal sequence #status predicted <SIG>
F:1-33/Region: hydrophobic #status predicted
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-729/Domain: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414
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Query Match      93.9%; Score 170; DB 1; Length 729;
Best Local Similarity 91.9%; Pred. No. 7.7e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 37
      |||||:|||||:|||||:|||||:|||||:|||||:
Db      560 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 596

RESULT 22
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C/Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A>Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <LIY>
A:Cross-references: GB:M93258
C/Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:489-843/Product: coat protein gp41 #status predicted <GP2>
F:489-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TM>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,
Query Match      93.9%; Score 170; DB 1; Length 843;
Best Local Similarity 91.9%; Pred. No. 9e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 37
      |||||:|||||:|||||:|||||:|||||:|||||:
Db      541 NLRAIEAQOHLQLTWGQIKQLQARILAVERYLKQ 577

RESULT 23
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: JQ0066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A>Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunoc
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162
A>Note: the authors translated the codon GCG for residue 523 as Arg
C/Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
```

F;502-846/Product: coat protein gp41 #status predicted <CP2>
 F;502-520/Domain: transmembrane #status predicted <TM1>
 F;674-692/Domain: transmembrane #status predicted <TM2>
 F;87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 93.9%; Score 170; DB 1; Length 846;
 Best Local Similarity 91.9%; Pred. No. 9e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 37
 DB 544 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 580

RESULT 24

T12016
 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: T12016

R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
 AIDS Res. Hum. Retroviruses 14, 329-337, 1998
 A/Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
 A/Reference number: Z17379; MUID:98178716; PMID:9519894
 A/Accession: T12016
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-852 <MCC>
 A/Cross-references: EMBL:U90934; NID:g32351783; PIDN:AAC59271.1; PID:g32351784
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

Query Match 93.9%; Score 170; DB 2; Length 852;
 Best Local Similarity 91.9%; Pred. No. 9.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 37
 DB 550 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 586

RESULT 25

VCLJ42
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate AŕV-2)
 N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C/Accession: A03976

R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-St
 Science 227, 484-492, 1985
 A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
 A/Reference number: A04003; MUID:85090453; PMID:2578227
 A/Accession: A03976
 A/Molecule type: DNA
 A/Residues: 1-855 <SAN>
 A/Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-508/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;510-855/Product: transmembrane glycoprotein #status predicted <TM1>
 F;87,129,140,158,184,190,204,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
 F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.9%; Score 170; DB 1; Length 855;
 Best Local Similarity 91.9%; Pred. No. 9.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 37

DB 553 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 589

RESULT 26

VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
 C/Accession: A24774

R;Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986
 A/Title: Identification and characterization of conserved and variable regions in the env
 A/Reference number: A24774; MUID:86218077; PMID:2423250
 A/Accession: A24774
 A/Molecule type: DNA
 A/Residues: 1-856 <STA>
 A/Cross-references: GB:K03455; GB:M38432; NID:g1906382
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-501/Product: coat protein gp120 #status predicted <GP1>
 F;502-847/Product: coat protein gp41 #status predicted <GP2>
 F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 93.9%; Score 170; DB 1; Length 856;
 Best Local Similarity 91.9%; Pred. No. 9.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 37
 DB 554 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 550

RESULT 27

A44963
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
 N/Alternate names: coat polyprotein
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
 C/Accession: A44963

R;Strinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989
 A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc
 A/Reference number: A44963; MUID:89228766; PMID:2713163
 A/Accession: A44963
 A/Molecule type: DNA
 A/Residues: 1-856 <SRI>
 A/Cross-references: GB:M15896; NID:g329392; PIDN:AAB5948.1; PID:g329394
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-520/Product: coat protein gp120 #status predicted <CP1>
 F;521-856/Product: coat protein gp41 #status predicted <CP2>
 F;684-705/Domain: transmembrane #status predicted <TM1>
 F;87,137,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 93.9%; Score 170; DB 1; Length 856;
 Best Local Similarity 94.6%; Pred. No. 9.1e-15;
 Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 37
 DB 554 NLRAIEAQQHLLQLTWQIKQQLARILAVERYLKDQ 550

RESULT 28

VCLJKB

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-9p41)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A:Reference number: A42995; MUID:92351552; PMID:1322587

A/Accession: A42995

A:Molecule type: mRNA

A:Residues: 1-861 <SH1>

A/Cross-references: GB:541266; GB:D01206

C/Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domain: extracellular #status predicted <EXT>

F:1-33/Domain: signal sequence #status predicted <SIG>

F:1-33/Region: hydrophobic #status predicted

F:34-517/Product: coat protein gp120 #status predicted <CP1>

F:514-517/Region: cleavage processing #status predicted

F:518-681/Product: coat protein gp41 #status predicted <CP2>

F:518-534/Region: hydrophobic #status predicted

F:690-711/Domain: transmembrane #status predicted <TM1>

F:712-681/Domain: intracellular #status predicted <INT>

F:756-772/Region: hydrophobic #status predicted

F:93,141,145,146,163,191,192,237,241,248,269,283,308,338,345,361,367,397,403,408,414

Query Match 93.9%; Score 170; DB 1; Length 861;

Best Local Similarity 91.9%; Pred. No. 9.2e-15;

Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIAQOHLQLTWQIKOLQARILAVERYLKQ 37

DB 560 NLRRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 596

RESULT 29

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C/Accession: B28922

R/Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta

Virology 164, 531-536, 1988

A:Title: Envelope sequences of two new United States HIV-1 isolates.

A:Reference number: A28922; MUID:88219542; PMID:3369091

A/Accession: B28922

A:Molecule type: DNA

A:Residues: 1-861 <GUR>

C/Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-861/Product: env polyprotein #status predicted <EPP>

F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 93.9%; Score 170; DB 1; Length 861;

Best Local Similarity 91.9%; Pred. No. 9.2e-15;

Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIAQOHLQLTWQIKOLQARILAVERYLKQ 37

DB 559 NLRRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 595

RESULT 30

VCLJH4

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: C25523

R/Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S.

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A:Reference number: A94136; MUID:87041461; PMID:3490666

A/Accession: C25523

A:Molecule type: DNA

A:Residues: 1-868 <DES>

A/Cross-references: GB:ML3137; NID:G326460; PIDN:AAA4311.1; PID:G326467

C/Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F:1-521/Product: coat protein gp120 #status predicted <GP1>

F:522-868/Product: coat protein gp41 #status predicted <GP2>

F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match 93.9%; Score 170; DB 1; Length 868;

Best Local Similarity 94.6%; Pred. No. 9.3e-15;

Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIAQOHLQLTWQIKOLQARILAVERYLKQ 37

DB 566 NLRRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 602

Search completed: June 2, 2004, 11:50:09

Job time: 10.0543 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 31.0679 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336A-179
Perfect score: 181
Sequence: 1 NLRLRAIEAOQHLLQLTWQIKQLQARIILAVERYIKDQ 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	96.7	852	15	Q8UJ55 human immun
2	174	96.1	129	15	Q9YVZ1 human immun
3	174	96.1	131	15	Q7SM43 human immun
4	174	96.1	132	15	Q9OQ52 human immun
5	174	96.1	132	15	Q7SLZ2 human immun
6	174	96.1	143	15	Q7SM06 human immun
7	174	96.1	144	15	Q7ZCD7 human immun
8	174	96.1	144	15	Q7ZCD6 human immun
9	174	96.1	145	15	Q7ZC52 human immun
10	174	96.1	153	15	Q7SM03 human immun
11	174	96.1	173	15	Q8JAJ9 human immun
12	174	96.1	357	15	Q78119 human immun
13	174	96.1	588	15	Q993A8 human immun
14	174	96.1	588	15	Q993A7 human immun
15	174	96.1	589	15	Q993B1 human immun
16	174	96.1	590	15	Q993A9 human immun

17	174	96.1	616	15	Q993B0 human immun
18	174	96.1	618	15	Q993B2 human immun
19	174	96.1	727	15	Q9Q723 human immun
20	174	96.1	747	15	Q70607 human immun
21	174	96.1	748	15	Q70606 human immun
22	174	96.1	752	15	Q70604 human immun
23	174	96.1	752	15	Q70605 human immun
24	174	96.1	752	15	Q70608 human immun
25	174	96.1	757	15	Q9Q722 human immun
26	174	96.1	811	15	Q9DVL6 human immun
27	174	96.1	826	15	Q9DVL1 human immun
28	174	96.1	842	15	Q73341 human immun
29	174	96.1	842	15	Q70895 human immun
30	174	96.1	842	15	Q73340 human immun
31	174	96.1	845	15	Q91D89 human immun
32	174	96.1	847	15	Q69996 human immun
33	174	96.1	851	15	Q78243 human immun
34	174	96.1	854	15	Q56566 human immun
35	174	96.1	854	15	Q85582 human immun
36	174	96.1	854	15	Q72502 human immun
37	174	96.1	854	15	Q90178 human immun
38	174	96.1	854	15	Q78705 human immun
39	174	96.1	855	15	Q8AQV7 human immun
40	174	96.1	855	15	Q8ADT7 human immun
41	174	96.1	856	15	Q74090 human immun
42	174	96.1	856	15	Q92877 human immun
43	174	96.1	856	15	Q74599 human immun
44	174	96.1	856	15	Q41772 human immun
45	174	96.1	857	15	Q92822 human immun
46	174	96.1	857	15	Q71013 human immun
47	174	96.1	857	15	Q89654 human immun
48	174	96.1	859	15	Q9WLJ1 human immun
49	174	96.1	864	15	Q9YP39 human immun
50	174	96.1	864	15	Q7ZJC8 human immun
51	174	96.1	866	15	Q9WPZ4 human immun
52	174	96.1	870	15	Q8Q2X1 human immun
53	174	96.1	870	15	Q8Q2X0 human immun
54	174	95.6	113	15	Q7ZCES human immun
55	173	95.6	125	15	Q91WP9 human immun
56	173	95.6	129	15	Q9YYV7 human immun
57	173	95.6	132	15	Q91WQ5 human immun
58	173	95.6	133	15	Q8UQZ6 human immun
59	173	95.6	133	15	Q8UQZ7 human immun
60	173	95.6	133	15	Q8UQZ8 human immun
61	173	95.6	133	15	Q8UQZ4 human immun
62	173	95.6	133	15	Q8UQZ3 human immun
63	173	95.6	133	15	Q9OQ20 human immun
64	173	95.6	134	15	Q91WQ6 human immun
65	173	95.6	137	15	Q9DQMO human immun
66	173	95.6	137	15	Q9DQO4 human immun
67	173	95.6	142	15	Q91WQ7 human immun
68	173	95.6	142	15	Q91WQ3 human immun
69	173	95.6	143	15	Q91WQ1 human immun
70	173	95.6	143	15	Q7ZC46 human immun
71	173	95.6	144	15	Q91WQ4 human immun
72	173	95.6	144	15	Q70207 human immun
73	173	95.6	144	15	Q7ZCE6 human immun
74	173	95.6	144	15	Q7ZCD8 human immun
75	173	95.6	144	15	Q7ZC6 human immun
76	173	95.6	144	15	Q7ZCC5 human immun
77	173	95.6	144	15	Q7ZCC2 human immun
78	173	95.6	144	15	Q7ZCB1 human immun
79	173	95.6	144	15	Q7ZCB0 human immun
80	173	95.6	144	15	Q7ZC96 human immun
81	173	95.6	144	15	Q7ZC95 human immun
82	173	95.6	144	15	Q7ZC89 human immun
83	173	95.6	144	15	Q7ZC88 human immun
84	173	95.6	144	15	Q7ZC71 human immun
85	173	95.6	144	15	Q7ZC70 human immun
86	173	95.6	144	15	Q7ZC45 human immun
87	173	95.6	145	15	Q7ZC57 human immun
88	173	95.6	145	15	Q7ZC53 human immun
89	173	95.6	145	15	Q7ZC51 human immun

90 173 95.6 145 15 Q7ZC50

Q7ZC50 human immun

ALIGNMENTS

RESULT 1

Q8UL55 PRELIMINARY; PRT; 852 AA.
 AC Q8UL55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GP160 protein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;
 RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells
 RT and Herpesvirus saimiri transformed T-cells is comparable.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ418531; CAD10941.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR00777; GP120.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 852 AA; 96711 MW; 57D8CA06A42P371F CRC64;

Query Match 96.7%; Score 175; DB 15; Length 852;
 Best Local Similarity 94.6%; Pred. No. 4.8e-16;
 Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 37
 Db 549 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 585

RESULT 2
 Q9YVZ1 PRELIMINARY; PRT; 129 AA.
 ID Q9YVZ1;
 AC Q9YVZ1;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GP41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=205.586;
 RC Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
 RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
 RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
 RT Uganda";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF006896; AAD01340.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.
 FT NON_TER 1

FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 15612 MW; 9CA606B58F42ADF CRC64;

Query Match 96.1%; Score 174; DB 15; Length 129;
 Best Local Similarity 97.3%; Pred. No. 9.1e-17;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 37
 Db 1 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 37

RESULT 3

Q7SM43 PRELIMINARY; PRT; 131 AA.
 ID Q7SM43;
 AC Q7SM43;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G1362;
 RA Gonzalez Perez M.P., Garcia Saliz A.;
 RT "Epidemiological and molecular characteristics of HIV and HTLV
 RT infection in Equatorial Guinea, 1996-1998";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF529973; AAP87704.1; -
 DR Envelope protein.
 FT NON_TER 1
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 131 AA; 15539 MW; C1B4FE8B1A860F CRC64;

Query Match 96.1%; Score 174; DB 15; Length 131;
 Best Local Similarity 97.3%; Pred. No. 9.3e-17;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 37
 Db 12 NLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 48

RESULT 4

Q90Q52 PRELIMINARY; PRT; 132 AA.
 ID Q90Q52;
 AC Q90Q52;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=99ES-MO1496;
 RC MEDLINE=21322034; PubMed=11429126;
 RX Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeo N., Asumu E.,
 RA Garcia-Salaz A.;
 RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea";
 RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
 DR EMBL; AF331089; AAK92300.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KM Transmembrane.

FT NON_TER 1 1
SO SEQUENCE 132 AA; 15708 MW; 519DB8AED574FAE CRC64;
Query Match 96.1%; Score 174; DB 15; Length 132;
Best Local Similarity 97.3%; Pred. No. 9.3e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 37
Db 11 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 47

RESULT 5
Q7SLZ2 ID Q7SLZ2 PRELIMINARY; PRT; 132 AA.

AC Q7SLZ2; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Envelope glycoprotein (Fragment).

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=GT970;

RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF530024; AAP87755.1; -

KM Envelope protein.

FT NON_TER 1 1

FT NON_TER 132 132

SO SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 132;
Best Local Similarity 97.3%; Pred. No. 9.3e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 37
Db 12 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 48

RESULT 6
Q7SM06 ID Q7SM06 PRELIMINARY; PRT; 143 AA.

AC Q7SM06; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Envelope glycoprotein (Fragment).

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=GT1138;

RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF530010; AAP87741.1; -

KM Envelope protein.

FT NON_TER 1 1

FT NON_TER 143 143

SO SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BE0 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 143;

Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 37
Db 12 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 48

RESULT 7
Q7ZCD7 ID Q7ZCD7 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD7; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-1;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY185383; AAO65658.1; -

DR GO: GO:0019031; C:Viral envelope; IEA.

DR GO: GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR000328; Env_Gp41.

DR Pfam: PF00517; GP41; 1.

KM Envelope protein.

FT NON_TER 1 1

FT NON_TER 144 144

SO SEQUENCE 144 AA; 16887 MW; A139D1C53D318EBE CRC64;

Query Match 96.1%; Score 174; DB 15; Length 144;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 37
Db 25 NLRRAIEAOQHLLQLTWGKIQOLQARILAVERYLKQ 61

RESULT 8
Q7ZCD6 ID Q7ZCD6 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD6; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;

RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-2;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY185384; AAO65659.1; -

DR GO: GO:0019031; C:Viral envelope; IEA.

DR GO: GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR000328; Env_Gp41.

DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C4218EBB CRC64;

Query Match 96.1%; Score 174; DB 15; Length 144;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 25 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 61

RESULT 9

ID Q7ZC52 PRELIMINARY; PRT; 145 AA.
AC Q7ZC52;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HR1UX18;
RA Roman F., Gonzalez D., Lambert C., Deroc S., Fischer A., Baurich T.,
RA Straub T., Bouime R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
RT subtype HIV-1-";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185468; AA065743.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR Interpro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 17020 MW; AC8C32E97B09D1A1 CRC64;
Query Match 96.1%; Score 174; DB 15; Length 145;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 23 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 59

RESULT 10

ID Q7SM03 PRELIMINARY; PRT; 153 AA.
AC Q7SM03;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT598;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530013; AAP87744.1; -.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 153 153
SQ SEQUENCE 153 AA; 18136 MW; 01FA9E1FFFC035 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 153;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 12 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 48

RESULT 11

ID Q8UAJ9 PRELIMINARY; PRT; 173 AA.
AC Q8UAJ9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96BRJ045;
RA Gutierrez M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF63445; AM90821.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR Interpro; IPR000328; Env_GP41.
DR Interpro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 173 173
SQ SEQUENCE 173 AA; 19858 MW; 300D69C94C03AD14 CRC64;
Query Match 96.1%; Score 174; DB 15; Length 173;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 57 NLRPAIEAOQHLLQLTWQIKQLQARILAVERYLKQ 93

RESULT 12

ID Q78119 PRELIMINARY; PRT; 357 AA.
AC Q78119;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.,
RT "distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid."
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61356; CAA43624.1; -.
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KM NON TER 1
FT SEQUENCE 357 AA; 4118 MW; FE4CAA7E122AB8E6 CRC64;
SQ
Query Match 96.1%; Score 174; DB 15; Length 357;
Best Local Similarity 97.3%; Pred. No. 2.7e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 37
Db 55 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 91
RESULT 13
ID Q993A8 PRELIMINARY; PRT; 588 AA.
AC Q993A8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240A8E CRC64;
Qy
Query Match 96.1%; Score 174; DB 15; Length 588;
Best Local Similarity 97.3%; Pred. No. 4.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 37
Db 497 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 533
RESULT 14
ID Q993A7 PRELIMINARY; PRT; 588 AA.
AC Q993A7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AAK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1
SQ SEQUENCE 589 AA; 65593 MW; 3FE7610B592EFC6D CRC64;
Qy
Query Match 96.1%; Score 174; DB 15; Length 588;
Best Local Similarity 97.3%; Pred. No. 4.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 37
Db 497 NLRATEAOQHLLQLTWVGKQARILAAVERYLKQ 533
RESULT 15
ID Q993B1 PRELIMINARY; PRT; 589 AA.
AC Q993B1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AAK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;
Qy
Query Match 96.1%; Score 174; DB 15; Length 589;
Best Local Similarity 97.3%; Pred. No. 4.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 37
Db 497 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 533

RESULT 16

Q993A9 PRELIMINARY; PRT; 590 AA.
ID Q993A9;
AC Q993A9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wc2;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221146; AAK20294.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP41; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT SEQUENCE 590 AA; 65902 MW; 91ED899C8F91CAF CRC64;
SQ
Query Match 96.1%; Score 174; DB 15; Length 590;
Best Local Similarity 97.3%; Pred. No. 4.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 37
Db 498 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 534

RESULT 17

Q993B0 PRELIMINARY; PRT; 616 AA.
ID Q993B0;
AC Q993B0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221145; AAK20293.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR00777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT SEQUENCE 616 AA; 69189 MW; 57A8E20F9A580A4F CRC64;
SQ

Query Match 96.1%; Score 174; DB 15; Length 616;
Best Local Similarity 97.3%; Pred. No. 4.7e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 37
Db 498 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 534

RESULT 18

Q993B2 PRELIMINARY; PRT; 618 AA.
ID Q993B2;
AC Q993B2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221143; AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;
SQ
Query Match 96.1%; Score 174; DB 15; Length 618;
Best Local Similarity 97.3%; Pred. No. 4.7e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 37
Db 500 NLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 536

RESULT 19

Q90723 PRELIMINARY; PRT; 727 AA.
ID Q90723;
AC Q90723;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=111Bx;

RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Haiften I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319 (1999).
DR EMBL: AF189158; AAF2567.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; P90FD626D26B9E66 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 727;
Best Local Similarity 97.3%; Pred. No. 5.6e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 37
Db 549 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 585
|||||

RESULT 20
Q70607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=LM87-1;
RC MEDLINE=95127297; PubMed=7826699;
RA Shaw G., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Raitz M., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB)." ;
RL AIDS Res. Hum. Retroviruses 10:1143-1155 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RA Mulder K.E.;
DR EMBL: U12034; AAA76669.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 747;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 37
Db 549 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 585
|||||

RESULT 21
Q70606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=LM881;
RC MEDLINE=95127297; PubMed=7826699;
RA Raitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB)." ;
RL AIDS Res. Hum. Retroviruses 10:1143-1155 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RA Mulder K.E.;
DR EMBL: U12032; AAA76668.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 96.1%; Score 174; DB 15; Length 748;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 37
Db 550 NLRAIEAOQHLLQLTWMOIKQLOARILAVERYLKQD 586
|||||

RESULT 22
Q70604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxId=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.1%; Score 174; DB 15; Length 752;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 37
Db 554 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 590

RESULT 23
Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxId=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
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DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.1%; Score 174; DB 15; Length 752;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 37
Db 554 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 590

RESULT 24
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxId=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AAA76670.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 752;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 37
Db 554 NLRAIEAOQHLLQLTWGIKQLQARILAVERYLKQ 590

RESULT 25
Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
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OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=9272698; Pubmed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; Pubmed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BDE CRC64;

Query Match 96.1%; Score 174; DB 15; Length 757;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 37
Db 549 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 585

RESULT 26
O9DVL6 PRELIMINARY; PRT; 811 AA.
AC O9DVL6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; Pubmed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tehimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401037; CAC15045.1; -.
GO: GO:0042025; C:host cell nucleus; IEA.

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DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 1 811
FT NON TER 1 811
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 811;
Best Local Similarity 97.3%; Pred. No. 6.3e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 37
Db 558 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 594

RESULT 27
O9DVL1 PRELIMINARY; PRT; 826 AA.
AC O9DVL1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97DC.KTB22;
RX MEDLINE=20499072; Pubmed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tehimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401042; CAC15050.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 1 826
FT NON TER 1 826
SQ SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 826;
Best Local Similarity 97.3%; Pred. No. 6.4e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 37
Db 541 NLRRAEAOQHLLQLTWQIKOLQARILAVERYLKDQ 577

RESULT 28
Q73341

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ID Q73341 PRELIMINARY; PRT; 842 AA.
AC Q73341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96303593; Pubmed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
  Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
  D, E, and F obtained from the World Health Organization Network for
  HIV Isolation and Characterization.";
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39236; AAB37173.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1E9F1 CRC64;

Query Match 96.1%; Score 174; DB 15; Length 842;
Best Local Similarity 97.3%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 540 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 576

RESULT 29
ID Q70895 PRELIMINARY; PRT; 842 AA.
AC Q70895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RX MEDLINE=98285725; Pubmed=9621027;
RA Gao F., Robertson D.L., Carruthers C.D., Morrison S.G., Jian B.,
  Chen Y., Barre-Sinoussi F., Girard M., Srinivasan A., Adimik A.G.,
  Shaw G.M., Sharp P.M., Hahn B.H.;
RT "A comprehensive panel of near-full-length clones and reference
  sequences for non-subtype B isolates of human immunodeficiency virus
  type 1.";
RL J. Virol. 72:5680-5698(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Gao F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005495; AAD03179.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

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DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94810 MW; F82041BD932DCAD CRC64;

Query Match 96.1%; Score 174; DB 15; Length 842;
Best Local Similarity 97.3%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 540 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 576

RESULT 30
ID Q73340 PRELIMINARY; PRT; 842 AA.
AC Q73340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96303593; Pubmed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
  Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
  D, E, and F obtained from the World Health Organization Network for
  HIV Isolation and Characterization.";
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39235; AAB37172.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94906 MW; 607B4F2A47B791BB CRC64;

Query Match 96.1%; Score 174; DB 15; Length 842;
Best Local Similarity 97.3%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 540 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 576

Search completed: June 2, 2004, 11:48:21
Job time : 32.0679 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 13.6739 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-179
Perfect score: 181
Sequence: 1 NLRALIAQOHLQLTWQIKQLQARILAVRYLKQD 37

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	100.0	38 4	US-08-973-952-82	Sequence 82, App1
2	174	96.1	37 4	US-09-515-965A-1757	Sequence 1757, App1
3	174	96.1	38 1	US-08-374-666-1	Sequence 1, App1
4	174	96.1	38 3	US-08-486-099-89	Sequence 89, App1
5	174	96.1	38 3	US-08-360-107A-99	Sequence 99, App1
6	174	96.1	38 3	US-08-360-107A-132	Sequence 132, App1
7	174	96.1	38 3	US-08-484-223B-89	Sequence 89, App1
8	174	96.1	38 3	US-08-919-597-89	Sequence 89, App1
9	174	96.1	38 3	US-08-475-668A-89	Sequence 89, App1
10	174	96.1	38 3	US-08-485-551A-99	Sequence 89, App1
11	174	96.1	38 3	US-08-471-913A-89	Sequence 89, App1
12	174	96.1	38 3	US-08-485-264A-89	Sequence 89, App1
13	174	96.1	38 3	US-09-082-279B-16	Sequence 16, App1
14	174	96.1	38 3	US-09-082-279B-507	Sequence 507, App1
15	174	96.1	38 3	US-09-082-279B-604	Sequence 604, App1
16	174	96.1	38 3	US-09-082-279B-660	Sequence 660, App1
17	174	96.1	38 4	US-08-474-349A-89	Sequence 89, App1
18	174	96.1	38 4	US-08-474-349A-441	Sequence 441, App1
19	174	96.1	38 4	US-09-315-304B-16	Sequence 16, App1
20	174	96.1	38 4	US-09-315-304B-507	Sequence 507, App1
21	174	96.1	38 4	US-09-315-304B-604	Sequence 604, App1
22	174	96.1	38 4	US-09-315-304B-660	Sequence 660, App1
23	174	96.1	38 4	US-08-255-208A-25	Sequence 25, App1
24	174	96.1	38 4	US-08-470-896-89	Sequence 89, App1
25	174	96.1	38 4	US-08-485-546A-89	Sequence 89, App1
26	174	96.1	38 4	US-09-796-202-11	Sequence 11, App1
27	174	96.1	38 4	US-09-834-784-16	Sequence 16, App1

28	174	96.1	38 4	US-09-834-784-507	Sequence 507, App1
29	174	96.1	38 4	US-09-834-784-604	Sequence 604, App1
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31	174	96.1	38 4	US-08-464-003-1	Sequence 1, App1
32	174	96.1	38 4	US-09-779-451-2	Sequence 2, App1
33	174	96.1	38 4	US-09-515-965A-16	Sequence 16, App1
34	174	96.1	38 4	US-09-515-965A-507	Sequence 507, App1
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36	174	96.1	38 4	US-09-515-965A-660	Sequence 660, App1
37	174	96.1	38 4	US-09-350-641C-16	Sequence 16, App1
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42	174	96.1	41 1	US-08-374-666-9	Sequence 9, App1
43	174	96.1	41 1	US-08-374-666-3	Sequence 3, App1
44	174	96.1	41 3	US-08-486-099-8	Sequence 8, App1
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46	174	96.1	41 3	US-08-484-223B-8	Sequence 8, App1
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48	174	96.1	41 3	US-08-484-223B-243	Sequence 243, App1
49	174	96.1	41 3	US-08-919-597-8	Sequence 8, App1
50	174	96.1	41 3	US-08-475-668A-8	Sequence 8, App1
51	174	96.1	41 3	US-08-485-551A-8	Sequence 8, App1
52	174	96.1	41 3	US-08-471-913A-8	Sequence 8, App1
53	174	96.1	41 3	US-08-554-616-8	Sequence 8, App1
54	174	96.1	41 3	US-08-485-264A-8	Sequence 8, App1
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58	174	96.1	41 3	US-09-082-279B-1163	Sequence 1163, App1
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62	174	96.1	41 4	US-09-315-304B-633	Sequence 633, App1
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64	174	96.1	41 4	US-08-255-208A-8	Sequence 8, App1
65	174	96.1	41 4	US-08-973-952-8	Sequence 8, App1
66	174	96.1	41 4	US-08-470-896-8	Sequence 8, App1
67	174	96.1	41 4	US-08-485-546A-8	Sequence 8, App1
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69	174	96.1	41 4	US-09-834-784-601	Sequence 601, App1
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73	174	96.1	41 4	US-08-464-003-9	Sequence 9, App1
74	174	96.1	41 4	US-09-515-965A-496	Sequence 496, App1
75	174	96.1	41 4	US-09-515-965A-601	Sequence 601, App1
76	174	96.1	41 4	US-09-515-965A-633	Sequence 633, App1
77	174	96.1	41 4	US-09-515-965A-1163	Sequence 1163, App1
78	174	96.1	41 4	US-09-350-641C-496	Sequence 496, App1
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80	174	96.1	41 4	US-09-350-641C-633	Sequence 633, App1
81	174	96.1	41 4	US-09-350-641C-1163	Sequence 1163, App1
82	174	96.1	44 1	US-08-374-666-10	Sequence 10, App1
83	174	96.1	44 1	US-08-464-003-3	Sequence 3, App1
84	174	96.1	45 3	US-09-082-279B-1164	Sequence 1164, App1
85	174	96.1	45 4	US-09-315-304B-1164	Sequence 1164, App1
86	174	96.1	45 4	US-09-834-784-1164	Sequence 1164, App1
87	174	96.1	45 4	US-09-779-451-9	Sequence 9, App1
88	174	96.1	45 4	US-09-515-965A-1164	Sequence 1164, App1
89	174	96.1	45 4	US-09-350-641C-1164	Sequence 1164, App1
90	174	96.1	49 4	US-09-796-202-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

```

; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORIAL THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/08/973,952A
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/481,957
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match      100.0%; Score 181; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 37
        |||||
Db      2 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 38

RESULT 2
US-09-515-965A-1757
; Sequence 1757, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: DeJemico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sietra, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1757
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1757

Query Match      96.1%; Score 174; DB 4; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 37
        |||||
Db      1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 37

RESULT 3
US-08-374-666-1
; Sequence 1, Application US/08374666
; Patent No. 5656480
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Bolognesi, Dani P.
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
```

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,666
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-374-666-1

Query Match      96.1%; Score 174; DB 1; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 37
        |||||
Db      2 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKDQ 38

RESULT 4
US-08-486-099-89
; Sequence 89, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 38

RESULT 5
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petterway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 38

RESULT 6

US-08-360-107A-132

Sequence 132, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petterway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-132

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWQIKQIARILAVERYLKQ 38

RESULT 7
US-08-484-223B-89

Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQIQAARILAVERYLKQD 37
DB 2 NLRAIEAQOHLQLTWQIKQIQAARILAVERYLKQD 38

RESULT 8
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQIQAARILAVERYLKQD 37
DB 2 NLRAIEAQOHLQLTWQIKQIQAARILAVERYLKQD 38

RESULT 9
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petterway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 37
Db 2 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 38

RESULT 10
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 37
Db 2 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 38

RESULT 11
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 37
Db 2 NLRAIEAOQHLLQLTWQIKQIQARILAVERYLKQ 38

RESULT 12
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:

```

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petreway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-264A-89

Query Match          96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 37
DB      2  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 38

RESULT 13
; US-09-082-279B-16
; Sequence 16, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-16

Query Match          96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 37
DB      2  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 38

RESULT 14
; US-09-082-279B-507
; Sequence 507, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-507

Query Match          96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 37
DB      2  NLRAIEAQOHLQLTWGKIQLOARILAVERYLKQ 38

RESULT 15
; US-09-082-279B-604
; Sequence 604, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-604
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Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 37
Db 2 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 38

RESULT 16
US-09-082-279B-660
Sequence 660, Application US/09082279B

Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 660
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-660

Query Match 96.1%; Score 174; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 37
Db 1 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 37

RESULT 17
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 37
Db 2 NLRRAEAOQHLLQLTWVGIKQLQARILAVERYLKQ 38

RESULT 18
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 19
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 20
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Core polypeptide
US-09-315-304B-507

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 21
US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 22
US-09-315-304B-660
Sequence 660, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 660
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-660

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37

RESULT 23

US-08-255-208A-25

; Sequence 25, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matchews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 24

; US-08-470-896-89
; Sequence 89, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matchews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 25

; US-08-485-546A-89
; Sequence 89, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matchews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING ESTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 26
US-09-796-202-11
Sequence 11, Application US/09796202
Patent No. 6546636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olsson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 27
US-09-834-784-16
Sequence 16, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:

APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Arner, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 28
US-09-834-784-507
Sequence 507, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Arner, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-507

Query Match 96.1%; Score 174; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
Db 2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 29
US-09-834-784-604
Sequence 604, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn

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1  APPLICANT: Guthrie, Kelly
2  APPLICANT: Merutka, Gene
3  APPLICANT: Amer, Mohamed
4  APPLICANT: Lambert, Dennis
5  TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
6  TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
7  FILE REFERENCE: 7872-043
8  CURRENT APPLICATION NUMBER: US/09/834,784
9  PRIOR FILING DATE: 2001-04-13
10 PRIOR APPLICATION NUMBER: 09/082,279
11 PRIOR FILING DATE: 1998-05-20
12 NUMBER OF SEQ ID NOS: 1515
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 604
15 LENGTH: 38
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Core polypeptide
20 US-09-834-784-604

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Query Match	96.1%	Score 174;	DB 4;	Length 38;
Best Local Similarity	97.3%	Pred. No. 1.4e-17;		
Matches 36;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Dy 1 NLRRAIEAQHLLQLTWNGIKQLQARILAVERYLKDQ 37
| | | | | | | | | | | | | | | | | | | | |
Db 2 NLRRAIEAQHLLQLTWNGIKQLQARILAVERYLKDQ 38

RESULT 30
 US-09-834-784-660
 Sequence 660, Application US/09834784
 Patent No. 6562787
 GENERAL INFORMATION:
 APPLICANT: Barney, Shawn
 APPLICANT: Guthrie, Kelly
 APPLICANT: Merutka, Gene
 APPLICANT: Arner, Mohamed
 APPLICANT: Lambert, Dennis
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
 FILE REFERENCE: 7872-043
 CURRENT APPLICATION NUMBER: US/09/834,784
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 09/082,279
 PRIOR FILING DATE: 1998-05-20
 NUMBER OF SEQ ID NOS: 1515
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 660
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Core polypeptide
 US-09-834-784-660

Query Match	96.1%;	Score 174;	DB 4;	Length 38;
Best Local Similarity	97.3%;	Pred. No. 1.4e-17;		
Matches 36;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 NLRAIEAQHLLQITWQGIKQLARILAVERYLKQ 377

Db 1 NLRAIEAQHLLQITWQGIKQLARILAVERYLKQ 377

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 34.0842 Seconds
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Title: US-09-657-336a-179
Perfect score: 181
Sequence: 1 NLRLAEAOQHLLQLTWQIKQLQARILAVRYLKQD 37

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Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	100.0	38	14	US-10-252-136-82
2	174	96.1	37	15	US-10-005-305-164
3	174	96.1	38	9	US-09-796-202-11
4	174	96.1	38	9	US-09-779-451-2
5	174	96.1	38	12	US-09-493-346-2
6	174	96.1	38	12	US-10-267-682-89
7	174	96.1	38	12	US-10-267-682-89
8	174	96.1	38	12	US-10-267-748-89
9	174	96.1	38	12	US-09-809-060-7
10	174	96.1	38	12	US-09-809-060-7
11	174	96.1	38	12	US-10-663-589-3
12	174	96.1	38	12	US-10-681-879-2
13	174	96.1	38	12	US-09-828-615-2
14	174	96.1	38	14	US-10-116-797-2
15	174	96.1	38	14	US-10-323-314-11

16	174	96.1	38	14	US-10-351-641-16	Sequence 16, Appl
17	174	96.1	38	14	US-10-351-641-507	Sequence 507, App
18	174	96.1	38	14	US-10-351-641-604	Sequence 604, App
19	174	96.1	38	14	US-10-351-641-660	Sequence 660, App
20	174	96.1	38	15	US-10-005-305-165	Sequence 165, App
21	174	96.1	38	15	US-10-005-305-202	Sequence 202, App
22	174	96.1	38	15	US-10-005-305-203	Sequence 203, App
23	174	96.1	38	15	US-10-420-194-1234	Sequence 1234, App
24	174	96.1	38	16	US-10-664-021-2	Sequence 2, Appli
25	174	96.1	38	16	US-10-671-316-2	Sequence 8, Appli
26	174	96.1	41	12	US-10-267-682-8	Sequence 8, Appli
27	174	96.1	41	12	US-10-267-748-8	Sequence 8, Appli
28	174	96.1	41	12	US-10-663-589-30	Sequence 30, Appli
29	174	96.1	41	12	US-10-663-589-33	Sequence 33, Appli
30	174	96.1	41	12	US-10-663-589-35	Sequence 35, Appli
31	174	96.1	41	14	US-10-252-136-8	Sequence 8, Appli
32	174	96.1	41	14	US-10-414-192-3	Sequence 9, Appli
33	174	96.1	41	14	US-10-414-192-9	Sequence 9, Appli
34	174	96.1	41	14	US-10-351-641-496	Sequence 496, App
35	174	96.1	41	14	US-10-351-641-601	Sequence 601, App
36	174	96.1	41	14	US-10-351-641-633	Sequence 633, App
37	174	96.1	41	14	US-10-351-641-1163	Sequence 1163, App
38	174	96.1	41	16	US-10-664-021-27	Sequence 27, Appl
39	174	96.1	41	16	US-10-671-316-27	Sequence 27, Appl
40	174	96.1	44	12	US-10-663-589-36	Sequence 36, Appl
41	174	96.1	44	14	US-10-414-192-10	Sequence 10, Appl
42	174	96.1	45	9	US-09-779-451-9	Sequence 9, Appli
43	174	96.1	45	12	US-09-809-060-50	Sequence 50, Appl
44	174	96.1	45	12	US-10-663-589-29	Sequence 29, Appl
45	174	96.1	45	14	US-10-351-641-1164	Sequence 1164, Ap
46	174	96.1	45	16	US-10-664-021-26	Sequence 26, Appl
47	174	96.1	45	16	US-10-671-316-26	Sequence 26, Appl
48	174	96.1	49	9	US-09-796-202-3	Sequence 3, Appli
49	174	96.1	49	14	US-10-323-314-3	Sequence 3, Appli
50	174	96.1	51	12	US-10-663-589-27	Sequence 27, Appl
51	174	96.1	51	16	US-10-351-641-745	Sequence 745, App
52	174	96.1	51	16	US-10-664-021-24	Sequence 24, Appl
53	174	96.1	52	14	US-10-671-316-24	Sequence 24, Appl
54	174	96.1	52	14	US-10-351-641-1119	Sequence 1119, Ap
55	174	96.1	53	14	US-10-351-641-955	Sequence 955, App
56	174	96.1	53	14	US-10-351-641-1062	Sequence 1062, Ap
57	174	96.1	55	9	US-09-779-451-1	Sequence 1, Appli
58	174	96.1	55	12	US-09-809-060-14	Sequence 14, Appl
59	174	96.1	57	15	US-10-438-691-1	Sequence 1, Appli
60	174	96.1	59	16	US-10-664-021-1	Sequence 1, Appli
61	174	96.1	59	16	US-10-671-316-1	Sequence 1, Appli
62	174	96.1	60	12	US-10-663-589-1	Sequence 1, Appli
63	174	96.1	63	12	US-10-267-682-201	Sequence 201, App
64	174	96.1	63	12	US-10-267-748-201	Sequence 201, App
65	174	96.1	63	14	US-10-252-136-54	Sequence 54, Appl
66	174	96.1	103	14	US-10-263-103-29	Sequence 29, Appl
67	174	96.1	103	15	US-10-438-691-3	Sequence 3, Appli
68	174	96.1	113	15	US-10-438-691-4	Sequence 4, Appli
69	174	96.1	177	14	US-10-040-349B-2	Sequence 2, Appli
70	174	96.1	188	9	US-09-854-816-88	Sequence 88, Appl
71	174	96.1	198	9	US-09-854-816-8	Sequence 8, Appl
72	174	96.1	200	14	US-10-263-103-25	Sequence 25, Appl
73	174	96.1	200	15	US-10-438-691-8	Sequence 8, Appli
74	174	96.1	232	14	US-10-059-271-81	Sequence 81, Appl
75	174	96.1	234	14	US-10-059-271-82	Sequence 82, Appl
76	174	96.1	256	14	US-10-059-271-97	Sequence 97, Appl
77	174	96.1	268	9	US-09-854-816-16	Sequence 16, Appl
78	174	96.1	268	9	US-09-854-816-17	Sequence 17, Appl
79	174	96.1	268	9	US-09-854-816-18	Sequence 18, Appl
80	174	96.1	268	9	US-09-854-816-19	Sequence 19, Appl
81	174	96.1	269	9	US-09-854-816-43	Sequence 43, Appl
82	174	96.1	338	12	US-10-267-682-90	Sequence 90, Appl
83	174	96.1	344	14	US-10-267-748-90	Sequence 90, Appl
84	174	96.1	345	9	US-10-040-349B-1	Sequence 1, Appli
85	174	96.1	345	14	US-09-779-451-1	Sequence 8, Appli
86	174	96.1	359	14	US-10-026-741-49	Sequence 49, Appl
87	174	96.1	359	14	US-10-214-670-58	Sequence 58, Appl
88	174	96.1	391	14	US-10-059-271-93	Sequence 93, Appl

89	174	96.1	488	8	US-08-911-824-95	Sequence 95, Appl
90	174	96.1	491	8	US-08-911-824-56	Sequence 56, Appl

ALIGNMENTS

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RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82
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Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 38

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US-10-005-305-164
; Sequence 164, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-164
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Query Match 96.1%; Score 174, DB 15; Length 37;
Best Local Similarity 97.3%; Pred. No. 9.7e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 37
DB 1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 37

```
RESULT 3
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11
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Query Match 96.1%; Score 174, DB 9; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 37
DB 2 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 38

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RESULT 4
US-09-779-451-2
; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2
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Query Match 96.1%; Score 174, DB 9; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 37
DB 2 NLRRAIEAQQHLLQLTWGQIKQLQARILAVERYLKQ 38

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RESULT 5
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
```

1 TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
2 FILE REFERENCE: 61009
3 CURRENT APPLICATION NUMBER: US/09/493,346
4 NUMBER OF SEQ ID NOS: 5
5 SOFTWARE: Patentin Ver. 2.0
6 SEQ ID NO: 2
7 LENGTH: 38
8 TYPE: PRT
9 ORGANISM: Artificial Sequence
10 FEATURE:
11 OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
12 US-09-493-346-2

Query Match 96.1%; Score 174; DB 10; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 6
US-10-267-682-89
Sequence 89, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown

1 MOLECULE TYPE: peptide
2 SEQUENCE DESCRIPTION: SEQ ID NO: 89:
3 US-10-267-682-89

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 7
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
2 NLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 8
US-09-809-060-6
; Sequence 6, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 37
DB 2 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 9
US-09-809-060-7
; Sequence 7, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 37
DB 2 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 10
US-10-663-589-3
; Sequence 3, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV

; TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 37
DB 2 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 11
US-10-681-879-2
; Sequence 2, Application US/10681879
; Publication No. US20040062767A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Madden, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/10/681,879
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/493,346
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 37
DB 2 NLRAIEAQQHLLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 12
US-09-828-615-2
; Sequence 2, Application US/09828615
; Publication No. US20020146415A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Madden, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672
; CURRENT APPLICATION NUMBER: US/09/828,615
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38

TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 96.1%; Score 174; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 37
DB 2 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 38

RESULT 13
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US2003004411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38.
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 37
DB 2 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 38

RESULT 14
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olsson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 37
DB 2 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 38

RESULT 15
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
Bolognesi, Daniel P.
Matthews, Thomas J.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/414,192
FILING DATE: 15-Apr-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 37
DB 2 NLRATFAOQHLLQLTWGIKQARILAVERYLKQ 38

RESULT 16
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthe, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279

;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 16
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 17
US-10-351-641-507

;; Sequence 507, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Amer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; PRIOR FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 507
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 18
US-10-351-641-604

;; Sequence 604, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Amer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100

;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 604
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 19
US-10-351-641-660

;; Sequence 660, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Amer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; PRIOR FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 660
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-660

Query Match 96.1%; Score 174; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
Db 2 NLRRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 37

RESULT 20
US-10-005-305-165

;; Sequence 165, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the

APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 165
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 96.1%; Score 174; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 21
US-10-005-305-202
Sequence 202, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match 96.1%; Score 174; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 22
US-10-005-305-203
Sequence 203, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services

TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 96.1%; Score 174; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 23
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US2004006035A1
GENERAL INFORMATION:
APPLICANT: MGSWigen, Jim
APPLICANT: Blact, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
TITLE OF INVENTION: Interactions
FILE REFERENCE: MBH02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences

NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match 96.1%; Score 174; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1;

QY 1 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 38

RESULT 24
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US20040076637A1

GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
PRIOR FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 96.1%; Score 174; DB 16; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1;

QY 1 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 38

RESULT 25
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1

GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: peptides, and trimers formed therefrom
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
PRIOR FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match 96.1%; Score 174; DB 16; Length 38;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1;

QY 1 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 37
DB 2 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 38

RESULT 26
US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Pettey, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-682-8

Query Match 96.1%; Score 174; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 1;

QY 1 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 37
DB 5 NLRAIEAQOHLQLTWGKIQARILAVERYLKQ 41

RESULT 27
US-10-267-748-8
Sequence 8, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.

Matchews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petterway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: unknown
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-748-8

Query Match 96.1%; Score 174; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 5 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 41

RESULT 28
US-10-663-589-30
Sequence 30, Application US/10663589
Publication No. US200400637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 41

TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-30

Query Match 96.1%; Score 174; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 5 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 41

RESULT 29
US-10-663-589-33
Sequence 33, Application US/10663589
Publication No. US200400637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-33

Query Match 96.1%; Score 174; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
DB 5 NLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 41

RESULT 30
US-10-663-589-35
Sequence 35, Application US/10663589
Publication No. US200400637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-35

Query Match 96.1%; Score 174; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
| | | | | | | | | | | | | | | | | | | | | |
Db 2 NLRAIEAQOHLQLTWGIIKQLQARILAVERYLKDQ 38
| | | | | | | | | | | | | | | | | | | | | |

Search completed: June 2, 2004, 12:29:25
Job time : 34.0842 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 45.0978 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-180
Sequence: 1 LRLRAIRAOQHLLQLTWQIKQLQARILAVERYIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	36	3	AAAB14738
2	175	100.0	36	4	AAAB55003
3	175	100.0	37	3	AAAB14739
4	175	100.0	37	4	AAAB55004
5	175	100.0	38	2	AAAB98408
6	175	100.0	38	4	AAAB54785
7	175	100.0	38	4	AAAB55005
8	175	100.0	38	4	AAAB54970
9	175	100.0	38	4	AAAB92244
10	175	100.0	38	4	AAAB14011
11	175	100.0	38	5	AAAB18771
12	171	97.7	35	3	AAAB14737
13	171	97.7	35	4	AAAB55002
14	170	97.1	37	4	AAAB14705
15	170	97.1	37	4	AAAB54969
16	168	96.0	36	3	AAAB52784
17	168	96.0	37	3	AAAB52785
18	168	96.0	38	2	AAAB55635
19	168	96.0	38	2	AAAB55636
20	168	96.0	38	2	AAAB47216
21	168	96.0	38	2	AAAB27614
22	168	96.0	38	3	AAAB86666
23	168	96.0	38	3	AAAB8730
24	168	96.0	38	3	AAAB8731
25	168	96.0	38	3	AAAB89145

26	168	96.0	38	3	AAAB99146	AAAB99146 Core poly
27	168	96.0	38	3	AAAB99243	AAAB99243 Core poly
28	168	96.0	38	3	AAAB14530	AAAB14530 HIV-1 iso
29	168	96.0	38	3	AAAB52824	AAAB52824 T21/DP107
30	168	96.0	38	3	AAAB52786	AAAB52786 T21/DP107
31	168	96.0	38	3	AAAB52823	AAAB52823 T21/DP107
32	168	96.0	38	4	AAAB63858	AAAB63858 Amino ac1
33	168	96.0	38	4	AAAB92349	AAAB92349 Virus rel
34	168	96.0	38	4	AAAB77021	AAAB77021 Core poly
35	168	96.0	38	4	AAAB77085	AAAB77085 Core poly
36	168	96.0	38	4	AAAB77086	AAAB77086 Core poly
37	168	96.0	38	4	AAAB7596	AAAB7596 Core poly
38	168	96.0	38	4	AAAB77851	AAAB77851 Core poly
39	168	96.0	38	4	AAAB77650	AAAB77650 Core poly
40	168	96.0	38	4	AAAB77500	AAAB77500 Core poly
41	168	96.0	38	4	AAAB77624	AAAB77624 Core poly
42	168	96.0	38	4	AAAB70185	AAAB70185 HIV viral
43	168	96.0	38	4	AAAB70184	AAAB70184 HIV viral
44	168	96.0	38	4	AAAB85690	AAAB85690 DP107 pep
45	168	96.0	38	4	AAAB01489	AAAB01489 Viral cor
46	168	96.0	38	4	AAAB00505	AAAB00505 Viral DP1
47	168	96.0	38	4	AAAB00656	AAAB00656 Viral DP1
48	168	96.0	38	4	AAAB00090	AAAB00090 Viral DP1
49	168	96.0	38	4	AAAB02077	AAAB02077 Viral cor
50	168	96.0	38	4	AAAB00025	AAAB00025 HIV-1 gp4
51	168	96.0	38	4	AAAB02133	AAAB02133 Viral cor
52	168	96.0	38	4	AAAB00089	AAAB00089 Viral DP1
53	168	96.0	38	4	AAAB00655	AAAB00655 Viral DP1
54	168	96.0	38	4	AAAB00504	AAAB00504 Viral DP1
55	168	96.0	38	4	AAAB00629	AAAB00629 Viral DP1
56	168	96.0	38	4	AAAB00601	AAAB00601 RSV Fl pr
57	168	96.0	38	4	AAAB01980	AAAB01980 Viral cor
58	168	96.0	38	4	AAAB02132	AAAB02132 Viral cor
59	168	96.0	38	4	AAAB12638	AAAB12638 DP178-11k
60	168	96.0	38	4	AAAB13203	AAAB13203 DP178-11k
61	168	96.0	38	4	AAAB13053	AAAB13053 DP178-11k
62	168	96.0	38	4	AAAB13149	AAAB13149 DP178-11k
63	168	96.0	38	4	AAAB13204	AAAB13204 DP178-11k
64	168	96.0	38	4	AAAB12574	AAAB12574 DP178-11k
65	168	96.0	38	4	AAAB12639	AAAB12639 DP178-11k
66	168	96.0	38	4	AAAB82962	AAAB82962 Anti-HIV
67	168	96.0	38	4	AAAB82962	AAAB82962 Anti-HIV
68	168	96.0	38	5	AAAB22292	AAAB22292 gp41 fusi
69	168	96.0	38	5	AAAB20152	AAAB20152 Hybrid po
70	168	96.0	38	5	AAAB20297	AAAB20297 Hybrid po
71	168	96.0	38	5	AAAB20153	AAAB20153 Hybrid po
72	168	96.0	38	5	AAAB20150	AAAB20150 Hybrid po
73	168	96.0	38	6	AAAB75976	AAAB75976 HIV-1 gp4
74	168	96.0	38	6	AAAB09553	AAAB09553 Peptide f
75	168	96.0	38	6	AAAB010245	AAAB010245 HIV-1 gp
76	168	96.0	38	7	AAAB92756	AAAB92756 DP-107 an
77	168	96.0	38	7	AAAB73011	AAAB73011 HIV gp41
78	168	96.0	41	2	AAAB52840	AAAB52840 DP-125 -
79	168	96.0	41	2	AAAB98406	AAAB98406 Peptide D
80	168	96.0	41	2	AAAB17019	AAAB17019 DP-178-11
81	168	96.0	41	2	AAAB27616	AAAB27616 Human imm
82	168	96.0	41	2	AAAB27622	AAAB27622 Human imm
83	168	96.0	41	3	AAAB89779	AAAB89779 Core poly
84	168	96.0	41	3	AAAB99240	AAAB99240 Core poly
85	168	96.0	41	3	AAAB89134	AAAB89134 Core poly
86	168	96.0	41	4	AAAB54791	AAAB54791 HIV anti
87	168	96.0	41	4	AAAB92250	AAAB92250 Virus rel
88	168	96.0	41	4	AAAB77593	AAAB77593 Core poly
89	168	96.0	41	4	AAAB78180	AAAB78180 Core poly
90	168	96.0	41	4	AAAB77489	AAAB77489 Core poly

ALIGNMENTS

RESULT 1
ID AAAB14738 standard; peptide; 36 AA.

AC ABA14738;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #67.
XX
KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX isolate LAI.
XX
XS Human immunodeficiency virus 1.
XX
FN WO20040616-A1.
PD
PD 13-JUL-2000.
PF
PF 10-JAN-2000; 2000WO-US000456.
PR
PR 08-JAN-1999; 99US-011540A.P.
PR 07-JAN-2000; 2000US-00480336.
XX
PA (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
PI Wild CT, Weiss CD;
DR WPI; 2000-465959/40.
PT Raising neutralising antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
PS Disclosure; Page 38; 97pp; English.

Sequence ABA14672-B14739 represent peptides derived from the N-helical domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B, isolate LAI. The invention relates to raising a neutralising antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of gp41 which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond to mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-helical segment), or the gp41 core 6-helix bundle, which is formed by the interaction of the N- and C-helical domains of three gp41 proteins. The peptides can be administered either singly or as a combination (particularly a combination of N-helical and C-helical peptides), and can be multimerised. For example, N- and C-helical domain peptides can be alternately linked together to form a peptide which mimics the core 6-helix bundle. Administration of the peptide(s) generates a humoral response, with the production of antibodies against gp41 structures involved in viral entry. As these portions of gp41 are well conserved, such antibodies may be effective against a broad range of HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 36 AA;

Peptide	Sequence	Score
QY	1 LRLRAEAOQHLLQTLVWQIKQLQARILAEVRYLKQ	36
Db	1 LRLRAEAOQHLLQTLVWQIKQLQARILAEVRYLKQ	36
RESULT 2		
AB55003	standard; peptide; 36 AA.	
ID		

RESULT 2

ID AAB55003 standard; peptide; 36 AA.

AC AAB55003 ;

DT 11-SEP-2003 (revised)

DE Anti-HIV peptide DP107 amino truncation peptide #33.

KM Long lasting fusion peptide inhibitor; viral infection; antiviral.
KM antileukemic; mobile blood component; measles virus; MeV; SiV.
KM simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV.
KM human respiratory syncytial virus; human immunodeficiency virus; HIV

OS Human immunodeficiency virus 1.

PN WO200069902-A1.

PD 23-NOV-2000

PF 17-MAY-2000; 2000WO-US013651.

PR	17-MAY-1999;	99US-0134406P.
DE	10-SEP-1999;	99US-0153406P.

XX
XX
(COVT \ CONTICHEM TNC

XX		
DT	Diferencia PD	Boudieljah N Pchitaillo M Milner PG:
DD		

DR WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino

PT human immunodeficiency virus.

PS Disclosure; Page 139; 211pp; English.

The present invention describes a modified anti-viral peptide (I) comprising a peptide that exhibits anti-viral activity and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds. (I) has anti-viral and anti-fusogenic activities. (I) inhibits viral infection of cells by inhibiting cell-cell fusion or free virus infection or to reduce the level of membrane fusion events between two or more entities, e.g., virus-cell or cell-cell, relative to the level of membrane fusion that occurs in the absence of the peptide. (I) is useful in the treatment of patients who are suffering from viral infection, e.g. HIV, RSV, HPV, MeV, and SIV. (I) may be administered prophylactically to previously uninfected individuals. This is useful in cases where an individual has been subjected to a high risk of exposure to a virus. By bonding of long-lived components of the blood, such as immunoglobulin, serum albumin, red blood cells and platelets the activity is extended for days to weeks. This is due to improved stability in vivo and a reduced susceptibility to proteolysis or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 to AAB55431 represent peptides used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match	100.0%	Score 175;	DB 4:	Length 36;
Best Local Similarity	100.0%	Pred. No. 9, 1e-16;		
Matches 36; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 LRAIEAQHLLQTVWQIKQLOARILAVERYLKDQ 36

DB 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 36

RESULT 3
AAB14739
XX AAB14739 standard; peptide; 37 AA.
XX
AC AAB14739;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
XX
DE HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX isolate LAI.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200040616-A1.
XX
PD 13-JUL-2000.
XX
XX 10-JAN-2000; 2000MO-US000456.
XX
PR 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
XX Wild CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
PT Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX Disclosure; Page 38; 97pp; English.

XX SQ Sequence 37 AA;
XX
XX Query Match 100.0%; Score 175; DB 3; Length 37;
XX Best Local Similarity 100.0%; Pred No. 9,3e-16;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 36
DB 2 LRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 4
ID AAB55004
XX AAB55004 standard; peptide; 37 AA.
XX
AC AAB55004;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 amino truncation peptide #34.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antitumorigenic; mobile blood component; measles virus; MeV; SiV;
XX simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Disclosure; Page 139; 211pp; English.

SQ Sequence 37 AA:

Query Match 100.0%; Score 175; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 9.3e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 36
 DB 2 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 37

RESULT 5

AAR98408
 ID AAR98408 standard; peptide; 38 AA.

XX AAR98408;

XX 16-OCT-2003 (revised)
 DT 17-FEB-1997 (first entry)

XX DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX WO9619495-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-US016733.

XX 20-DEC-1994; 94US-00360107.
 PR 06-JUN-1995; 95US-00470896.

XX (UYDU-) UNIV DUKE.
 PA (TRIM-) TRIMERIS INC.

PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
 PI Pecteway SR, Langlois AJ;

XX WPI; 1996-309517/31.

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence
 PT search motif.

XX Disclosure; Page 30; 471pp; English.

XX The sequences given in AAR98398-408 represent peptides which exhibit
 CC antifusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALLMOTIS, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 38 AA:

Query Match 100.0%; Score 175; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 36
 DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 6

AAB54785
 ID AAB54785 standard; peptide; 38 AA.

XX AAB54785;

XX 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)

XX HIV antiviral activity exhibiting peptide SEQ ID NO:2.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus 1.

XX WO200069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013651.

XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.

PA (CONU-) CONUCHEM INC.

PI Bridon DF, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.

XX Claim 6; Page 173; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB5431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 38 AA:

Query Match 100.0%; Score 175; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 36
 DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 7

AAB55005
 ID AAB55005 standard; peptide; 38 AA.

AC AAB55005;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #35.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 OS WO200069902-A1.
 PN
 XX
 XX 23-NOV-2000.
 PD
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONT-) CONJUCHEM INC.
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX WPI; 2001-007496/01.
 DR
 XX
 PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 38 AA:
 XX
 QY Query Match 100.0%; Score 175; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LRAIAEQHLLQTLTWQIKOLQARITLAVERYLKQ 36
 3 LRAIAEQHLLQTLTWQIKOLQARITLAVERYLKQ 38
 RESULT 8
 ID AAB54970 standard; peptide; 38 AA.
 XX
 AC AAB54970;
 XX

XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #35.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 OS WO200069902-A1.
 PN
 XX
 XX 23-NOV-2000.
 PD
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONT-) CONJUCHEM INC.
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX WPI; 2001-007496/01.
 DR
 XX
 PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 137; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 38 AA:
 XX
 QY Query Match 100.0%; Score 175; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LRAIAEQHLLQTLTWQIKOLQARITLAVERYLKQ 36
 3 LRAIAEQHLLQTLTWQIKOLQARITLAVERYLKQ 38
 RESULT 9
 ID AAB92244 standard; peptide; 38 AA.
 XX
 AC AAB92244;
 XX


```

KW gp41.
XX
OS Human immunodeficiency virus.
XX
XX WO200256902-A2.
XX
PD 25-UTL-2002.
XX
XX 17-DEC-2001; 2001WO-US048802.
XX
PR 19-DEC-2000; 2000US-0256657P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Baroudy BM;
XX
XX WPI; 2002-636513/68.
XX
PT Treatment of HIV infection in an individual involves administration of a
PT combination of chemokine co-receptor five antagonist and a specified HIV
PT envelope polypeptide.
XX
PS Disclosure; Page 34; 52pp; English.
XX
XX The present invention relates to a method of treating an HIV infection in
XX an individual, which involves administering in combination a chemokine co-
XX receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
XX derivative. Other viral infections can also be treated using the method.
XX The present sequence is a peptide derived from HIV and useful in the
XX method of the invention
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 175; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 9, 6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LRAIEAQOHLQLTWQIKQARILAVERYLKDQ 36
3 LRAIEAQOHLQLTWQIKQARILAVERYLKDQ 38
Db
RESULT 12
AAB14737
ID AAB14737 standard; peptide; 35 AA.
XX
AC AAB14737;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #66.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
XX isolate LAI.
XX
XX Human immunodeficiency virus 1.
XX
XX OS
XX
XX PN WO200040616-A1.
XX
PD 13-UTL-2000.
XX
PF 10-JAN-2000; 2000WO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
XX
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
XX
XX (WEIS/) WEIS C D.
XX

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PI Wild CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
XX comprises administering a polypeptide capable of forming a stable coiled-
XX coil solution structure.
XX
PS Disclosure; Page 38; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
XX domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
XX isolate LAI. The invention relates to raising a neutralizing antibody
XX response to a broad spectrum of HIV (human immunodeficiency virus)
XX strains and isolates, comprising the administration of a peptide which
XX corresponds to or mimics highly conserved portions of gp41 which are
XX important in mediating the process of viral entry into host cells. Such
XX peptides can correspond to or mimic the coiled coil solution structure of
XX the N-helical domain (the heptad repeat region), or can correspond or
XX mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
XX helical segment), or the gp41 core 6-helix bundle, which is formed by the
XX interaction of the N- and C-helical domains of three gp41 proteins. The
XX peptides can be administered either singly or as a combination
XX (particularly a combination of N-helical and C-helical peptides), and can
XX be multimerised. For example, N- and C-helical domain peptides can be
XX alternately linked together to form a peptide which mimics the core 6-
XX helix bundle. Administration of the peptide(s) generates a humoral
XX response, with the production of antibodies against gp41 structures
XX involved in viral entry. As these portions of gp41 are well conserved,
XX such antibodies may be effective against a broad range of HIV strains and
XX isolates. The peptide compositions may be administered as a prophylactic
XX or therapeutic vaccine to generate antibodies which reduce or inhibit the
XX ability of HIV to infect uninfected cells. A composition comprising
XX polyclonal or monoclonal antibodies can be administered to reduce HIV
XX infection of uninfected cells. Antibodies raised against entry-relevant
XX gp41 structures may also be used therapeutically and as tools to further
XX elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
SQ Sequence 35 AA;
XX
Query Match 97.7%; Score 171; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2, 9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 LRAIEAQOHLQLTWQIKQARILAVERYLKDQ 36
1 LRAIEAQOHLQLTWQIKQARILAVERYLKDQ 35
Db
RESULT 13
AAB55002
ID AAB55002 standard; peptide; 35 AA.
XX
AC AAB55002;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 amino truncation peptide #32.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX OS
XX
XX PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX

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XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 PI WPI; 2001-007496/01.
 XX
 DR A modified peptide and a reactive group which is reactive with amino
 XX PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,
 CC MEV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 35 AA;
 Query Match 97.7%; Score 171; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
 Db 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35
 RESULT 14
 AAB14705
 ID AAB14705 standard; peptide; 37 AA.
 XX
 AC AAB14705;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
 XX
 KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KW isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN MO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.

XX 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 XX (WILD/) WILD C.T.
 PA (WEISS/) WEISS C.D.
 XX
 PI Wild CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Disclosure; Page 36; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralising antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 37 AA;
 Query Match 97.1%; Score 170; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 4.2e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKD 35
 Db 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKD 37
 RESULT 15
 AAB54969
 ID AAB54969 standard; peptide; 37 AA.
 XX
 AC AAB54969;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
 XX
 KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KW anti-fusogenic; mobile blood component; measles virus; MEV; SIV;
 KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX

OS Human immunodeficiency virus 1.
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONT.) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX Disclosure; Page 137; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MeV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptide. AAB54784 to
XX AAB54531 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 37 AA:
SO
Query Match 97.1%; Score 170; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKD 35
Db 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKD 37
RESULT 16
AAB52784
ID AAB52784 standard; peptide; 36 AA.
XX
XX AAB52784;
XX
XX 12-SEP-2003 (revised)
XX 23-FEB-2001 (first entry)
XX
XX T21/DPI07 peptide fragment #66.
XX
XX Antinflammatory; T21/DPI07; gp41 ectodomain; HIV-1 fusion;
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;
XX chemottractant.
XX
XX Human immunodeficiency virus 1.
XX

PN WO200066622-A1.
XX
XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang JM, Oppenheim JU, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
XX partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor antagonist
XX is used to modulate inflammation.
XX
XX Claim 12; Page 29; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DPI07. T21/DPI07 is a
XX helical segment of the ectodomain of HIV-1 protein gp41. T21/DPI07 is
XX located in the amino terminus of the gp41 ectodomain. gp41 plays a
XX critical role in the fusion of HIV-1 and host cell membranes. T21/DPI07
XX interacts with members of the formyl peptide receptor (FPR) family and
XX thereby up-regulates an inflammatory response, and acts as a potent
XX chemottractant and activator of human peripheral blood phagocytes (but
XX not T cells). The present peptide can be used to modulate an inflammatory
XX response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 36 AA:
SQ
Query Match 96.0%; Score 168; DB 3; Length 36;
Best Local Similarity 97.2%; Pred. No. 7.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
RESULT 17
AAB52785
ID AAB52785 standard; peptide; 37 AA.
XX
XX AAB52785;
XX
XX 12-SEP-2003 (revised)
XX 23-FEB-2001 (first entry)
XX
XX T21/DPI07 peptide fragment #67.
XX
XX Antinflammatory; T21/DPI07; gp41 ectodomain; HIV-1 fusion;
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;
XX chemottractant.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200066622-A1.
XX
XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang JM, Oppenheim JU, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
XX

PT	partial length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT	is used to modulate inflammation.
XX	
XX	
PS	Claim 12; Page 29; 148pp; English.
XX	
CC	The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC	helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC	located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC	critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemottractant and activator of human peripheral blood phagocytes (but
CC	not T cells). The present peptide can be used to modulate an inflammatory
CC	response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 37 AA;
Qy	
Db	1 LLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQD 36 2 LLRAIEAQOHLLQLTWQIGIKQLQARILAVERYLKQD 37
RESULT 18	
ID	AAR55635
XX	AAR55635 standard; peptide; 38 AA.
AC	AAR55635;
XX	
DT	25-MAR-2003 (revised)
DT	25-JUL-1994 (first entry)
XX	
DE	DP-139 - DP-107 analogue.
XX	
KW	Leucine zipper; HIV-1; human immunodeficiency virus;
KM	transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM	antiviral; gp41.
XX	
OS	Synthetic.
XX	
FN	W09402505-A1.
XX	
PD	03-FEB-1994.
XX	
PF	19-JUL-1993; 93WO-US006769.
XX	
PR	20-JUL-1992; 92US-00916540.
PR	07-AUG-1992; 92US-00927532.
XX	
PA	(UYDU-) UNIV DUKE.
XX	
PI	Wild CT, Matthews TJ, Bolognesi DP;
XX	
DR	WPI; 1994-048790/06.
PT	New peptides corresponding to HIV transmembrane protein - used for
PT	inhibiting infection of cells by an enveloped virus, partic. for
PT	inhibiting HIV-induced cell fusion.
PS	
PS	Disclosure; Page 25; 38pp; English.
XX	
CC	Peptide DP-107 (AAR7216); a peptide comprising 14-60 amino acids capable
CC	of forming a heterodimer with DP-107; or a multimer of these peptides can
CC	be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC	fusion. DP-107 is based on a highly conserved region in the transmembrane
CC	protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC	amphipathic alpha-helix with structural analogues in the TM proteins of
CC	several fusogenic viruses. Other peptides studied and DP-107 analogues
CC	are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC	correct PN field.)

[illegible]

XX ID AAR47216 standard; peptide; 38 AA.
XX AC AAR47216;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 25-JUL-1994 (first entry)
XX DE DP-107 - HIV-1 TM protein (558-595).
XX XX
XX KM leucine zipper; HIV-1; human immunodeficiency virus;
XX KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
XX KM antiviral; gp41.
XX OS Synthetic.
XX XX
XX FH Key location/Qualifiers
XX FT Misc-difference 12 /note= "residue 12 of the sequence in Fig 1 is H; residue
XX FT 12 of the sequence in Table 4 is G"
XX PN MO9402505-A1.
XX PD 03-FEB-1994.
XX PF 19-JUL-1993; 93WO-US006769.
XX XX
XX PR 20-JUL-1992; 92US-00916540.
XX PR 07-AUG-1992; 92US-00927532.
XX PA (UYDU-) UNIV DUKE.
XX XX
XX PI Wild CT, Matthews TJ, Bolognesi DP;
XX XX WPI; 1994-048790/06.
XX DR
XX XX
XX PT New peptides corresponding to HIV transmembrane protein - used for
XX PT inhibiting infection of cells by an enveloped virus, partic. for
XX PT inhibiting HIV-induced cell fusion.
XX XX
XX PS Claim 1; Page 27; 38pp; English.
XX CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
XX CC of forming a heterodimer with DP-107; or a multimer of these peptides can
XX CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
XX CC fusion. DP-107 is based on a highly conserved region in the transmembrane
XX CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
XX CC amphipathic alpha-helix with structural analogues in the TM proteins of
XX CC several fusogenic viruses. Other peptides studied and DP-107 analogues
XX CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX XX
XX SQ Sequence 38 AA;
XX
XX Query Match 96.0%; Score 168; DB 2; Length 38;
XX Best Local Similarity 97.2%; Pred. No. 7.9e-15;
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LRAIEAQOHLQLTWGIKQIARILAVERYIKDQ 36
XX 3 LRAIEAQOHLQLTWGIKQIARILAVERYIKDQ 38
XX DB
XX
XX RESULT 21
XX AAR27614
XX ID AAR27614 standard; peptide; 38 AA.
XX AC AAR27614;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 22-DEC-1997 (first entry)
XX XX
XX DE Human immunodeficiency virus gp41 derived peptide DP-107.
XX XX

XX KM Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
XX KM inhibition; induction; cell fusion; transmission; type 1.
XX OS Human immunodeficiency virus.
XX PN US5656480-A.
XX PD 12-AUG-1997.
XX PF 27-JAN-1995; 95US-00374666.
XX XX
XX PR 20-JUL-1992; 92US-00916540.
XX PR 07-AUG-1992; 92US-00927532.
XX PR 19-JUL-1993; 93WO-US006769.
XX XX
XX PA (UYDU-) UNIV DUKE.
XX XX
XX PI Bolognesi DP, Wild CT, Matthews TJ;
XX XX WPI; 1997-414595/38.
XX DR
XX XX
XX PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
XX PT syncytia formation and transmission.
XX PS Claim 1; Col 13-14; 18pp; English.
XX XX
XX CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein
XX CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
XX CC cell fusion in a culture and cell free HIV transmission in a culture to a
XX CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
XX CC MAR-2003 to correct PF field.)
XX XX
XX SQ Sequence 38 AA;
XX
XX Query Match 96.0%; Score 168; DB 2; Length 38;
XX Best Local Similarity 97.2%; Pred. No. 7.9e-15;
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LRAIEAQOHLQLTWGIKQIARILAVERYIKDQ 36
XX 3 LRAIEAQOHLQLTWGIKQIARILAVERYIKDQ 38
XX DB
XX
XX RESULT 22
XX AAY88666
XX ID AAY88666 standard; peptide; 38 AA.
XX AC AAY88666;
XX XX
XX DT 23-MAY-2000 (first entry)
XX XX
XX DE Core polypeptide fragment T No. 21.
XX XX
XX KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX KM anti-fusogenic; differentiation factor; interleukin; interferon;
XX KM colony stimulating factor; hormone; angiogenic factor.
XX XX
XX OS Unidentified.
XX PN WO9959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PR 20-MAY-1998; 98US-00082279.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX XX WPI; 2000-136792/12.
XX DR

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
XX Disclosure; Page 21, 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 1 LRAIEAQQHLQLTWQIKQLQARILAVERYLKDQ 36
3 LRAIEAQQHLQLTWQIKQLQARILAVERYLKDQ 38
Db
RESULT 23
AAY86730 standard; peptide; 38 AA.
XX
AC AAY86730;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 85.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX PN W09959615-A1.
XX
XX PD 25-NOV-1999.
XX
XX PF 20-MAY-1999; 99WO-US011219.
XX
XX PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX PI Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22, 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 1 LRAIEAQQHLQLTWQIKQLQARILAVERYLKDQ 36
3 LRAIEAQQHLQLTWQIKQLQARILAVERYLKDQ 38
Db
RESULT 24
AAY86731
ID AAY86731 standard; peptide; 38 AA.
XX
AC AAY86731;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 86.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX PN W09959615-A1.
XX
XX PD 25-NOV-1999.
XX
XX PF 20-MAY-1999; 99WO-US011219.
XX
XX PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX PI Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22, 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral

infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AA188651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides

[illegible]

	Query Match	96.0%;	Score 168;	DB 3;	Length 38;
	Best Local Similarity	Pred. 97.2%;	Pred. No. 7.9e-15;		
	Matches	Conservative 35;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LRAIEAOQHLLQLTWQIKOLQAIIIVAVERTLKQO	36		
Db	3	LRAIEAOQHLLQLTWQIGIKOLAIIIVAVERTLKQO	38		

RESULT 26	
AA89146	
ID	AA89146 standard; peptide; 38 AA.
XX	
AC	AA89146;
XX	
DT	23-MAY-2000 (first entry)

RESULT 25	
AAV89145	
ID	AAV89145 standard; peptide; 38 AA.
XX	
AC	AAV89145;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	Core polypeptide fragment T No. 583.

XX	
KX	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1
KW	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM	anti-fusogenic; differentiation factor; interleukin; interferon;
KW	colony stimulating factor; hormone; angiogenic factor.
XX	
OS	Unidentified.
XX	
FN	M09J95615-A1.

SQ	Sequence 38 AA;	
Query Match	96.0%	Score 168; DB 3; Length 38;
Best Local Similarity	97.2%;	Pred. No. 7.9e-15;

RESULT 27
AA189243

```

ID AAY89243 standard; peptide: 38 AA.
XX
XX AAY89243;
XX
DT 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 681.
DE
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
OS
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 32; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAY88651-Y90055 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
XX Sequence 38 AA;
SQ
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
RESULT 28
AAB14530
XX AAB14530 standard; peptide: 38 AA.
XX
XX AAB14530;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).
XX

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XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
XX
XX 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
XX (WEIS/) WEISS C D.
XX
XX Wild CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
XX comprises administering a polypeptide capable of forming a stable coiled-
XX coil solution structure.
XX
XX Claim 5; Page 56; 97pp; English.
XX
XX Sequences AAB14529-B14531 and AAB14537-B14568 represent specifically
XX claimed peptides derived from the N-helical domain of the gp41 envelope
XX glycoprotein from a variety of HIV-1 isolates. The invention relates to
XX raising a neutralizing antibody response to a broad spectrum of HIV
XX (human immunodeficiency virus) strains and isolates, comprising the
XX administration of a peptide which corresponds to or mimics highly
XX conserved portions of gp41 which are important in mediating the process
XX of viral entry into host cells. Such peptides can correspond to or mimic
XX the coiled coil solution structure of the N-helical domain (the heptad
XX repeat region), or can correspond or mimic the C-helical domain (the
XX transmembrane-proximal amphipathic alpha-helical segment), or the gp41
XX core 6-helix bundle, which is formed by the interaction of the N- and C-
XX helical domains of three gp41 proteins. The peptides can be administered
XX either singly or as a combination (particularly a combination of N-
XX helical and C-helical peptides), and can be multimerised. For example, N-
XX and C-helical domain peptides can be alternately linked together to form
XX a peptide which mimics the core 6-helix bundle. Administration of the
XX peptide(s) generates a humoral response, with the production of
XX antibodies against gp41 structures involved in viral entry. As these
XX portions of gp41 are well conserved, such antibodies may be effective
XX against a broad range of HIV strains and isolates. The peptide
XX compositions may be administered as a prophylactic or therapeutic vaccine
XX to generate antibodies which reduce or inhibit the ability of HIV to
XX infect uninfected cells. A composition comprising polyclonal or
XX monoclonal antibodies can be administered to reduce HIV infection of
XX uninfected cells. Antibodies raised against entry-relevant gp41
XX structures may also be used therapeutically and as tools to further
XX elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 38 AA;
SQ
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
RESULT 29
AAB52824
XX AAB52824 standard; peptide: 38 AA.
XX

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XX AC AAB52824;
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX DE T21/DP107 peptide fragment #101.
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX OS Human immunodeficiency virus 1.
XX PN WO200066622-A1.
XX PD 09-NOV-2000.
XX PF 05-MAY-2000; 2000WO-US012371.
XX PR 05-MAY-1999; 99US-0132686P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX PS Disclosure; Page 28; 148pp; English.
XX CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX SQ
SQ Sequence 38 AA;
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 36
Db 3 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 38
RESULT 30
AAB52786
ID AAB52786 standard; peptide; 38 AA.
XX AC AAB52786;
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX DE T21/DP107 peptide fragment #68.
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX OS Human immunodeficiency virus 1.
XX PN WO200066622-A1.

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XX PD 09-NOV-2000.
XX PF 05-MAY-2000; 2000WO-US012371.
XX PR 05-MAY-1999; 99US-0132686P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX PS Claim 12; Page 29; 148pp; English.
XX CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX SQ
SQ Sequence 38 AA;
Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 7.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 36
Db 3 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 38

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Search completed: June 2, 2004, 11:41:44
 Job time : 45.0978 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 9.78261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336A-180
Perfect score: 175
Sequence: 1 LRAIRAQOHLQLFTWQIKQLQARILAVERYIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	168	96.0	357	2	envelope protein g
2	168	96.0	851	2	env polypotein -
3	168	96.0	853	2	envelope polypote
4	168	96.0	854	2	env protein - huma
5	168	96.0	855	1	env polypotein pr
6	168	96.0	856	1	env polypotein pr
7	168	96.0	856	1	env polypotein pr
8	168	96.0	861	1	env polypotein pr
9	167	95.4	357	2	envelope protein g
10	167	95.4	357	2	envelope protein g
11	167	95.4	357	2	envelope protein g
12	167	95.4	358	2	envelope protein g
13	167	95.4	358	2	envelope protein g
14	167	95.4	358	2	envelope protein g
15	165	94.3	357	2	envelope protein g
16	165	94.3	357	2	envelope protein g
17	165	94.3	357	2	envelope protein g
18	164	93.7	859	1	env polypotein pr
19	164	93.7	445	2	env polypotein p
20	164	93.7	454	2	env polypotein M
21	164	93.7	729	1	env polypotein D
22	164	93.7	843	1	env polypotein pr
23	164	93.7	846	1	env polypotein pr
24	164	93.7	852	1	envelope glycoprot
25	164	93.7	855	1	env polypotein pr
26	164	93.7	856	1	env polypotein pr
27	164	93.7	861	1	env polypotein pr
28	164	93.7	861	1	env polypotein pr
29	164	93.7	861	1	env polypotein pr

30	164	93.7	868	1	VCLJH4	env polypotein -
31	163	93.1	859	2	T01672	envelope polypote
32	160	91.4	358	2	S21998	envelope protein g
33	156	89.1	852	1	VCLJBR	env polypotein -
34	153	87.4	854	1	VCLJST	env polypotein pr
35	150	85.7	847	2	T09448	envelope glycoprot
36	150	85.7	847	2	S13289	env protein - huma
37	120	68.6	104	2	S52930	GP41 ENV protein -
38	119	68.0	864	1	VCLJG4	env polypotein -
39	119	68.0	877	2	C46356	env polypotein -
40	117	66.9	877	2	S49197	envelope protein p
41	115	65.7	366	2	B41565	env polypotein -
42	114	65.1	732	2	S46352	env polypotein -
43	113	64.6	712	1	VCLJG4	env polypotein pr
44	113	64.6	851	2	S12159	env protein - huma
45	113	64.6	852	1	VCLJG2	env polypotein pr
46	113	64.6	859	1	VCLJST	env polypotein pr
47	113	64.6	869	1	S53098	envelope polypote
48	112	64.0	859	1	VCLJCT	env polypotein pr
49	111	63.4	855	2	A45713	env transmembrane
50	111	63.4	858	1	VCLJG2	env polypotein pr
51	111	63.4	881	2	S03068	env protein - huma
52	111	63.4	885	2	S04322	env polypotein -
53	111	63.4	886	2	T11555	env protein - simi
54	110	62.9	881	1	VCLJG3	env protein - huma
55	109	62.3	859	2	S24571	env protein - huma
56	109	62.3	869	2	A53034	env polypotein -
57	109	62.3	869	2	A47665	env protein gpi20 (
58	108	61.7	880	1	VCLJG2	env polypotein pr
59	107	61.1	151	2	S30458	env protein - huma
60	107	61.1	786	2	S28084	env polypotein -
61	107	61.1	889	1	VCLJG5	env polypotein -
62	106	60.6	887	2	T11566	envelope glycoprot
63	105	60.0	151	2	S30448	env protein - huma
64	105	60.0	151	2	S30453	env protein - huma
65	105	60.0	151	2	S30452	env protein - huma
66	105	60.0	151	2	S30450	env protein - huma
67	105	60.0	151	2	S30451	env protein - huma
68	103	58.9	151	2	S30459	env protein - huma
69	103	58.9	151	2	S30457	env protein - huma
70	103	58.9	151	2	S30456	env protein - huma
71	103	58.9	151	2	S30455	env protein - huma
72	103	58.9	151	2	S30454	env protein - huma
73	85	48.6	68	2	S60695	env protein - huma
74	85	48.6	68	2	S60693	env protein - huma
75	85	48.6	68	2	S60696	env protein - huma
76	85	48.6	68	2	S60705	env protein - huma
77	85	48.6	68	2	S60707	env protein - huma
78	85	48.6	68	2	S60694	env protein - huma
79	85	48.6	68	2	S60687	env protein - huma
80	85	48.6	69	2	S60706	env protein - huma
81	83	47.4	68	2	S60692	env protein - huma
82	77	44.0	68	2	S60688	env protein - huma
83	74	42.3	69	2	S60690	env protein - huma
84	74	42.3	69	2	S60689	env protein - huma
85	74	42.3	69	2	S60691	env protein - huma
86	70	40.0	294	2	S60525	envelope polypote
87	70	40.0	297	2	S60538	envelope polypote
88	69	39.4	372	2	S46344	env polypotein -
89	69	39.4	375	2	S46345	env polypotein -
90	66	37.7	294	2	S60545	envelope polypote

ALIGNMENTS

RESULT 1
S21996
envelope protein gpi20/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1; HIV-1
C:Date: 20-Feb-1995 #Sequence_rev: revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hegenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A/Reference number: S70417; MUID:92144209; PMID:11736940

A/Accession: S70422

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-357 <ST2>

A/Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:g1067129

A/Experimental source: patient 27L

A/Note: submitted to the EMBL Data Library, July 1991

C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 168; DB 2; Length 357;

Best Local Similarity 97.2%; Pred. No. 3.8e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 36
Db 56 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 91

RESULT 2

S33985

env polyprotein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C/Accession: S33985

R/Contributor: F.

Submitted to the EMBL Data Library, November 1991

A/Reference number: S33979

A/Accession: S33985

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-851 <CAR>

A/Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:g60199

C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 168; DB 2; Length 851;

Best Local Similarity 97.2%; Pred. No. 9.9e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 36
Db 550 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 585

RESULT 3

S54384

envelope polyprotein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C/Accession: S54384

R/Contributor: T.; Buckler-White, A.J.

Submitted to the EMBL Data Library, July 1989

A/Reference number: S54377

A/Accession: S54384

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-853 <THB>

A/Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: polyprotein

Query Match 96.0%; Score 168; DB 2; Length 853;

Best Local Similarity 97.2%; Pred. No. 9.9e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 36
Db 552 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 587

RESULT 4

S13288

env protein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C/Accession: S13288

R/O'Brien, W.A.; Koyanagi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A/Reference number: S13288; MUID:91043044; PMID:2172833

A/Accession: S13288

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-854 <OBK>

C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 168; DB 2; Length 854;

Best Local Similarity 97.2%; Pred. No. 9.9e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 36
Db 553 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 588

RESULT 5

VCL2ZR

env polyprotein precursor - human immunodeficiency virus Zr-6

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus Zr-6

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C/Accession: D26192

R/Srinivasan, A.; Anand, R.; Ranganathan, P.; Teorino, P.; Schochetman, G.; Cui

Gene 52, 71-82, 1987

A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleocic

A/Reference number: A26192; MUID:87248097; PMID:3036660

A/Accession: D26192

A/Molecule type: DNA

A/Residues: 1-855 <SRI>

A/Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C/Genetic: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-855/Product: env polyprotein #status predicted <MAT>

F:501-855/Product: exterior membrane glycoprotein #status predicted <EXTR>

F:87,129,140,145,154,158,166,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 96.0%; Score 168; DB 1; Length 855;

Best Local Similarity 97.2%; Pred. No. 1e-14;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 36
Db 554 LRAIEAQQHLLQLTWGIKQLQARILAVERYLKDQ 589

RESULT 6

VCL2H3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C/Accession: A03973

R/Reiner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Sarcich, B.; Josephs, S.F.; Dorar

berger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A/Reference number: A93553; MUID:85111123; PMID:2578615

A/Accession: A03973

A/Molecule type: DNA

A:Residues: 1-856 <RAT>
 A/Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326383; PIDN:AAA442
 C/Genetics:
 A:Gene: env
 C/Superfamily: type B retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:/1-30/Domain: signal sequence #status predicted <SIG>
 F:/31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
 Query Match 96.0%; Score 168; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 1e-14;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 36
 DB 555 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 590

RESULT 7
 VCLJVL
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
 N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C/Accession: A03974
 R/Huesting, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
 Nature 313, 450-458, 1985
 A/Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
 A/Reference number: A93355; MUID:85111157; PMID:2982104
 A/Accession: A03974
 A:Molecule type: DNA
 A:Residues: 1-856 <MOE>
 A/Cross-references: GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559
 C/Genetics:
 A:Gene: env
 C/Superfamily: type B retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:/1-30/Domain: signal sequence #status predicted <SIG>
 F:/31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
 Query Match 96.0%; Score 168; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 1e-14;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 36
 DB 555 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 590

RESULT 8
 VCLJVL
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
 N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C/Accession: A03975
 R/Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
 Cell 40, 9-17, 1985
 A/Title: Nucleotide sequence of the AIDS virus, LAV.
 A/Reference number: A90866; MUID:85099333; PMID:2981635
 A/Accession: A03975
 A:Molecule type: DNA
 A:Residues: 1-861 <NAI>
 A/Cross-references: GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
 C/Genetics:

A:Gene: env
 C/Superfamily: type B retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:/1-30/Domain: signal sequence #status predicted <SIG>
 F:/31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:/517-861/Product: transmembrane glycoprotein #status predicted <TM>
 F:/88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
 F:/516,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
 Query Match 96.0%; Score 168; DB 1; Length 861;
 Best Local Similarity 97.2%; Pred. No. 1e-14;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 36
 DB 560 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 595

RESULT 9
 S22006
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C/Accession: S70420; S22006
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70420
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A/Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
 A:Experimental source: patient L
 A/Note: submitted to the EMBL Data Library, July 1991
 C/Superfamily: type B retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 357;
 Best Local Similarity 94.4%; Pred. No. 5.3e-15;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 36
 DB 56 LRAIAEQHLLQLTWGIKQLQARILAVERYLKQ 91

RESULT 10
 S21994
 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Variety: isolate 27B
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C/Accession: S21994; S70421
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A/Reference number: S21990
 A/Accession: S21994
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A/Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
 A/Reference number: S70417; MUID:92144209; PMID:1736940
 A/Accession: S70421
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <ST2>
 A/Cross-references: EMBL:X61355; NID:G60179
 C/Superfamily: type B retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 357;

Best Local Similarity 94.4%; Pred. No. 5.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 56 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 91

RESULT 11

S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 4B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:g60188
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 5.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 56 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 91

RESULT 12

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:g60186
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 5.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 36
Db 57 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 92

RESULT 13

S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 5.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 57 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 92

RESULT 14

S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.4%; Score 167; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 5.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 57 LRAIEAQOHLQLTWGIKQLQARVLAVERYLKDQ 92

RESULT 15

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Seuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70423
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polyprotein

Query Match 94.3%; Score 165; DB 2; Length 357;
Best Local Similarity 91.7%; Pred. No. 9.8e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 36
Db 56 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 16
S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70424; S21992
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70424
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61358; NID:960177; PIDN:CAA43628.1; PID:960178
A:Experimental source: patient 22
A>Note: Submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 94.3%; Score 165; DB 2; Length 357;
Best Local Similarity 91.7%; Pred. No. 9.8e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 36
Db 56 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 17
VCLJMN
env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: A28922
R;Guirgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, G.
Virology 164, 531-536, 1988
A>Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <GUR>
C:Genetics: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein; gp120; gp41; signal sequence; #status predicted <IG>
F;1-29/Domain: signal sequence #status predicted <IG>
F;30-859/Product: env polyprotein #status predicted <EP>
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.3%; Score 165; DB 1; Length 859;
Best Local Similarity 91.7%; Pred. No. 2.6e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 36
Db 559 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 594

RESULT 18
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
C:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015
A>Note: This virus was isolated from the mother's sexual partner
C:Genetics: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein; gp120; gp41; signal sequence; #status predicted <GP1>
F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;424-443/Domain: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: carboxyl

Query Match 93.7%; Score 164; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 1.7e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 36
Db 295 LRAIEAQOHMLQLTWGIKQLQARVLAVERYLKQ 330

RESULT 19
A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
C:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: A41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: A41621
A:Molecule type: DNA
A:Residues: 1-445 <BUR>
A:Cross-references: GB:M77228; NID:9328627; PIDN:AAB03790.1; PID:9555013
A>Note: This virus was isolated from the mother
C:Genetics: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein; gp120; gp41; signal sequence; #status predicted <GP1>
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/Domain: transmembrane #status predicted <TMN>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site: carboxyl

Query Match 93.7%; Score 164; DB 2; Length 445;
Best Local Similarity 91.7%; Pred. No. 1.7e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

Oy      1  LLRAIEAQOHLLQTLTWQIQKOLQARILAVERYLKDQ 36
      |||||
Db      297 LLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKDQ 332

RESULT 20
env polypeptide D - human immunodeficiency virus type 1 (fragment)
B1621
N:Alternate names: coat polypeptide
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C:Accession: B1621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gull, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A1621; MUID:92107924; PMID:1763038
A:Accession: B1621
A:Molecule type: DNA
A:Residues: 1-454 <BUR>
A:Cross-references: GB:M77279
A:Note: this virus was isolated from the daughter
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:435-454/Domain: transmembrane #status predicted <TMN>
F:9,23,36,42,46,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo

Query March      93.7%; Score 164; DB 2; Length 454;
Beet Local Similarity 91.7%; Pred. No. 1.7e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1  LLRAIEAQOHLLQTLTWQIQKOLQARILAVERYLKDQ 36
      |||||
Db      306 LLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKDQ 341

VCLIMX
env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polypeptide
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-517/Region: hydrophobic #status predicted
F:514-517/Product: coat protein gp120 #status predicted <CP1>
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-554/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-729/Domain: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414,
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

```

[illegible]

F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 93.7%; Score 164; DB 1; Length 846;
Best Local Similarity 91.7%; Pred. No. 3.4e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 36
DB 545 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 580

RESULT 24
T12016

envelope glycoprotein - human immunodeficiency virus type 1 (strain sec14.3)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T12016
R/McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A/Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A/Reference number: Z17379; MUID:98178716; PMID:9519894
A/Accession: T12016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-852 <MCC>
A/Cross-references: EMBL:U90934; NID:G2351783; PIDN:AAC5271.1; PID:G2351784
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein

Query Match 93.7%; Score 164; DB 2; Length 852;
Best Local Similarity 91.7%; Pred. No. 3.5e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 36
DB 551 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 586

RESULT 25
VCLJAJ2

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03976
R/Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-S
Science 227, 484-492, 1985
A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A/Reference number: A04003; MUID:85090453; PMID:2578227
A/Accession: A03976
A/Molecule type: DNA
A/Residues: 1-855 <SAN>
A/Cross-references: GB:K02007; NID:G328658; PIDN:AAB59882.1; PID:G328666
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.7%; Score 164; DB 1; Length 855;
Best Local Similarity 91.7%; Pred. No. 3.5e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 36

DB 554 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 589

RESULT 26
VCLJ3W

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C/Accession: A24774
R/Starch, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986
A/Title: Identification and characterization of conserved and variable regions in the env
A/Reference number: A24774; MUID:86218077; PMID:2423250
A/Accession: A24774
A/Molecule type: DNA
A/Residues: 1-856 <STA>
A/Cross-references: GB:K03455; GB:M38432; NID:G1906382
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <CP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 93.7%; Score 164; DB 1; Length 856;
Best Local Similarity 91.7%; Pred. No. 3.5e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 36
DB 555 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 590

RESULT 27
A44963

env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
N/Alternate names: coat polyprotein
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
C/Accession: A44963
R/Stinvaasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc
A/Reference number: A44963; MUID:89228766; PMID:2713163
A/Accession: A44963
A/Molecule type: DNA
A/Residues: 1-856 <SRI>
A/Cross-references: GB:M15896; NID:G329392; PIDN:AAB53948.1; PID:G329394
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-520/Product: coat protein gp120 #status predicted <GP1>
F:521-856/Product: coat protein gp41 #status predicted <CP2>
F:684-705/Domain: transmembrane #status predicted <TM>
F:87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 93.7%; Score 164; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 3.5e-14;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 36
DB 555 LRAIAEQHLLDTWQIKQLQARILAVERYLKDQ 590

RESULT 28

VCLJKB

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-SP41)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A/Reference number: A42995; MUID:92351552; PMID:1323587

A/Accession: A42995

A/Molecule type: mRNA

A/Residues: 1-861 <SH1>

A/Cross-references: GB:S41266; GB:D01206

C/Genetic:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F/1-689/Domain: extracellular #status predicted <EXT>

F/1-33/Domain: signal sequence #status predicted <SIG>

F/17-33/Region: hydrophobic #status predicted <CP1>

F/34-517/Product: coat protein gp120 #status predicted <CP1>

F/514-517/Region: cleavage processing #status predicted <CP2>

F/518-861/Product: coat protein gp41 #status predicted <CP2>

F/518-534/Region: hydrophobic #status predicted <CP2>

F/690-711/Domain: transmembrane #status predicted <TM1>

F/712-861/Domain: intracellular #status predicted <INT>

F/756-772/Region: hydrophobic #status predicted

F/93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.7%; Score 164; DB 1; Length 861;
 Best Local Similarity 91.7%; Pred. No. 3,5e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 29

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C/Accession: B28922

R/Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta

Virology 164, 531-536, 1988

A/Title: Envelope sequences of two new United States HIV-1 isolates.

A/Reference number: A28922; MUID:88219542; PMID:3369091

A/Accession: B28922

A/Molecule type: DNA

A/Residues: 1-861 <GUR>

C/Genetic:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-861/Product: env polyprotein #status predicted <EP>

F/87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 93.7%; Score 164; DB 1; Length 861;
 Best Local Similarity 91.7%; Pred. No. 3,5e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 30

VCLJHA

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: C25523

R/Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A/Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human i

A/Reference number: A94136; MUID:87041461; PMID:3490666

A/Accession: C25523

A/Molecule type: DNA

A/Residues: 1-868 <DES>

A/Cross-references: GB:M13137; NID:G326460; PIDN:AAA44311.1; PID:G326467

C/Genetic:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F/1-521/Product: coat protein gp120 #status predicted <GP1>

F/522-868/Product: coat protein gp41 #status predicted <GP2>

F/89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match 93.7%; Score 164; DB 1; Length 868;
 Best Local Similarity 94.4%; Pred. No. 3,5e-14;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: June 2, 2004, 11:50:10
 Job time: 10.7826 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 5.86957 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-180
Perfect score: 175
Sequence: 1 LRRAIEAQOHLQLFTWQIKQLARILAAVERLIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	168	96.0	853	1	ENV_HV1EL
2	168	96.0	853	1	ENV_HV1MF
3	168	96.0	853	1	ENV_HV122
4	168	96.0	855	1	ENV_HV126
5	168	96.0	856	1	ENV_HV181
6	168	96.0	856	1	ENV_HV182
7	168	96.0	856	1	ENV_HV183
8	168	96.0	856	1	ENV_HV184
9	168	96.0	856	1	ENV_HV185
10	168	96.0	856	1	ENV_HV186
11	167	95.4	855	1	ENV_HV187
12	167	95.4	855	1	ENV_HV188
13	165	94.3	848	1	ENV_HV189
14	165	94.3	856	1	ENV_HV190
15	164	93.7	843	1	ENV_HV191
16	164	93.7	846	1	ENV_HV192
17	164	93.7	851	1	ENV_HV193
18	164	93.7	852	1	ENV_HV194
19	164	93.7	855	1	ENV_HV195
20	164	93.7	856	1	ENV_HV196
21	164	93.7	856	1	ENV_HV197
22	164	93.7	856	1	ENV_HV198
23	164	93.7	861	1	ENV_HV199
24	164	93.7	865	1	ENV_HV200
25	164	93.7	867	1	ENV_HV201
26	164	93.7	868	1	ENV_HV202
27	163	93.1	847	1	ENV_HV203
28	161	92.0	847	1	ENV_HV204
29	159	90.9	863	1	ENV_HV205
30	156	89.1	852	1	ENV_HV206
31	153	87.4	854	1	ENV_HV207
32	119	68.0	865	1	ENV_HV208
33	119	68.0	877	1	ENV_HV209

34	116	66.3	854	1	ENV_HV210	Q02837 simian immu
35	113	64.6	712	1	ENV_HV211	P32536 human immu
36	113	64.6	851	1	ENV_HV212	P17755 human immu
37	113	64.6	851	1	ENV_HV213	P18040 human immu
38	113	64.6	856	1	ENV_HV214	P05883 human immu
39	113	64.6	859	1	ENV_HV215	P20872 human immu
40	112	64.0	859	1	ENV_HV216	P24105 human immu
41	111	63.4	380	1	ENV_HV217	P08810 simian immu
42	111	63.4	858	1	ENV_HV218	P04577 human immu
43	111	63.4	885	1	ENV_HV219	P12492 simian immu
44	111	63.4	889	1	ENV_HV220	P19503 simian immu
45	110	62.9	768	1	ENV_HV221	P27577 simian immu
46	110	62.9	882	1	ENV_HV222	P05885 simian immu
47	109	62.3	859	1	ENV_HV223	P18531 human immu
48	108	61.7	880	1	ENV_HV224	P11267 simian immu
49	107	61.1	821	1	ENV_HV225	P22380 simian immu
50	107	61.1	846	1	ENV_HV226	P12449 human immu
51	107	61.1	881	1	ENV_HV227	P05884 simian immu
52	106	60.6	857	1	ENV_HV228	P04126 human immu
53	106	60.6	860	1	ENV_HV229	P18094 human immu
54	106	60.6	860	1	ENV_HV230	P27926 rat mus norv
55	105	59.4	2564	1	ENV_HV231	P09254 homo sapien
56	105	59.4	2564	1	ENV_HV232	P09254 homo sapien
57	105	59.4	2564	1	ENV_HV233	P09254 homo sapien
58	105	59.4	2564	1	ENV_HV234	P09254 homo sapien
59	105	59.4	2564	1	ENV_HV235	P09254 homo sapien
60	105	59.4	2564	1	ENV_HV236	P09254 homo sapien
61	105	59.4	2564	1	ENV_HV237	P09254 homo sapien
62	105	59.4	2564	1	ENV_HV238	P09254 homo sapien
63	105	59.4	2564	1	ENV_HV239	P09254 homo sapien
64	105	59.4	2564	1	ENV_HV240	P09254 homo sapien
65	105	59.4	2564	1	ENV_HV241	P09254 homo sapien
66	105	59.4	2564	1	ENV_HV242	P09254 homo sapien
67	105	59.4	2564	1	ENV_HV243	P09254 homo sapien
68	105	59.4	2564	1	ENV_HV244	P09254 homo sapien
69	105	59.4	2564	1	ENV_HV245	P09254 homo sapien
70	105	59.4	2564	1	ENV_HV246	P09254 homo sapien
71	105	59.4	2564	1	ENV_HV247	P09254 homo sapien
72	105	59.4	2564	1	ENV_HV248	P09254 homo sapien
73	105	59.4	2564	1	ENV_HV249	P09254 homo sapien
74	105	59.4	2564	1	ENV_HV250	P09254 homo sapien
75	105	59.4	2564	1	ENV_HV251	P09254 homo sapien
76	105	59.4	2564	1	ENV_HV252	P09254 homo sapien
77	105	59.4	2564	1	ENV_HV253	P09254 homo sapien
78	105	59.4	2564	1	ENV_HV254	P09254 homo sapien
79	105	59.4	2564	1	ENV_HV255	P09254 homo sapien
80	105	59.4	2564	1	ENV_HV256	P09254 homo sapien
81	105	59.4	2564	1	ENV_HV257	P09254 homo sapien
82	105	59.4	2564	1	ENV_HV258	P09254 homo sapien
83	105	59.4	2564	1	ENV_HV259	P09254 homo sapien
84	105	59.4	2564	1	ENV_HV260	P09254 homo sapien
85	105	59.4	2564	1	ENV_HV261	P09254 homo sapien
86	105	59.4	2564	1	ENV_HV262	P09254 homo sapien
87	105	59.4	2564	1	ENV_HV263	P09254 homo sapien
88	105	59.4	2564	1	ENV_HV264	P09254 homo sapien
89	105	59.4	2564	1	ENV_HV265	P09254 homo sapien
90	105	59.4	2564	1	ENV_HV266	P09254 homo sapien

ALIGNMENTS

RESULT 1
ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (BLI isolate) (HIV-1).

OC viruses; Retrovirda viruses; Retrovirda; Lenticivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP MEDLINE=66245056; PubMed=2424612;
 RX Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 of two isolates from African patients";
 RL Cell 46:63-74(1986).
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 CC EMBL; K03454; AAA44329.1; -;
 DR EMBL; A07108; CA00616.1; -;
 DR HIV; K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 340 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MM; PSCDB64DAAD00755 CRC64;
 Query Match 96.0%; Score 168; DB 1; Length 853;

Best Local Similarity 97.2%; Pred. No. 1.2e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LRAIRAOQHLLQLTWQIKQLQARILAVERYKQD 36
 Db 552 LRAIRAOQHLLQLTWQIKQLQARILAVERYKQD 587
 RESULT 2
 ENV_HVLMF STANDARD; PRT; 853 AA.
 ID ENV_HVLMF
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retrovirda viruses; Retrovirda; Lenticivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP MEDLINE=90317877; PubMed=1695254;
 RX Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
 RA Maslak A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1
 RT variants diminished in the ability to induce syncytium-independent
 RT cytolysis";
 RL J. Virol. 64:3792-3803(1990).
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 CC -----
 CC EMBL; M33943; AAA44850.1; -;
 DR PDB; 1A1K; 16-JUN-97.
 DR HIV; M33943; ENVSMFA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 509
 FT CHAIN 510 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 329 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).


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FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22A8A CRC64;

Query Match 96.0%; Score 168; DB 1; Length 853;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQUTWQIKQLQARILAVERYLKDQ 36
Db 553 LRAIEAQHLLQUTWQIKQLQARILAVERYLKDQ 588

RESULT 3
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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DR EMBL; M22639; AAA45370.1; -.
DR PIR; S54384; S54384.
DR HIV; M22639; ENV22226.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KM Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.

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FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query Match 96.0%; Score 168; DB 1; Length 853;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQUTWQIKQLQARILAVERYLKDQ 36
Db 552 LRAIEAQHLLQUTWQIKQLQARILAVERYLKDQ 587

RESULT 4
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82(1987).
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CC -----
DR EMBL; K03458; AAA45380.1; -.
DR PIR; D26192; VCLJ2R.
DR HIV; K03458; ENV526.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
FT DISULFID 230 241
FT DISULFID 298 332
FT DISULFID 378 444
FT DISULFID 385 417
FT CARBOHYD 87 129
FT CARBOHYD 129 140
FT CARBOHYD 140 145
FT CARBOHYD 145 154
FT CARBOHYD 154 158
FT CARBOHYD 158 186
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FT CARBOHYD 340 355
FT CARBOHYD 355 386
FT CARBOHYD 386 392
FT CARBOHYD 392 398
FT CARBOHYD 398 404
FT CARBOHYD 404 443
FT CARBOHYD 443 447
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FT CARBOHYD 460 461
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FT CARBOHYD 615 624
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SQ SEQUENCE 855 AA; 96971 MW; 3B4D3D6E239C3457 CRC64;

Query March 96.0%; Score 168; DB 1; Length 855;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LRAIAEQHLLQTTWQIKQLQARILAVERYLKQ 36
Db 554 LRAIAEQHLLQTTWQIKQLQARILAVERYLKQ 589

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DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RT Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RL J. Biol. Chem. 265:10373-10382(1990).
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CC -----
DR EMBL; M15654; AAA44205.1; -.
DR PIR; A03973; VCLJH3.
DR HIV; M15654; ENV5BH102.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
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FT SIGNAL 1 30
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FT DISULFID 54 74
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FT DISULFID 131 157
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FT DISULFID 378 445
FT DISULFID 385 418
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FT CARBOHYD 136 136
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SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931B827 CRC64;

Query Match 96.0%; Score 168; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1,2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 LRAIEAQQHLLQLTWGIKQARILAVERYLKQ 36
555 LRAIEAQQHLLQLTWGIKQARILAVERYLKQ 590

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11706;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8729196; Pubmed=3040055;
RA Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN REVISIONS.
RA Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
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CC or send an email to license@ebi.ac.uk).
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DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF03819; AAC82596.1; -
DR PDB; 1DPA; 26-JAN-00.
DR PDB; 1DPS; 26-JAN-00.
DR PDB; 1DUB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K3J; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
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FT CHAIN 512 856
FT DISULFID 54 74
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FT DISULFID 131 157
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FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
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FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FA816AF85107FE0 CRC64;

Query Match 96.0%; Score 168; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1,2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 LRAIEAQQHLLQLTWGIKQARILAVERYLKQ 36
555 LRAIEAQQHLLQLTWGIKQARILAVERYLKQ 590

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 10-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11707;
RN REVISIONS.
RP SEQUENCE FROM N.A.

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Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261
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Db	555	LRRAIEAQHLLQLTWQIQKQQLARIATVRYLKDQ	590
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AC	Q70626;		
DT	15-JUL-1998	(Rel. 36, Created)	
DT	15-JUL-1998	(Rel. 36, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Envelope polypeptide gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.		
OX	NCBI_Taxid=82834;		
RA	SEQUENCE FROM N.A.		
RA	MEDLINE=95127297; PubMed=7826699;		
RA	Reitz M.S. Jr., Hall U., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.;		
RT	"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIB)."		
RL	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).		
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CC	-----		
DR	EMBL; U12055; AAA76690.1; -.		
DR	PDB; 1IF3; Q2-MAY-01.		
DR	GlycosylatedB; Q70626; -. Env GP41.		
DR	InterPro; IPR000328; Env GP41.		
DR	InterPro; IPR000777; GP120.		
DR	Pfam; PF00516; GP120; 1.		
DR	Pfam; PF00517; GP41; 1.		
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FT	DISULFID	385	418
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FT	DISULFID	378	445
FT	DISULFID	385	418
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FT	CARBOHYD	160	160
FT	CARBOHYD	186	186</

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

Query Match 96.0%; Score 168; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 1.2e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 36
 555 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 590

Db 555 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 590

RESULT 9
 ENV_HV1PV STANDARD; PRT; 856 AA.
 ID ENV_HV1PV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Pv22 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11700;
 RX MEDLINE=5111157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laasy L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
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 CC -----
 CC EMBL: K02083; AAB59873.1; --
 DR EMBL: X01762; CAA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT CHAIN 31 30
 FT CHAIN 511 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCB1DC3C1209B3 CRC64;

Query Match 96.0%; Score 168; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 1.2e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 36
 555 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 590

Db 555 LRAIAEQHLLQTLTWQIKOLQARILAVERYLKQ 590

RESULT 10
 ENV_HV1BR STANDARD; PRT; 861 AA.
 ID ENV_HV1BR
 AC P03377;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11686;
 RX MEDLINE=5099333; PubMed=2981635;
 RA Main-Hobson S., Sonigo P., Dancos O., Cole S., Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RL Cell 40:9-17(1985).
 CC -----
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 CC -----

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CC -----
DR EMBL; K02013; AAB59751.1; -.
DR EMBL; A04321; CAA00352.1; -.
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV5BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 506
FT CHAIN 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 235 235
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 337 337
FT CARBOHYD 344 344
FT CARBOHYD 361 361
FT CARBOHYD 391 391
FT CARBOHYD 397 397
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 453 453
FT CARBOHYD 468 468
FT CARBOHYD 616 616
FT CARBOHYD 621 621
FT CARBOHYD 630 630
FT CARBOHYD 642 642
FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE3B4D4E4FD63A CRC64;

Query Match 96.0%; Score 168; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQTVWIKQLQARILAVERYLDDQ 36
Db 560 LRAIAEQHLLQTVWIKQLQARILAVERYLDDQ 595

RESULT 11
ENV HV1S1
AC P19550; STANDARD; PRT; 847 AA.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP120 precursor [Contains: Exterior membrane
DE glycoprotein (GP120), Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RT J. Virol. 64:4390-4398(1990).
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M65024; AAA45072.1; -.
DR PDB; IOBE; 15-MAY-97.
DR HIV; M38428; ENV5SF162.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT CHAIN 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT DISULFID 87 87
FT CARBOHYD 135 135
FT CARBOHYD 154 154
FT CARBOHYD 186 186
FT CARBOHYD 195 195
FT CARBOHYD 232 232
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 293 293
FT CARBOHYD 299 299
FT CARBOHYD 329 329
FT CARBOHYD 336 336
FT CARBOHYD 352 352
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 401 401
FT CARBOHYD 438 438
FT CARBOHYD 454 454
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FDFE2AB CRC64;

Query Match 95.4%; Score 167; DB 1; Length 847;
Best Local Similarity 94.4%; Pred. No. 1.6e-15;

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Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKOLQARILAVERYLKQ 36
 Db 546 LRAIAEQHLLQITWQIKOLQARILAVERYLKQ 581

RESULT 12
 ENV_HV10Y STANDARD; PRT; 855 AA.

AC P20868;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Bhett T.; Dazza M.C.; Brun-Vezinet F.; Roelants G.E.; Wain-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot."
 RL AIDS 3:707-715(1989).
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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 CC -----
 CC EMBL; M26727; AAA83397.1; -.
 CC HIV; M26727; ENVSOYI.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR00777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509
 FT 510 855
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 442
 FT DISULFID 388 415
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 142 142
 FT CARBOHYD 145 145
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 192 192
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 306 306

FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADB62DA CRC64;

Query Match 95.4%; Score 167; DB 1; Length 855;
 Best Local Similarity 94.4%; Pred. No. 1, 7e-15;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKOLQARILAVERYLKQ 36
 Db 554 LRAIAEQHLLQITWQIKOLQARILAVERYLKQ 589

RESULT 13
 ENV_HV10Y STANDARD; PRT; 848 AA.

AC P20871;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (URCSF isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11688;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koyanagi S.; Chen I.S.Y.;
 RL Submitted (DEC-1988) to the HIV data bank.
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 CC -----
 CC EMBL; M38429; AAB03749.1; -.
 CC PDB; 1CE4; 18-MAR-99.
 DR HIV; M38429; ENV5JRCFSF.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR00777; GP120.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 503
 FT 504 848
 FT DISULFID 53 73
 FT DISULFID 118 203
 FT DISULFID 125 194
 FT DISULFID 130 154
 FT DISULFID 135 154
 FT DISULFID 216 245
 FT DISULFID 226 237
 FT DISULFID 294 328
 FT DISULFID 374 437
 FT DISULFID 381 410
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 137 137

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FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;

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Query March 94.3%; Score 165; DB 1; Length 848;
Best Local Similarity 91.7%; Pred. No. 3.1e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 LRAIEAQOHLQLTWQIKQLARILAVERYLKQ 36
Db 547 LRAIEAQOHLQLTWQIKQLARILAVERYLKQ 582

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RESULT 14
ENV_HV1MN STANDARD; PRT; 856 AA.
ID ENV_HV1MN
AC P05877;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
  Parrelli K., Wong-Staal P., Gallo R.C., Reitz M.S. Jr.;
  "Envelope sequences of two new United States HIV-1 isolates.";
  Virology 164:531-536(1988).
RT -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
  PATIENT IN 1984.
CC

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  or send an email to license@isb-sib.ch).
CC

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CC EMBL; M17449; AAA44857.1; -.
DR PDB; 1AC7; 31-JUL-94.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1N1Z; 25-FEB-03.
DR PDB; 1N0J; 25-FEB-03.
DR HIV; M17449; ENVSMN.

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DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
  3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 513
FT CHAIN 514 856
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 445
FT DISULFID 388 418
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 140 140
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 336 336
FT CARBOHYD 343 343
FT CARBOHYD 359 359
FT CARBOHYD 365 365
FT CARBOHYD 395 395
FT CARBOHYD 401 401
FT CARBOHYD 405 405
FT CARBOHYD 406 406
FT CARBOHYD 413 413
FT CARBOHYD 448 448
FT CARBOHYD 465 465
FT CARBOHYD 612 612
FT CARBOHYD 617 617
FT CARBOHYD 626 626
FT CARBOHYD 638 638
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

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Query March 94.3%; Score 165; DB 1; Length 856;
Best Local Similarity 91.7%; Pred. No. 3.2e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 LRAIEAQOHLQLTWQIKQLARILAVERYLKQ 36
Db 556 LRAIEAQOHLQLTWQIKQLARILAVERYLKQ 591

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RESULT 15
ENV_HV1Y2 STANDARD; PRT; 843 AA.
ID ENV_HV1Y2
AC P35561;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;

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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA57DE2B83 CRC64;

Query Match 93.7%; Score 164; DB 1; Length 846;
 Best Local Similarity 91.7%; Pred. No. 4.3e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQTLTWGKIQARILAVERYLKQ 36
 Db 545 LRAIEAQHLLQTLTWGKIQARILAVERYLKQ 580

RESULT 17
 ENV_HV1B8 STANDARD; PRT; 851 AA.
 AC P04582;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 OS ENV.
 GN Human immunodeficiency virus type 1 (B8 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11684;
 [1]
 RA Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).

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 CC or send an email to license@isb-sib.ch).

 CC
 DR EMBL, K02011; AAA44661.1; .
 DR PDB, 1DDH; 13-JAN-99.
 DR PDB, 1HHG; 31-OCT-93.
 DR PDB, 1QO3; 02-JAN-00.
 DR PDB, 1S2T; 24-DEC-97.
 DR HIV, K02011; ENV5B8.
 DR Glycosylated; P04582; .
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.

FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 440 BY SIMILARITY.
 FT DISULFID 385 413 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 93.7%; Score 164; DB 1; Length 851;
 Best Local Similarity 94.4%; Pred. No. 4.3e-15;
 Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQTLTWGKIQARILAVERYLKQ 36
 Db 550 LRAIEAQHLLQTLTWGKIQARILAVERYLKQ 585

RESULT 18
 ENV_HV1S3 STANDARD; PRT; 852 AA.
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 OS ENV.
 GN Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11690;
 [1]
 RA Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).

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 CC or send an email to license@isb-sib.ch).

 CC
 DR EMBL, K02011; AAA44661.1; .
 DR PDB, 1DDH; 13-JAN-99.
 DR PDB, 1HHG; 31-OCT-93.
 DR PDB, 1QO3; 02-JAN-00.
 DR PDB, 1S2T; 24-DEC-97.
 DR HIV, K02011; ENV5B8.
 DR Glycosylated; P04582; .
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.

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CC EMBL; AY352275; A017031.1; --

DR PDB; 1ME0; 11-DEC-02.

DR HIV; M38427; ENV5SF33.

DR InterPro; IPR000328; Env_GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;

KM 3D-structure.

FT SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 89 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 852 AA; 96663 MW; E57B8D23C910D CRC64;

Query Match 93.7%; Score 164; DB 1; Length 852;

Best Local Similarity 91.7%; Pred. No. 4.3e-15;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEAOHLLQITWQIKOLARILAVERYLKDQ 36

DB 551 LRAIAEAOHLLQITWQIKOLARILAVERYLKDQ 586

RESULT 19

ENV_HV1A2 STANDARD; PRT; 855 AA.

ID ENV_HV1A2

AC P03378;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=65090453; PubMed=2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steiner K.S.,

RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)."

RT Science 227:484-492 (1985).

CC -----

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CC EMBL; K02007; AAB59882.1; --

DR PIR; A03976; VCLJL2.

DR HIV; K02007; ENV5SF2.

DR InterPro; IPR000328; Env_GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KM 3D-structure.

FT SIGNAL 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 30 509 TRANSMEMBRANE GLYCOPROTEIN.

FT CHAIN 510 855

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 208 BY SIMILARITY.

FT DISULFID 125 199 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 221 250 BY SIMILARITY.

FT DISULFID 231 242 BY SIMILARITY.

FT DISULFID 299 333 BY SIMILARITY.

FT DISULFID 380 442 BY SIMILARITY.

FT DISULFID 387 415 BY SIMILARITY.

FT CARBOHYD 87 89 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
 Query Match 93.7%; Score 164; DB 1; Length 855;
 Best Local Similarity 91.7%; Pred. No. 4,4e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQARIVLAVERYLKDQ 36
 DB 554 LRAIEAQHLLQLTWQIKQARIVLAVERYLKDQ 589

RESULT 20
 ENV_HV1SC STANDARD; PRT; 856 AA.
 AC POS878;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68219542; PubMed=3369091;
 RA Garro C., Guo H.-G., Franchini G., Aldrovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Rietz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates";
 RL Virology 164:531-536 (1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN 1984 IN SOUTHERN CALIFORNIA.

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 CC -----

CC EMBL; M17450; -; NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 93.7%; Score 164; DB 1; Length 856;
 Best Local Similarity 91.7%; Pred. No. 4,4e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQARIVLAVERYLKDQ 36
 DB 555 LRAIEAQHLLQLTWQIKQARIVLAVERYLKDQ 590

RESULT 21
 ENV_HV1M1 STANDARD; PRT; 856 AA.
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MMU1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66218077; PubMed=2423250;
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of Cell 45:637-648 (1986).
 CC -1- MISCELLANEOUS: ISOLATES MMU1, MMU2, AND MMU3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC PIR; A24774; VCLJ3W.
 DR PDB; 1LBO; 04-DEC-02.
 DR PDB; 1LCK; 04-DEC-02.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM SIGNAL.
 FT 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.

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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E34C0404DB9 CRC64;

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Query Match 93.7%; Score 164; DB 1; Length 856;
Best Local Similarity 91.7%; Pred. No. 4,4e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 1 LRAIRAGQHLLQLTWQIKOLARILAVERYLKDQ 36
555 LRAIRAGQHLLQLTWQIKOLARILAVERYLKDQ 590

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RESULT 22
ENV_HV1ZH STANDARD; PRT; 856 AA.
AC P05881;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11692;
RN [1]
RX MEDLINE=99228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D., Jannoun-Nasr R., Getchell J.,
McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of hybrid HIV-1."
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
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or send an email to license@ebi.ac.uk).
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CC -----
DR EMBL; M15896; AAB53948.1; -
DR PIR; A44963; A44963.
DR HIV; M15896; ENV52321.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW signal.
FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 30 511 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 512 856 BY SIMILARITY.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 153 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 379 445 BY SIMILARITY.
FT DISULFID 386 418 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;

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Query Match 93.7%; Score 164; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 4,4e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 LRAIRAGQHLLQLTWQIKOLARILAVERYLKDQ 36
555 LRAIRAGQHLLQLTWQIKOLARILAVERYLKDQ 590

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RESULT 23

ENV_HV1KB STANDARD; PRT; 861 AA.

AC P31819;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 93.7%; Score 164; DB 1; Length 865;
 Best Local Similarity 91.7%; Pred. No. 4,4e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAOQHLLQLTWQIKOLARILAVERYLKDQ 36
 Db 566 LRAIEAOQHLLQLTWQIKOLARILAVERYLKDQ 599

RESULT 25
 ENV_HV1J3 STANDARD; PRT; 867 AA.
 AC P12485;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11694;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352108; PubMed=2669897;
 RA Komiya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria."
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
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 CC -----
 CC EMBL: M21138; AAB03526.1; -
 DR HIV; M21138; ENV5JH3.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR007777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; signal.
 FT SIGNAL 1 30
 FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 217 BY SIMILARITY.
 FT DISULFID 125 208 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 230 259 BY SIMILARITY.
 FT DISULFID 240 251 BY SIMILARITY.
 FT DISULFID 308 342 BY SIMILARITY.
 FT DISULFID 388 457 BY SIMILARITY.
 FT DISULFID 395 430 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 867 AA; 98399 MW; 5F23101468B8680 CRC64;

Query Match 93.7%; Score 164; DB 1; Length 867;
 Best Local Similarity 94.4%; Pred. No. 4,4e-15;
 Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LRAIEAOQHLLQLTWQIKOLARILAVERYLKDQ 36
 Db 566 LRAIEAOQHLLQLTWQIKOLARILAVERYLKDQ 601

RESULT 26
 ENV_HV1C4 STANDARD; PRT; 868 AA.
 AC P05879;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11687;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041461; PubMed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
 RT "Molecular cloning and primary nucleotide sequence analysis of a RT distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RL [2]
 RP SEQUENCE OF 34-43.

[illegible]

Oy		1	LIRAIEAQCHLQLTWIOIQLOARIILAVERYLKDQ	36
Dd		567	LIRAIKAOQHLLQTWGIGIKQLARILAVERLYLKDQ	602
 RESULT_27				
ID	_ENV_HV1MA	STANDARD;	PRT;	859 AA.
AC	P04583;			
DT	13-AUG-1987	(Rel. 05, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	15-JUN-1999	(Rel. 38, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
CN	ENV.			
OS	Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11697;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=66245056; PubMed=2424612.			
RA	Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;			
RT	"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";			
RL	Cell 46:63-74(1986).			
CC	-----			
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CC	-----			
DR	EMBL; X04415; CAA28016.1; -.			
DR	EMBL; A07116; CAA00623.1; -.			
DR	PIR; T01672; T01672.			
DR	HIV; K03456; ENV\$MAL.			
DR	InterPro; IPR00328; Env_GP41..			
DR	InterPro; IPR00777; GP120.			
KM	Pfam; PF00516; GP120; 1.			
KX	Pfam; PF00517; GP41; 1.			
KS	AIDS; Coat protein; polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL.	1	30	
FT	CHAIN	31	513	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	514	859	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	210	BY SIMILARITY.
FT	DISULFID	125	201	BY SIMILARITY.
FT	DISULFID	130	162	BY SIMILARITY.
FT	DISULFID	223	252	BY SIMILARITY.
FT	DISULFID	233	244	BY SIMILARITY.
FT	DISULFID	301	334	BY SIMILARITY.
FT	DISULFID	380	445	BY SIMILARITY.
FT	DISULFID	387	418	BY SIMILARITY.
FT	CARBOHYD	87		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	146	146	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	193	193	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	281	281	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	306	306	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	357	357	N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 819 819 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 859 AA; 97109 MW; DECP9AAS2E3ABF29 CRC64;

Query Match 93.1%; Score 163; DB 1; Length 859;
 Best Local Similarity 91.7%; Pred. No. 6e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKQARILAVERYLKQD 36
 Db 557 LRAIAEQHLLQITWQIKQARILAVERYLKQD 592

RESULT 28
 ENV_HV1W2 STANDARD; PRT; 847 AA.

AC P05880;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.B., Redfield R.R., Markham P.D.,
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.,
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS."
 RL Science 233:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEPARATELY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
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 CC -----
 CC EMBL: M12507; AAB12990.1; -
 DR HIV: M12507; ENV:WMJ2.
 DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; signal.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
 FT DISULFID 379 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73AAS5BCAE CRC64;

Query Match 92.0%; Score 161; DB 1; Length 847;
 Best Local Similarity 88.9%; Pred. No. 1.1e-14;
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKQARILAVERYLKQD 36
 Db 546 LRAIAEQHLLQITWQIKQARILAVERYLKQD 581

RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.

AC P05882;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; PubMed=3395517;
 RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.,
 RT "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.
 CC -----
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 CC -----

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CC -----
DR EMBL: J03653; AAA44684.1; -.
DR HIV: J03653; ENVSJY1.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00517; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KM Signal.
FT SIGNAL 1 29
FT CHAIN 30 518 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 519 863 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 452 BY SIMILARITY.
FT DISULFID 388 452 BY SIMILARITY.
FT DISULFID 395 425 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729C85A6FAD1641 CRC64;

Query Match 90.9%; Score 159; DB 1; Length 863;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2789516;
RA Amand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia."
RT Virology 168:79-89(1989).
CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21098; AAA44221.1; -.
DR PIR: A31677; VCLJBR.
DR PDB: 1IM7; 23-OCT-02.
DR HIV: M21098; ENVSBRVA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KM 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 155 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 439 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match 89.1%; Score 156; DB 1; Length 852;
Best Local Similarity 86.1%; Pred. No. 5.7e-14;

Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LIRAIEAQCHILQITWQIKQLQARILAVERYLKDQ 36
|||:|||||:|||||:|||||
Db 551 LMAIEAQCHIMLETWGIKQLQARVLAVERYLKDQ 586

Search completed: June 2, 2004, 11:42:57
Job time : 5.86957 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 30.2283 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-180
Perfect score: 175
Sequence: 1 LRLRAIQOHILQTLTWQIKQARILAVERYIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169	96.6	852	15	Q8UJ55 human immun
2	168	96.0	129	15	Q9YI21 human immun
3	168	96.0	131	15	Q7SM43 human immun
4	168	96.0	132	15	Q9Q522 human immun
5	168	96.0	132	15	Q7SL22 human immun
6	168	96.0	143	15	Q7SM06 human immun
7	168	96.0	144	15	Q7ZCD7 human immun
8	168	96.0	144	15	Q7ZCD6 human immun
9	168	96.0	145	15	Q7ZC52 human immun
10	168	96.0	153	15	Q7SM03 human immun
11	168	96.0	173	15	Q8JAJ9 human immun
12	168	96.0	357	15	Q78119 human immun
13	168	96.0	588	15	Q993A8 human immun
14	168	96.0	588	15	Q993A7 human immun
15	168	96.0	589	15	Q993B1 human immun
16	168	96.0	590	15	Q993A9 human immun

17	168	96.0	616	15	Q993B0 human immun
18	168	96.0	618	15	Q993B2 human immun
19	168	96.0	727	15	Q9Q723 human immun
20	168	96.0	747	15	Q70607 human immun
21	168	96.0	748	15	Q70606 human immun
22	168	96.0	752	15	Q70604 human immun
23	168	96.0	752	15	Q70605 human immun
24	168	96.0	752	15	Q70608 human immun
25	168	96.0	757	15	Q9Q722 human immun
26	168	96.0	811	15	Q9QV16 human immun
27	168	96.0	826	15	Q9QV11 human immun
28	168	96.0	842	15	Q73341 human immun
29	168	96.0	842	15	Q70895 human immun
30	168	96.0	842	15	Q73340 human immun
31	168	96.0	845	15	Q91D89 human immun
32	168	96.0	847	15	Q69996 human immun
33	168	96.0	851	15	Q78243 human immun
34	168	96.0	854	15	Q68566 human immun
35	168	96.0	854	15	Q85582 human immun
36	168	96.0	854	15	Q72502 human immun
37	168	96.0	854	15	Q90178 human immun
38	168	96.0	854	15	Q78705 human immun
39	168	96.0	855	15	Q8AKV7 human immun
40	168	96.0	855	15	Q8ADT7 human immun
41	168	96.0	856	15	Q74090 human immun
42	168	96.0	856	15	Q92877 human immun
43	168	96.0	856	15	Q74599 human immun
44	168	96.0	856	15	Q41772 human immun
45	168	96.0	857	15	Q92822 human immun
46	168	96.0	857	15	Q71013 human immun
47	168	96.0	857	15	Q89654 human immun
48	168	96.0	859	15	Q9WLJ1 human immun
49	168	96.0	864	15	Q9YP39 human immun
50	168	96.0	864	15	Q7ZJC8 human immun
51	168	96.0	866	15	Q9WP24 human immun
52	168	96.0	870	15	Q8Q2X1 human immun
53	168	96.0	870	15	Q8Q2X0 human immun
54	167	95.4	113	15	Q7ZC85 human immun
55	167	95.4	125	15	Q91WP9 human immun
56	167	95.4	127	15	Q9YXX9 human immun
57	167	95.4	127	15	Q9YXX0 human immun
58	167	95.4	129	15	Q9YIY7 human immun
59	167	95.4	132	15	Q91WQ5 human immun
60	167	95.4	133	15	Q8UQ26 human immun
61	167	95.4	133	15	Q8UQ27 human immun
62	167	95.4	133	15	Q8UQ28 human immun
63	167	95.4	133	15	Q8UQ24 human immun
64	167	95.4	133	15	Q8UQ23 human immun
65	167	95.4	133	15	Q9Q020 human immun
66	167	95.4	134	15	Q91WQ6 human immun
67	167	95.4	137	15	Q9QOM0 human immun
68	167	95.4	137	15	Q9QOM4 human immun
69	167	95.4	142	15	Q91WQ7 human immun
70	167	95.4	142	15	Q91WQ3 human immun
71	167	95.4	143	15	Q91WQ1 human immun
72	167	95.4	143	15	Q7ZC46 human immun
73	167	95.4	144	15	Q91WQ4 human immun
74	167	95.4	144	15	Q70207 human immun
75	167	95.4	144	15	Q7ZCB6 human immun
76	167	95.4	144	15	Q7ZCD8 human immun
77	167	95.4	144	15	Q7ZC68 human immun
78	167	95.4	144	15	Q7ZCC5 human immun
79	167	95.4	144	15	Q7ZCC2 human immun
80	167	95.4	144	15	Q7ZCB1 human immun
81	167	95.4	144	15	Q7ZCB0 human immun
82	167	95.4	144	15	Q7ZC96 human immun
83	167	95.4	144	15	Q7ZC95 human immun
84	167	95.4	144	15	Q7ZC89 human immun
85	167	95.4	144	15	Q7ZC88 human immun
86	167	95.4	144	15	Q7ZC71 human immun
87	167	95.4	144	15	Q7ZC70 human immun
88	167	95.4	144	15	Q7ZC45 human immun
89	167	95.4	145	15	Q7ZC57 human immun

90 167 95.4 145 15 Q7ZC53 Q7ZC53 human immun

ALIGNMENTS

RESULT 1

Q8UL55 PRELIMINARY; PRT; 852 AA.
AC Q8UL55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp160 protein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;
RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells
RT and Herpesvirus saimiri transformed T-cells is comparable."
RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418531; C:AD10941.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 852 AA; 96711 MW; 57D8CA06A42F371F CRC64;
Query Match 96.6%; Score 169; DB 15; Length 852;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 36
Db 550 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 585
RESULT 2
Q9YYZ1 PRELIMINARY; PRT; 129 AA.
AC Q9YYZ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataha P.R., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda."
RU Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006886; AAD01340.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1 1

FT NON_TER 129 129
SQ SEQUENCE 129 AA; 15612 MW; 9CA606B5B8F42ADF CRC64;

Query Match 96.0%; Score 168; DB 15; Length 129;
Best Local Similarity 97.2%; Pred. No. 6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 36
Db 2 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 37

RESULT 3

Q7SM43 PRELIMINARY; PRT; 131 AA.
AC Q7SM43;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998."
RU Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529573; AAP87704.1; -
DR Env Envelope protein.
FT NON_TER 1 1
SQ SEQUENCE 131 AA; 15539 MW; C11B4FEFB1A860F CRC64;
Query Match 96.0%; Score 168; DB 15; Length 131;
Best Local Similarity 97.2%; Pred. No. 6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 36
Db 13 LRAIEAQQHLLQTLTWQIKQLQARILAVERYIKDQ 48

RESULT 4

Q9Q052 PRELIMINARY; PRT; 132 AA.
AC Q9Q052;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=99ES-MOI496;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeo N., Asuna E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."
RU AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331089; AK92300.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.

FT NON_TER 1 1
SQ SEQUENCE 132 AA; 15708 MW; 519DB8AED574FAE CRC64;

Query Match
Best Local Similarity 96.0%; Score 168; DB 15; Length 132;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
12 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 47

RESULT 5

07SLZ2 PRELIMINARY; PRT; 132 AA.

AC 07SLZ2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=GP970;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF530024; AAP87755.1; -.
KM Envelope protein.
FT NON_TER 1 1
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;

Query Match
Best Local Similarity 96.0%; Score 168; DB 15; Length 132;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
13 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 48

RESULT 6

07SM06 PRELIMINARY; PRT; 143 AA.

AC 07SM06;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF530010; AAP87741.1; -.
KM Envelope protein.
FT NON_TER 1 1
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BEO CRC64;

Query Match
96.0%; Score 168; DB 15; Length 143;

Best Local Similarity 97.2%; Pred. No. 6.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
13 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 48

RESULT 7

07ZCD7 PRELIMINARY; PRT; 144 AA.

AC 07ZCD7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Derou S., Fischer A., Baurith T.,
RT "Unccommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185383; AA06558.1; -.
DR GO: GO:0019031; C:Viral envelope; IEA.

DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1 1
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318EBE CRC64;

Query Match
Best Local Similarity 96.0%; Score 168; DB 15; Length 144;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
26 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 61

RESULT 8

07ZCD6 PRELIMINARY; PRT; 144 AA.

AC 07ZCD6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-2;
RA Roman F., Gonzalez D., Lambert C., Derou S., Fischer A., Baurith T.,
RT "Unccommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185384; AA06559.1; -.
DR GO: GO:0019031; C:Viral envelope; IEA.

DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EBB CRC64;

Query Match 96.0%; Score 168; DB 15; Length 144;
 Best Local Similarity 97.2%; Pred. No. 6.7e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 36
 Db 26 LRAIEAQHLLQLTWGIKQLQARILAVERYLKQ 61

RESULT 9

07ZCS2 PRELIMINARY; PRT; 145 AA.

AC 07ZCS2; (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=HRLX18;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
 RA Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
 RT "Uncommun mutations at residue positions critical for enfuvirtide (T-
 RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
 RT subtype HIV-1.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: A1185468; AA065743.1; -

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1
 FT NON_TER 145 145

SQ SEQUENCE 145 AA; 17020 MW; AC8C32B97B09D1A1 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 145;
 Best Local Similarity 97.2%; Pred. No. 6.7e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 36
 Db 24 LRAIEAQHLLQLTWGIKQLQARILAVERYLKQ 59

RESULT 10

07SM03 PRELIMINARY; PRT; 153 AA.

AC 07SM03; (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=GT598;

RA Gonzalez Perez M.P., Garcia Saitz A.;
 RT "Epidemiological and molecular characteristics of HIV and HTLV
 RT infection in Equatorial Guinea, 1996-1998.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF530013; AA87744.1; -
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 153 153
 SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1F8FPC03 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 153;
 Best Local Similarity 97.2%; Pred. No. 7.1e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 36
 Db 13 LRAIEAQHLLQLTWGIKQLQARILAVERYLKQ 48

RESULT 11

08JAJ9 PRELIMINARY; PRT; 173 AA.

AC 08JAJ9; (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=88BRJ045;

RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
 RA Morgado M.G.;
 RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
 RT Southeastern and Southern regions.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF463445; AA90821.1; -

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR00777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

FT NON_TER 1
 FT NON_TER 173 173

SQ SEQUENCE 173 AA; 19858 MW; 300D69C94C03AD14 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 173;
 Best Local Similarity 97.2%; Pred. No. 8.1e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 36
 Db 58 LRAIEAQHLLQLTWGIKQLQARILAVERYLKQ 93

RESULT 12

07B119 PRELIMINARY; PRT; 357 AA.

AC 07B119; (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last annotation update)
 DE Envelope protein, gp120 (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=92144209; Pubmed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.,
RT "distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61356; CAA43624.1; -.
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON TER
FT NON TER
SQ SEQUENCE 357 AA; 4118 MW; FE4CAA7E122AB8E6 CRC64;
Query Match 96.0%; Score 168; DB 15; Length 357;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 36
Db 56 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 91
RESULT 13
Oy 0993A8 PRELIMINARY; PRT; 588 AA.
AC 0993A8;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240A88 CRC64;
Query Match 96.0%; Score 168; DB 15; Length 588;
Best Local Similarity 97.2%; Pred. No. 2.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 36
Db 498 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 533
RESULT 14
Oy 0993A7 PRELIMINARY; PRT; 588 AA.
AC 0993A7;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321148; AAK20296.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;
Query Match 96.0%; Score 168; DB 15; Length 588;
Best Local Similarity 97.2%; Pred. No. 2.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 36
Db 498 LRAIAEQHLLQLTWGIKOLARILAVERYLKQD 533
RESULT 15
Oy 0993B1 PRELIMINARY; PRT; 589 AA.
AC 0993B1;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AAK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;
Query Match 96.0%; Score 168; DB 15; Length 589;
Best Local Similarity 97.2%; Pred. No. 2.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Craiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity";
RL J. Virol. 73:10310-10319(1999).
DR EMBL; AF189158; AAF25627.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD626D26B9E6 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 727;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKOLQARILAVERYLKQ 36
Db 550 LRAIAEQHLLQLTWQIKOLQARILAVERYLKQ 585

RESULT 20
Q70607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 96.0%; Score 168; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKOLQARILAVERYLKQ 36
Db 550 LRAIAEQHLLQLTWQIKOLQARILAVERYLKQ 585

RESULT 21
Q70606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 96.0%; Score 168; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
[1]
RC SEQUENCE FROM N.A.
RC STRAIN=LW851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12030; AAA76666.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.0%; Score 168; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 36
Db 555 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 590
|||||
RESULT 23
ID Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
[1]
RC SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA MEDLINE=95127297; PubMed=7826699;
RX Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12031; AAA76667.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.

DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.0%; Score 168; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 36
Db 555 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 590
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RESULT 24
ID Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
[1]
RC SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
EMBL: U12035; AAA7670.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0B88 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 36
Db 555 LRAIEAQHLLQITWGIKOLARILAVERYLKQ 590
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RESULT 25
ID Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.

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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=9272698; Pubmed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; Pubmed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.U., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -.
DR FTR: A53591; A53591.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AFB8263BD2E CRC64;

Query Match 96.0%; Score 168; DB 15; Length 757;
Best Local Similarity 97.2%; Pred. No. 3.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 550 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 585

RESULT 26
Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; Pubmed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401037; CAC15045.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
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DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 811;
Best Local Similarity 97.2%; Pred. No. 4.1e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 559 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 594

RESULT 27
Q9DVL1 PRELIMINARY; PRT; 826 AA.
AC Q9DVL1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=97DC.KTB22;
RX MEDLINE=20499072; Pubmed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401042; CAC15050.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 826;
Best Local Similarity 97.2%; Pred. No. 4.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 542 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 577

RESULT 28
Q73341
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ID 073341 PRELIMINARY; PRT; 842 AA.
AC 073341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96303593; PubMed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RA Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization."
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39236; AAB37173.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 842 AA; 9496 MW; 02B9CB76D3D1E9F1 CRC64;

Query Match 96.0%; Score 168; DB 15; Length 842;
Best Local Similarity 97.2%; Pred. No. 4.3e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 36
Db 541 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 576

RESULT 29
070895 PRELIMINARY; PRT; 842 AA.
AC 070895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=93br029;
RX MEDLINE=98285725; PubMed=9621027;
RA Gao F., Robertson D.L., Carruthers C.D., Morrison S.G., Jian B.,
RA Chen Y., Barre-Sinoussi F., Girard M., Srinivasan A., Adimku A.G.,
RA Shaw G.M., Sharp P.M., Hahn B.H.;
RT "A comprehensive panel of near-full-length clones and reference
RT sequences for non-subtype B isolates of human immunodeficiency virus
RT type 1."
RL J. Virol. 72:5680-5698(1998).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Gao F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005495; AAD03179.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

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DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 842 AA; 94810 MW; F82041BD932DCAD CRC64;

Query Match 96.0%; Score 168; DB 15; Length 842;
Best Local Similarity 97.2%; Pred. No. 4.3e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 36
Db 541 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 576

RESULT 30
073340 PRELIMINARY; PRT; 842 AA.
ID 073340;
AC 073340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96303593; PubMed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RA Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization."
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39235; AAB37172.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 842 AA; 94906 MW; 607B4F2447B791EB CRC64;

Query Match 96.0%; Score 168; DB 15; Length 842;
Best Local Similarity 97.2%; Pred. No. 4.3e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 36
Db 541 LRAIEAQHLLQLTWQIKQLARILAVERYIKDQ 576

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Job time : 30.2283 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 13.3043 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-180
Perfect score: 175
Sequence: 1 LRLRAIQOHLLQLTWQIKQLARILAVERYIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	168	96.0	38	1	US-08-374-666-1
5	168	96.0	38	1	US-08-486-099-89
6	168	96.0	38	3	US-08-360-107A-99
7	168	96.0	38	3	US-08-360-107A-132
8	168	96.0	38	3	US-08-484-223B-89
9	168	96.0	38	3	US-08-919-597-89
10	168	96.0	38	3	US-08-475-668A-89
11	168	96.0	38	3	US-08-485-551A-89
12	168	96.0	38	3	US-08-471-913A-89
13	168	96.0	38	3	US-08-485-264A-89
14	168	96.0	38	3	US-09-082-279B-16
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16	168	96.0	38	3	US-09-082-279B-604
17	168	96.0	38	3	US-09-082-279B-659
18	168	96.0	38	3	US-09-082-279B-660
19	168	96.0	38	4	US-08-474-349A-89
20	168	96.0	38	4	US-08-474-349A-441
21	168	96.0	38	4	US-09-315-304B-16
22	168	96.0	38	4	US-09-315-304B-507
23	168	96.0	38	4	US-09-315-304B-604
24	168	96.0	38	4	US-09-315-304B-659
25	168	96.0	38	4	US-09-315-304B-660
26	168	96.0	38	4	US-08-255-208A-25
27	168	96.0	38	4	US-08-470-896-89

28	168	96.0	38	4	US-08-485-546A-89	Sequence 89, App1
29	168	96.0	38	4	US-09-796-202-11	Sequence 11, App1
30	168	96.0	38	4	US-09-834-784-16	Sequence 16, App1
31	168	96.0	38	4	US-09-834-784-507	Sequence 507, App
32	168	96.0	38	4	US-09-834-784-604	Sequence 604, App
33	168	96.0	38	4	US-09-834-784-659	Sequence 659, App
34	168	96.0	38	4	US-09-834-784-660	Sequence 660, App
35	168	96.0	38	4	US-08-464-003-1	Sequence 1, App1
36	168	96.0	38	4	US-09-779-451-2	Sequence 2, App1
37	168	96.0	38	4	US-09-515-965A-16	Sequence 16, App1
38	168	96.0	38	4	US-09-515-965A-507	Sequence 507, App
39	168	96.0	38	4	US-09-515-965A-604	Sequence 604, App
40	168	96.0	38	4	US-09-515-965A-659	Sequence 659, App
41	168	96.0	38	4	US-09-515-965A-660	Sequence 660, App
42	168	96.0	38	4	US-09-350-641C-16	Sequence 16, App1
43	168	96.0	38	4	US-09-350-641C-507	Sequence 507, App
44	168	96.0	38	4	US-09-350-641C-604	Sequence 604, App
45	168	96.0	38	4	US-09-350-641C-659	Sequence 659, App
46	168	96.0	38	4	US-09-350-641C-660	Sequence 660, App
47	168	96.0	41	1	US-08-073-028-8	Sequence 8, App1
48	168	96.0	41	1	US-08-374-666-3	Sequence 3, App1
49	168	96.0	41	1	US-08-374-666-9	Sequence 9, App1
50	168	96.0	41	3	US-08-486-099-8	Sequence 8, App1
51	168	96.0	41	3	US-08-360-107A-8	Sequence 8, App1
52	168	96.0	41	3	US-08-484-223B-8	Sequence 8, App1
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54	168	96.0	41	3	US-08-484-223B-243	Sequence 243, App
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58	168	96.0	41	3	US-08-471-913A-8	Sequence 8, App1
59	168	96.0	41	3	US-08-554-616-8	Sequence 8, App1
60	168	96.0	41	3	US-08-485-264A-8	Sequence 8, App1
61	168	96.0	41	3	US-09-082-279B-496	Sequence 496, App
62	168	96.0	41	3	US-09-082-279B-601	Sequence 601, App
63	168	96.0	41	3	US-09-082-279B-633	Sequence 633, App
64	168	96.0	41	3	US-09-082-279B-1163	Sequence 1163, App
65	168	96.0	41	4	US-08-474-349A-8	Sequence 8, App1
66	168	96.0	41	4	US-09-315-304B-496	Sequence 496, App
67	168	96.0	41	4	US-09-315-304B-601	Sequence 601, App
68	168	96.0	41	4	US-09-315-304B-633	Sequence 633, App
69	168	96.0	41	4	US-09-315-304B-1163	Sequence 1163, App
70	168	96.0	41	4	US-08-255-208A-8	Sequence 8, App1
71	168	96.0	41	4	US-08-973-952-8	Sequence 8, App1
72	168	96.0	41	4	US-08-470-896-8	Sequence 8, App1
73	168	96.0	41	4	US-08-485-546A-8	Sequence 8, App1
74	168	96.0	41	4	US-09-834-784-496	Sequence 496, App
75	168	96.0	41	4	US-09-834-784-601	Sequence 601, App
76	168	96.0	41	4	US-09-834-784-633	Sequence 633, App
77	168	96.0	41	4	US-09-834-784-1163	Sequence 1163, App
78	168	96.0	41	4	US-08-464-003-3	Sequence 3, App1
79	168	96.0	41	4	US-08-464-003-9	Sequence 9, App1
80	168	96.0	41	4	US-09-515-965A-496	Sequence 496, App
81	168	96.0	41	4	US-09-515-965A-601	Sequence 601, App
82	168	96.0	41	4	US-09-515-965A-633	Sequence 633, App
83	168	96.0	41	4	US-09-515-965A-1163	Sequence 1163, App
84	168	96.0	41	4	US-09-350-641C-496	Sequence 496, App
85	168	96.0	41	4	US-09-350-641C-601	Sequence 601, App
86	168	96.0	41	4	US-09-350-641C-633	Sequence 633, App
87	168	96.0	41	4	US-09-350-641C-1163	Sequence 1163, App
88	168	96.0	44	1	US-08-374-666-10	Sequence 10, App1
89	168	96.0	44	4	US-08-464-003-10	Sequence 10, App1
90	168	96.0	45	3	US-09-082-279B-1164	Sequence 1164, App

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

```
APPLICANT: Johnson, M. Rose
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORIAL THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,955A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82
```

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Query Match 100.0%; Score 175; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 6,9e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 38
```

RESULT 2

```
US-09-515-965A-1756
Sequence 1756, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 1756
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1756
```

```
Query Match 96.0%; Score 168; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 6,2e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 36
```

RESULT 3

```
US-09-515-965A-1757
Sequence 1757, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
```

```
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 1757
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1757
```

```
Query Match 96.0%; Score 168; DB 4; Length 37;
Best Local Similarity 97.2%; Pred. No. 6,4e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 2 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 37
```

RESULT 4

```
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1
```

```
Query Match 96.0%; Score 168; DB 1; Length 38;
```


Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 36
Db 3 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 38

RESULT 5

US-08-486-099-89
; Sequence 89, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 36
Db 3 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 38

RESULT 6

US-08-360-107A-99
; Sequence 99, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 36
Db 3 LRAIAEQHLLQITWQIKOLARILAVERYLKQ 38

RESULT 7

US-08-360-107A-132
; Sequence 132, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKQLQARILAVERYLKQ 36
Db 3 LRAIAEQHLLQITWQIKQLQARILAVERYLKQ 38

RESULT 8
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQITWQIKQLQARILAVERYLKQ 36
Db 3 LRAIAEQHLLQITWQIKQLQARILAVERYLKQ 38

RESULT 9
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6034265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQITWGIKQARILAVERYLKQ 36
DB 3 LRAIAEQHLLQITWGIKQARILAVERYLKQ 38

RESULT 10

US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475.668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQITWGIKQARILAVERYLKQ 36
DB 3 LRAIAEQHLLQITWGIKQARILAVERYLKQ 38

RESULT 11

US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQITWGIKQARILAVERYLKQ 36
DB 3 LRAIAEQHLLQITWGIKQARILAVERYLKQ 38

RESULT 12

US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 36
Db 3 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 38

RESULT 13

US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matheue, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 36
Db 3 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 38

RESULT 14

US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Wernicka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 96.0%; Score 168; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 36
Db 3 LRAIEAQHLLDTWQIKQLARILAVERYLKDQ 38

RESULT 15

US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Wernicka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match
Best Local Similarity 97.2%; Score 168; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 16
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match
Best Local Similarity 97.2%; Score 168; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 17
US-09-082-279B-659
Sequence 659, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 659
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-659

Query Match
Best Local Similarity 97.2%; Score 168; DB 3; Length 38;

Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36

RESULT 18
US-09-082-279B-660
Sequence 660, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 660
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-660

Query Match
Best Local Similarity 97.2%; Score 168; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 2 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 19
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 633395

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 36
Db 3 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 38

RESULT 20
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 36
Db 3 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 38

RESULT 21
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 36
Db 3 LRLRAIEAQHLLDTLWTWQIKQLQARILAVERYLKDQ 38

RESULT 22
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-507

Query Match	96.0%;	Score 168;	DB 4;	Length 38;
Best Local Similarity	97.2%;	Pred. No. 6.6e-17;		
Matches 35; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	1	LRAIEAQDHLLQLTWQIKQLARILAVERYLKDQ	36
D5	3	LRAIEAQDHLLQLTWGKIKQLARILAVERYLKDQ	38

RESULT 23
US-09-315

US-09-315--304B-604

```

? Sequence 604, Application US/09315304B
? Patent No. 6348568
? GENERAL INFORMATION:
? APPLICANT: Barney, S.
? APPLICANT: Guthrie, K.
? APPLICANT: Merutka, G.
? APPLICANT: Amer, M.
? APPLICANT: Lambert, D.
? TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
? TITLE OF INVENTION: PROPERTIES
? FILE REFERENCE: 7872-052
? CURRENT APPLICATION NUMBER: US/09/315,304B
? CURRENT FILING DATE: 1999-05-20
? PRIOR APPLICATION NUMBER: 09/082,279
? PRIOR FILING DATE: 1998-05-20
? NUMBER OF SEQ. ID NOS: 1667
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 604
? LENGTH: 38
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Core polypeptide
? US-09-315-304B-604

```

Query Match	96.0%;	Score 168;	DB 4;	Length 38;
Best Local Similarity	97.2%;	Pred. No. 6.6e-17;		
Matches 35; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

```
Qy 1 LRLRAEAQOHLLOLTWQIKOLQARILAVERYLKDQ 36
    |||||
Db 3 LRLRAEAQOHLLOLTWQIKOLQARILAVERYLKDQ 38
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RESULT 24
ITS-09-315

US-09-315-304B-655

```

Sequence: 659, Application US/09915504B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETICS
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIORITY APPLICATION NUMBER: 09/082,279
PRIORITY FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 659
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-659

```

Query Match	96.0%;	Score 168;	DB 4;	Length 38;
Best Local Similarity	97.2%;	Pred. No. 6.6e-17;		
Matches .35;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	1	L	R	A	I	E	A	Q	H	L	L	T	W	I	K	I	K	O	A	R	I	A	V	E	R	I	K	D	36
D5	1	L	R	A	I	E	A	Q	H	L	L	T	W	I	K	I	K	O	A	R	I	A	V	E	R	I	K	D	36

RESULT 25
IIS-09-315

US-09-315-304B-660

```

Sequence 660, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/080,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 660
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-660

```

Query Match	96.0%;	Score 168;	DB 4;	Length 38;
Best Local Similarity	97.2%;	Pred. No. 6.6e-17;		
Matches 35; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

```

QY      1 LRLRAIEAQOQHLLQLTWQIQIKQIQARILAVERYLKDQ 3
         |||||
DB      2 LRLRAIEAQOQHLLQLTWQIGIKQIQARILAVERYLKDQ 3

```

RESULT 26
INC-09-358

US-08-255-208A-25

Sequence 25, Application US/08255208A
Patent No. 6440656

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,208A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 36
Db 3 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 38

RESULT 27
US-08-470-896-89
Sequence 89, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 36
Db 3 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 38

RESULT 28
US-08-485-546A-89
Sequence 89, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 36
Db 3 LRAIEAQHLLQLTWQIKQLARILAVERYLKQ 38

RESULT 29
US-09-796-202-11

; Sequence 11, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/CPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
|||
Db 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 30
US-09-834-784-16
; Sequence 16, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 96.0%; Score 168; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
|||
Db 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

Search completed: June 2, 2004, 11:52:39
Job time: 14.3043 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 / Search time 33.163 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-180
Perfect score: 175
Sequence: 1 LIRAIQAQOHLLQITWQIKQIARILAVERYIKDQ 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	100.0	38	14	US-10-252-136-82
2	168	96.0	37	15	US-10-005-305-163
3	168	96.0	37	15	US-10-005-305-164
4	168	96.0	38	9	US-09-796-202-51
5	168	96.0	38	9	US-09-779-451-2
6	168	96.0	38	10	US-09-493-346-2
7	168	96.0	38	12	US-10-267-682-89
8	168	96.0	38	12	US-10-267-748-89
9	168	96.0	38	12	US-09-809-060-6
10	168	96.0	38	12	US-09-809-060-7
11	168	96.0	38	12	US-10-663-589-2
12	168	96.0	38	12	US-10-681-879-2
13	168	96.0	38	12	US-09-828-615-2
14	168	96.0	38	14	US-10-116-797-2
15	168	96.0	38	14	US-10-323-314-11

16	168	96.0	38	14	US-10-414-192-1	Sequence 1, Appli
17	168	96.0	38	14	US-10-351-641-16	Sequence 16, Appl
18	168	96.0	38	14	US-10-351-641-507	Sequence 507, App
19	168	96.0	38	14	US-10-351-641-604	Sequence 604, App
20	168	96.0	38	14	US-10-351-641-659	Sequence 659, App
21	168	96.0	38	14	US-10-351-641-660	Sequence 660, App
22	168	96.0	38	15	US-10-005-305-165	Sequence 165, App
23	168	96.0	38	15	US-10-005-305-202	Sequence 202, App
24	168	96.0	38	15	US-10-005-305-203	Sequence 203, App
25	168	96.0	38	15	US-10-420-194-1334	Sequence 1234, Ap
26	168	96.0	38	16	US-10-664-021-2	Sequence 2, Appli
27	168	96.0	38	16	US-10-671-316-2	Sequence 2, Appli
28	168	96.0	41	12	US-10-267-682-8	Sequence 8, Appli
29	168	96.0	41	12	US-10-267-748-8	Sequence 8, Appli
30	168	96.0	41	12	US-10-663-589-30	Sequence 30, Appli
31	168	96.0	41	12	US-10-663-589-33	Sequence 33, Appli
32	168	96.0	41	12	US-10-663-589-35	Sequence 35, Appli
33	168	96.0	41	14	US-10-252-136-8	Sequence 8, Appli
34	168	96.0	41	14	US-10-414-192-3	Sequence 3, Appli
35	168	96.0	41	14	US-10-414-192-9	Sequence 9, Appli
36	168	96.0	41	14	US-10-351-641-496	Sequence 496, App
37	168	96.0	41	14	US-10-351-641-601	Sequence 601, App
38	168	96.0	41	14	US-10-351-641-633	Sequence 633, App
39	168	96.0	41	14	US-10-351-641-1163	Sequence 1163, Ap
40	168	96.0	41	16	US-10-664-021-27	Sequence 27, Appli
41	168	96.0	41	16	US-10-671-316-27	Sequence 27, Appli
42	168	96.0	44	12	US-10-663-589-36	Sequence 36, Appli
43	168	96.0	44	14	US-10-414-192-10	Sequence 10, Appli
44	168	96.0	44	9	US-09-779-451-9	Sequence 9, Appli
45	168	96.0	45	12	US-09-809-060-50	Sequence 50, Appli
46	168	96.0	45	12	US-10-663-589-29	Sequence 29, Appli
47	168	96.0	45	14	US-10-351-641-1164	Sequence 1164, Ap
48	168	96.0	45	16	US-10-664-021-26	Sequence 26, Appli
49	168	96.0	45	16	US-10-671-316-26	Sequence 26, Appli
50	168	96.0	49	9	US-09-796-202-3	Sequence 3, Appli
51	168	96.0	49	14	US-10-323-314-3	Sequence 3, Appli
52	168	96.0	51	12	US-10-663-589-27	Sequence 27, Appli
53	168	96.0	51	14	US-10-351-641-745	Sequence 745, App
54	168	96.0	51	16	US-10-664-021-24	Sequence 24, Appli
55	168	96.0	51	16	US-10-671-316-24	Sequence 24, Appli
56	168	96.0	52	14	US-10-351-641-1119	Sequence 1119, Ap
57	168	96.0	53	14	US-10-351-641-955	Sequence 955, App
58	168	96.0	53	14	US-10-351-641-1062	Sequence 1062, Ap
59	168	96.0	55	9	US-09-779-451-1	Sequence 1, Appli
60	168	96.0	55	12	US-09-809-060-14	Sequence 14, Appli
61	168	96.0	57	15	US-10-438-691-1	Sequence 1, Appli
62	168	96.0	59	16	US-10-664-021-1	Sequence 1, Appli
63	168	96.0	59	16	US-10-671-316-1	Sequence 1, Appli
64	168	96.0	60	12	US-10-663-589-1	Sequence 1, Appli
65	168	96.0	63	12	US-10-267-748-201	Sequence 201, App
66	168	96.0	63	12	US-10-267-748-201	Sequence 201, App
67	168	96.0	63	14	US-10-252-136-54	Sequence 54, Appli
68	168	96.0	103	14	US-10-263-103-29	Sequence 29, Appli
69	168	96.0	103	15	US-10-438-691-3	Sequence 3, Appli
70	168	96.0	113	15	US-10-438-691-4	Sequence 4, Appli
71	168	96.0	177	14	US-10-040-349B-2	Sequence 8, Appli
72	168	96.0	198	9	US-09-854-816-88	Sequence 88, Appli
73	168	96.0	198	9	US-09-854-816-89	Sequence 89, Appli
74	168	96.0	200	14	US-10-263-103-25	Sequence 25, Appli
75	168	96.0	200	15	US-10-438-691-8	Sequence 8, Appli
76	168	96.0	222	14	US-10-059-271-81	Sequence 81, Appli
77	168	96.0	254	14	US-10-059-271-82	Sequence 82, Appli
78	168	96.0	256	14	US-10-059-271-97	Sequence 97, Appli
79	168	96.0	268	9	US-09-854-816-16	Sequence 16, Appli
80	168	96.0	268	9	US-09-854-816-17	Sequence 17, Appli
81	168	96.0	268	9	US-09-854-816-18	Sequence 18, Appli
82	168	96.0	268	9	US-09-854-816-19	Sequence 19, Appli
83	168	96.0	269	9	US-09-854-816-43	Sequence 43, Appli
84	168	96.0	338	12	US-10-267-682-90	Sequence 90, Appli
85	168	96.0	338	12	US-10-267-748-90	Sequence 90, Appli
86	168	96.0	344	14	US-10-040-349B-1	Sequence 1, Appli
87	168	96.0	345	9	US-09-779-451-8	Sequence 8, Appli
88	168	96.0	345	14	US-10-026-741-49	Sequence 49, Appli

89 168 96.0 359 14 US-10-214-670-58
90 168 96.0 391 14 US-10-059-271-93

ALIGNMENTS

RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 175; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 2
US-10-005-305-163
; Sequence 163, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-163

Query Match 96.0%; Score 168; DB 15; Length 36;
Best Local Similarity 97.2%; Pred. No. 5.3e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36

RESULT 3
US-10-005-305-164
; Sequence 164, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-164

Query Match 96.0%; Score 168; DB 15; Length 37;
Best Local Similarity 97.2%; Pred. No. 5.5e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 2 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 4
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBLATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT FILING DATE: 2001-02-28
; CURRENT APPLICATION NUMBER: US/09/796,202
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.0%; Score 168; DB 9; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 5
US-09-779-451-2
; Sequence 2, Application US/09779451

Patent No. US2002009452A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
PRIORITY FILING DATE: 2001-08-17
PRIORITY APPLICATION NUMBER: US 60/235,901
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: US 60/181,543
PRIORITY FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 96.0%; Score 168; DB 9; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 36
DB 3 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 6
US-09-493-346-2
Sequence 2, Application US/09493346
Publication No. US20030082185A1
GENERAL INFORMATION:
APPLICANT: Olson, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/09/493,346
PRIORITY FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 96.0%; Score 168; DB 10; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 36
DB 3 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 7
US-10-267-682-89
Sequence 89, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
MATCHES: Matthews, Thomas J.
WILD, Carl T.
BARNEY, Shawn O.
PETTEWAY, Stephen R.
LANGLOIS, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 36
DB 3 LRAIRAEQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 8
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
MATCHES: Matthews, Thomas J.
WILD, Carl T.
BARNEY, Shawn O.
PETTEWAY, Stephen R.
LANGLOIS, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIAEQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 9
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIAEQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 10
US-09-809-060-7
Sequence 7, Application US/09809060

Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIAEQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 11
US-10-663-589-3
Sequence 3, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIAEQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 12
US-10-681-879-2
Sequence 2, Application US/10681879
Publication No. US20040062767A1
GENERAL INFORMATION:
APPLICANT: Olson, William C
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
TITLE OF INVENTION: Infection
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/10/681,879
CURRENT FILING DATE: 2003-10-09

PRIOR APPLICATION NUMBER: US/09/493,346
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 38

RESULT 13
US-09-828-615-2
Sequence 2, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 96.0%; Score 168; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 38

RESULT 14
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 36

DB 3 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 38

RESULT 15
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWGIKOLQARILAVERYLKDQ 38

RESULT 16
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
Bolognesi, Daniel P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 17
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 18
US-10-351-641-507
Sequence 507, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 19
US-10-351-641-604
Sequence 604, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 20
US-10-351-641-659
Sequence 659, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.

;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 659
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
;; US-10-351-641-659

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 36
Db 1 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 36

RESULT 21
US-10-351-641-660
;; Sequence 660, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Anwer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; TITLE OF INVENTION: PROPERTIES
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 660
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
;; US-10-351-641-660

Query Match 96.0%; Score 168; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 36
Db 2 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 37

RESULT 22
US-10-005-305-165
;; Sequence 165, Application US/10005305

;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 165
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
;; US-10-005-305-165

Query Match 96.0%; Score 168; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 36
Db 3 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 38

RESULT 23
US-10-005-305-202
;; Sequence 202, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 202
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
;; US-10-005-305-202

Query Match 96.0%; Score 168; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 5.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 36
Db 3 LRAIAEQHLLQLTWGIKQLARILAVERYLKQ 38

RESULT 24
US-10-005-305-203
;; Sequence 203, Application US/10005305
;; Publication No. US20030203841A1

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORNYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 96.0%; Score 168; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 25
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US2004006035A1
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Blact, Larry
APPLICANT: Macetjak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
TITLE OF INVENTION: Interactions
FILE REFERENCE: MBH02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/361,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(38)
US-10-420-194-1234

Query Match 96.0%; Score 168; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 26
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US2004007637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
TITLE OF INVENTION: Immunodeficiency Virus
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 96.0%; Score 168; DB 16; Length 38;
Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 36
Db 3 LRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 27
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: peptides, and trimers formed therefrom
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match 96.0%; Score 168; DB 16; Length 38;

Best Local Similarity 97.2%; Pred. No. 5,6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 3 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 28

US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US2004003235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.

Wild, Carl T.
Barney, Shawn O.

Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-267-632-8

Query Match 96.0%; Score 168; DB 12; Length 41;

Best Local Similarity 97.2%; Pred. No. 6,1e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 6 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 41

RESULT 29

US-10-267-748-8
Sequence 8, Application US/10267748

Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.

Wild, Carl T.
Barney, Shawn O.

Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-267-748-8

Query Match 96.0%; Score 168; DB 12; Length 41;

Best Local Similarity 97.2%; Pred. No. 6,1e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 36
DB 6 LRAIAEQHLLQLTWQIKQLQARILAVERYLKDQ 41

RESULT 30

US-10-663-589-30

Sequence 30, Application US/10663589

Publication No. US20040063637A1

GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV

FILE REFERENCE: TRM-003

CURRENT APPLICATION NUMBER: US/10/663,589

PRIOR APPLICATION NUMBER: US 60/414,441

PRIOR FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 95

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 43.8451 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-181
Sequence: 1 LRAIEAQOHLQLTWQIQXQARILAVERYLKQ 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	35	3	AAB14737 HIV-1 iso
2	171	100.0	35	4	AAB55002 Anti-HIV
3	171	100.0	36	3	AAB14738 HIV-1 iso
4	171	100.0	36	4	AAB55003 Anti-HIV
5	171	100.0	37	3	AAB14739 HIV-1 iso
6	171	100.0	37	4	AAB55004 Anti-HIV
7	171	100.0	38	4	AAR98408 DP107 cor
8	171	100.0	38	4	AAB54785 HIV antiiv
9	171	100.0	38	4	AAB55005 Anti-HIV
10	171	100.0	38	4	AAB54970 Anti-HIV
11	171	100.0	38	4	AAB92244 Virus rel
12	171	100.0	38	4	AAU14011 DP107 pep
13	171	100.0	38	5	AAO18771 HIV gp41
14	167	97.7	34	4	AAB14736 HIV-1 iso
15	167	97.7	34	4	AAB55001 Anti-HIV
16	166	97.1	37	3	AAB14705 HIV-1 iso
17	166	97.1	37	4	AAB54969 Anti-HIV
18	164	95.9	35	3	AAB52783 T21/DP107
19	164	95.9	36	3	AAB52784 T21/DP107
20	164	95.9	37	3	AAB52785 T21/DP107
21	164	95.9	38	2	AAR55635 DP-139 -
22	164	95.9	38	2	AAR55636 DP-140 -
23	164	95.9	38	2	AAR47216 DP-107 -
24	164	95.9	38	2	AAW27614 Human imm
25	164	95.9	38	3	AAV88666 Core poly

26	164	95.9	38	3	AAV88730 Core poly
27	164	95.9	38	3	AAV88731 Core poly
28	164	95.9	38	3	AAV89145 Core poly
29	164	95.9	38	3	AAV89146 Core poly
30	164	95.9	38	3	AAV89243 Core poly
31	164	95.9	38	3	AAV89243 Core poly
32	164	95.9	38	3	AAV89243 Core poly
33	164	95.9	38	3	AAV89243 Core poly
34	164	95.9	38	3	AAV89243 Core poly
35	164	95.9	38	3	AAV89243 Core poly
36	164	95.9	38	4	AAV89243 Core poly
37	164	95.9	38	4	AAV89243 Core poly
38	164	95.9	38	4	AAV89243 Core poly
39	164	95.9	38	4	AAV89243 Core poly
40	164	95.9	38	4	AAV89243 Core poly
41	164	95.9	38	4	AAV89243 Core poly
42	164	95.9	38	4	AAV89243 Core poly
43	164	95.9	38	4	AAV89243 Core poly
44	164	95.9	38	4	AAV89243 Core poly
45	164	95.9	38	4	AAV89243 Core poly
46	164	95.9	38	4	AAV89243 Core poly
47	164	95.9	38	4	AAV89243 Core poly
48	164	95.9	38	4	AAV89243 Core poly
49	164	95.9	38	4	AAV89243 Core poly
50	164	95.9	38	4	AAV89243 Core poly
51	164	95.9	38	4	AAV89243 Core poly
52	164	95.9	38	4	AAV89243 Core poly
53	164	95.9	38	4	AAV89243 Core poly
54	164	95.9	38	4	AAV89243 Core poly
55	164	95.9	38	4	AAV89243 Core poly
56	164	95.9	38	4	AAV89243 Core poly
57	164	95.9	38	4	AAV89243 Core poly
58	164	95.9	38	4	AAV89243 Core poly
59	164	95.9	38	4	AAV89243 Core poly
60	164	95.9	38	4	AAV89243 Core poly
61	164	95.9	38	4	AAV89243 Core poly
62	164	95.9	38	4	AAV89243 Core poly
63	164	95.9	38	4	AAV89243 Core poly
64	164	95.9	38	4	AAV89243 Core poly
65	164	95.9	38	4	AAV89243 Core poly
66	164	95.9	38	4	AAV89243 Core poly
67	164	95.9	38	4	AAV89243 Core poly
68	164	95.9	38	4	AAV89243 Core poly
69	164	95.9	38	4	AAV89243 Core poly
70	164	95.9	38	4	AAV89243 Core poly
71	164	95.9	38	4	AAV89243 Core poly
72	164	95.9	38	4	AAV89243 Core poly
73	164	95.9	38	4	AAV89243 Core poly
74	164	95.9	38	4	AAV89243 Core poly
75	164	95.9	38	5	AAE22292 gp41 fusi
76	164	95.9	38	5	AAE22292 gp41 fusi
77	164	95.9	38	5	AAE22292 gp41 fusi
78	164	95.9	38	5	AAE22292 gp41 fusi
79	164	95.9	38	5	AAE22292 gp41 fusi
80	164	95.9	38	5	AAE22292 gp41 fusi
81	164	95.9	38	5	AAE22292 gp41 fusi
82	164	95.9	38	5	AAE22292 gp41 fusi
83	164	95.9	38	5	AAE22292 gp41 fusi
84	164	95.9	38	5	AAE22292 gp41 fusi
85	164	95.9	38	5	AAE22292 gp41 fusi
86	164	95.9	38	5	AAE22292 gp41 fusi
87	164	95.9	38	5	AAE22292 gp41 fusi
88	164	95.9	38	5	AAE22292 gp41 fusi
89	164	95.9	38	5	AAE22292 gp41 fusi
90	164	95.9	38	5	AAE22292 gp41 fusi

ALIGNMENTS

RESULT 1
AAB14737 standard; peptide; 35 AA.

XX AAB14737;
 AC 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #66.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000WO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 PI WILD CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Disclosure; Page 38; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralizing antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond to or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 35 AA;
 XX

Query Match 100.0%; Score 171; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLARILAVERYLKQ 35
 Db 1 LRAIEAQOHLLQLTWQIKQLARILAVERYLKQ 35
 XX
 AC AAB55002 standard; peptide, 35 AA.
 XX
 AC AAB55002;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #32.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifusogenic; mobile blood component; measles virus; MeV; SiV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PA (COND-) CONJUCHEM INC.
 PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007436/01.
 XX
 PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (II)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SiV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 35 AA;
 XX

Query Match 100.0%; Score 171; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LRAIEAQOHLLQLTWQIKQLARILAVERYLKQ 35

```

Db      1 LRAIEAQOHLQLTWQIKOLQARILLAVERYLKQ 35
|||||
RESULT 3
AAB14738
ID      AAB14738 standard; peptide; 36 AA.
XX
XX      AAB14738;
AC
XX
XX      12-SEP-2003 (revised)
DT
XX      24-NOV-2000 (first entry)
DE
XX      HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #67.
XX
XX      HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX      core 6-helix bundle; viral entry inhibitor; immunogenic; antibody;
XX      humoral response; broad spectrum vaccine; anti-HIV;
XX      envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX      isolate LAI.
XX
XX      Human immunodeficiency virus 1.
OS
XX      WO200040616-A1.
XX
XX      13-JUL-2000.
PD
XX
XX      10-JAN-2000; 2000WO-US000456.
PF
XX      08-JAN-1999; 99US-0115404P.
XX      07-JAN-2000; 2000US-00480336.
PR
XX
XX      (WILD/) WILD C T.
XX      (WEIS/) WEISS C D.
PA
XX
XX      WILD CT, Weiss CD;
PI
XX      WPI; 2000-465959/40.
DR
XX
XX      Raising neutralizing antibody response to human immunodeficiency virus,
PT      comprises administering a polypeptide capable of forming a stable coiled-
PT      coil solution structure.
XX
XX      Disclosure; Page 38; 97pp; English.
XX
XX      Sequences AAB14672-B14739 represent peptides derived from the N-helical
XX      domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
XX      isolate LAI. The invention relates to raising a neutralizing antibody
XX      response to a broad spectrum of HIV (human immunodeficiency virus)
XX      strains and isolates, comprising the administration of a peptide which
XX      corresponds to or mimics highly conserved portions of gp41 which are
XX      important in mediating the process of viral entry into host cells. Such
XX      peptides can correspond to or mimic the coiled coil solution structure of
XX      the N-helical domain (the heptad repeat region), or can correspond or
XX      mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
XX      helical segment), or the gp41 core 6-helix bundle, which is formed by the
XX      interaction of the N- and C-helical domains of three gp41 proteins. The
XX      peptides can be administered either singly or as a combination
XX      (particularly a combination of N-helical and C-helical peptides), and can
XX      be multimerised. For example, N- and C-helical domain peptides can be
XX      alternately linked together to form a peptide which mimics the core 6-
XX      helix bundle. Administration of the peptide(s) generates a humoral
XX      response, with the production of antibodies against gp41 structures
XX      involved in viral entry. As these portions of gp41 are well conserved,
XX      such antibodies may be effective against a broad range of HIV strains and
XX      isolates. The peptide compositions may be administered as a prophylactic
XX      or therapeutic vaccine to generate antibodies which reduce or inhibit the
XX      ability of HIV to infect uninfected cells. A composition comprising
XX      polyclonal or monoclonal antibodies can be administered to reduce HIV
XX      infection of uninfected cells. Antibodies raised against entry-relevant
XX      gp41 structures may also be used therapeutically and as tools to further
XX      elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
XX      standardise OS field)

```

```

XX      SQ      Sequence 36 AA;
XX
XX      Query Match      100.0%; Score 171; DB 3; Length 36;
XX      Best Local Similarity 100.0%; Pred. No. 1.8e-15;
XX      Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 LRAIEAQOHLQLTWQIKOLQARILLAVERYLKQ 35
Db      2 LRAIEAQOHLQLTWQIKOLQARILLAVERYLKQ 36
|||||
RESULT 4
AAB55003
ID      AAB55003 standard; peptide; 36 AA.
XX
XX      AAB55003;
AC
XX
XX      11-SEP-2003 (revised)
DT
XX      05-MAR-2001 (first entry)
DE
XX      Anti-HIV peptide DP107 amino truncation peptide #33.
XX
XX      Long laesting fusion peptide inhibitor; viral infection; antiviral;
XX      antitubercogenic; mobile blood component; measles virus; MeV; SIV;
XX      simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX      human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX      Human immunodeficiency virus 1.
OS
XX      WO200069902-A1.
XX
XX      23-NOV-2000.
PD
XX
XX      17-MAY-2000; 2000WO-US013651.
PF
XX      17-MAY-1999; 99US-0134406P.
XX      10-SEP-1999; 99US-0153406P.
PR
XX
XX      (CONU-) CONUTCHEM INC.
PA
XX
XX      Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI
XX      WPI; 2001-007496/01.
DR
XX
XX      A modified peptide and a reactive group which is reactive with amino
XX      groups, hydroxyl groups, or thiol groups on blood components to form
XX      stable covalent bonds useful for treatment of viral infections, e.g.
XX      human immunodeficiency virus.
XX
XX      Disclosure; Page 139; 211pp; English.
XX
XX      The present invention describes a modified anti-viral peptide (I)
XX      comprising a peptide that exhibits anti-viral activity and a reactive
XX      group which is reactive with amino groups, hydroxyl groups, or thiol
XX      groups on blood components to form stable covalent bonds. (I) has anti-
XX      viral and anti-fusogenic activities. (I) inhibits viral infection of
XX      cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX      the level of membrane fusion events between two or more entities, e.g.,
XX      virus-cell or cell-cell, relative to the level of membrane fusion that
XX      occurs in the absence of the peptide. (I) is useful in the treatment of
XX      patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX      MeV, and SIV. (I) may be administered prophylactically to previously
XX      uninfected individuals. This is useful in cases where an individual has
XX      been subjected to a high risk of exposure to a virus. By bonding of long-
XX      lived components of the blood, such as immunoglobulin, serum albumin, red
XX      blood cells and platelets the activity is extended for days to weeks.
XX      This is due to improved stability in vivo and a reduced susceptibility to
XX      peptidase or protease degradation. This minimises the need for more
XX      frequent, or even continual, administration of the peptides. AAB54784 to
XX      AAB55431 represent peptides used in the exemplification of the present
XX      invention. (Updated on 11-SEP-2003 to standardise OS field)
XX

```

SQ Sequence 36 AA;

Query Match 100.0%; Score 171; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQLQARIILAVERYLKQ 35
 2 LRAIEAQHLLQLTWQIKQLQARIILAVERYLKQ 36

Db

RESULT 5
 AAB14739
 ID AAB14739 standard; peptide; 37 AA.
 XX AAB14739;
 AC
 XX
 DT 12-SEP-2003 (revised)
 XX 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 XX 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 XX (WEIS/) WEIS C D.
 PI
 XX WILD CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 PT
 PS Disclosure; Page 38; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralizing antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic

CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX

SQ Sequence 37 AA;

Query Match 100.0%; Score 171; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQLQARIILAVERYLKQ 35
 3 LRAIEAQHLLQLTWQIKQLQARIILAVERYLKQ 37

Db

RESULT 6
 AAB55004
 ID AAB55004 standard; peptide; 37 AA.
 XX AAB55004;
 AC
 XX
 DT 11-SEP-2003 (revised)
 XX 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #34.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 XX 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONU-) CONUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007496/01.
 XX
 CC A modified peptide and a reactive group which is reactive with amino
 CC groups, hydroxyl groups, or thiol groups on blood components to form
 CC stable covalent bonds useful for treatment of viral infections, e.g.
 CC human immunodeficiency virus.
 CC
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By binding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red

CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB54784 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 171; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
DB 3 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 37
RESULT 7
AAR98408
ID AAR98408 standard; peptide; 38 AA.
XX
AC AAR98408;
XX
DT 16-OCT-2003 (revised)
DT 17-FEB-1997 (first entry)
XX
DE DPL07 corresponds to residues 558-595 of HIV-1(LAI) gp41.
XX
KM Antifusogenic activity; antiviral capability; coiled-coil peptide;
KM ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
KM influenza virus; hepatitis B virus.
XX
XX Human immunodeficiency virus 1.
OS
XX WO9619495-A1.
XX
XX 27-JUN-1996.
XX
XX 20-DEC-1995; 95WO-US016733.
XX
XX 20-DEC-1994; 94US-00360107.
XX
XX 06-JUN-1995; 95US-00470896.
XX
XX (UYDU-) UNIV DUKE.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Bolognesi DP, Mathews TV, Wild CT, Barney S, Lambert DM;
XX
XX Peteway SR, Langlois AJ;
XX
XX WPI; 1996-309517/31.
XX
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
XX
XX isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence
XX
XX search motif.
XX
XX
XX Disclosure; Page 30; 471pp; English.
XX
XX The sequences given in AAR98398-408 represent peptides which exhibit
XX
XX antifusogenic activity, antiviral capability and/or the ability to
XX
XX modulate intracellular processes involving coiled-coil peptide
XX
XX structures. These peptides are recognised by the ALLMOT15, 107x178x4 and
XX
XX PLZIP search motifs. These peptides may be used to inhibit the
XX
XX transmission of a virus, pref. HIV, influenza virus, or hepatitis B
XX
XX virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 171; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35

DB 4 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
RESULT 8
AAB54785
ID AAB54785 standard; peptide; 38 AA.
XX
XX
AC AAB54785;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX
DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX
XX antifusogenic; mobile blood component; measles virus; MeV; SiV;
XX
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjelal N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX
XX A modified peptide and a reactive group which is reactive with amino
XX
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX
XX human immunodeficiency virus.
XX
XX
XX Claim 6; Page 173; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
XX
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX
XX the level of membrane fusion events between two or more entities, e.g.,
XX
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX
XX MeV, and SiV. (I) may be administered prophylactically to previously
XX
XX uninfected individuals. This is useful in cases where an individual has
XX
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX
XX blood cells and platelets the activity is extended for days to weeks.
XX
XX This is due to improved degradation. This minimises the need for more
XX
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX
XX AAB54784 represent peptides used in the exemplification of the present
XX
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 171; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35

Db 4 LRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 9

ID AAB55005 standard; peptide; 38 AA.

AC AAB55005;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 amino truncation peptide #35.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX Human immunodeficiency virus 1.
OS WO200069902-A1.

PN 23-NOV-2000.

PD 17-MAY-2000; 2000MO-US013651.

PF 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

XX Disclosure; Page 139; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MeV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX CC AAB55431 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 10

ID AAB54970 standard; peptide; 38 AA.

AC AAB54970;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 carboxy truncation peptide #35.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX Human immunodeficiency virus 1.
OS WO200069902-A1.

PN 23-NOV-2000.

PD 17-MAY-2000; 2000MO-US013651.

PF 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

XX Disclosure; Page 137; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MeV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX CC AAB55431 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 11
 AAB92244
 ID AAB92244 standard; peptide; 38 AA.
 XX
 AC AAB92244;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Virus related peptide SEQ ID NO:1420.
 XX
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimide group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Malner PG, Holmes DL, Tribaudieu K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 662; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 38 AA;
 XX
 QY Query Match 100.0%; Score 171; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKQ 35
 4 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKQ 38
 XX
 RESULT 12
 AAU14011
 ID AAU14011 standard; peptide; 38 AA.
 XX
 AC AAU14011;

XX
 DT 11-SEP-2003 (revised)
 DT 21-NOV-2001 (first entry)
 XX
 DE DP107 peptide from HIV-1 transmembrane protein gp41.
 XX
 KM Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KM antitumorigenic; antiviral; HIV transmission.
 XX
 OS Human immunodeficiency virus 1; isolate LAI.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 1..35
 FT /note="amino acids 1-35 can be optionally and serially
 FT deleted from the N-terminus"
 FT Misc-difference 4..38
 FT /note="amino acids 4-38 can be optionally and serially
 FT deleted from the C-terminus"
 XX
 PN WO200151673-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 05-JUL-2000; 2000MO-US035727.
 XX
 PR 09-JUL-1999; 99US-00350841.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merruck G;
 XX
 DR WPI; 2001-442157/47.
 XX
 PT Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitumorigenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Page 33; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antitumorigenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 38 AA;
 XX
 QY Query Match 100.0%; Score 171; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKQ 35
 4 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKQ 38
 XX
 RESULT 13
 AA018771
 ID AA018771 standard; peptide; 38 AA.
 XX

AA018771;
29-OCT-2002 (first entry)
HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
gp41.
Human Immunodeficiency virus.
MO200256902-A2.
25-JUL-2002.
17-DEC-2001; 2001WO-US048802.
19-DEC-2000; 2000US-0256657P.
(SCHE) SCHERING CORP.
Baroudy BM;
WPI; 2002-636513/68.
Treatment of HIV infection in an individual involves administration of a
combination of chemokine co-receptor five antagonist and a specified HIV
envelope polypeptide.
Disclosure; Page 34; 52pp; English.
The present invention relates to a method of treating an HIV infection in
an individual, which involves administering in combination a chemokine co-
receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
derivative. Other viral infections can also be treated using the method.
The present sequence is a peptide derived from HIV and useful in the
method of the invention
Sequence 38 AA;
Query Match 100.0%; Score 171; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35
4 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
RESULT 14
AAB14736
ID AAB14736 standard; peptide; 34 AA.
AAB14736;
12-SEP-2003 (revised)
24-NOV-2000 (first entry)
HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #65.
HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
humoral response; broad spectrum vaccine; anti-HIV;
envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
isolate LAI.
Human immunodeficiency virus 1.
MO200040616-A1.
13-JUL-2000.
10-JAN-2000; 2000WO-US000456.

08-JAN-1999; 99US-0115404P.
07-JAN-2000; 2000US-00480336.
(WILD/) WILD C T.
(WEIS/) WEISS C D.
Wild CT, Weiss CD;
WPI; 2000-465959/40.
Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
coil solution structure.
Disclosure; Page 38; 97pp; English.
Sequences AAB14672-B14739 represent peptides derived from the N-helical
domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
isolate LAI. The invention relates to raising a neutralizing antibody
response to a broad spectrum of HIV (human immunodeficiency virus)
strains and isolates, comprising the administration of a peptide which
corresponds to or mimics highly conserved portions of gp41 which are
important in mediating the process of viral entry into host cells. Such
peptides can correspond to or mimic the coiled coil solution structure of
the N-helical domain (the heptad repeat region), or can correspond to
mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
helical segment), or the gp41 core 6-helix bundle, which is formed by the
interaction of the N- and C-helical domains of three gp41 proteins. The
peptides can be administered either singly or as a combination
(particularly a combination of N-helical and C-helical peptides), and can
be multimerised. For example, N- and C-helical domain peptides can be
alternately linked together to form a peptide which mimics the core 6-
helix bundle. Administration of the peptide(s) generates a humoral
response, with the production of antibodies against gp41 structures
involved in viral entry. As these portions of gp41 are well conserved,
such antibodies may be effective against a broad range of HIV strains and
isolates. The peptide compositions may be administered as a prophylactic
or therapeutic vaccine to generate antibodies which reduce or inhibit the
ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
infection of uninfected cells. Antibodies raised against entry-relevant
gp41 structures may also be used therapeutically and as tools to further
elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
standardise OS field)
Sequence 34 AA;
Query Match 97.7%; Score 167; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.8e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 RAIEAQOHLQLTWQIKQARILAVERYLKQ 35
1 RAIEAQOHLQLTWQIKQARILAVERYLKQ 34
RESULT 15
AAB55001
ID AAB55001 standard; peptide; 34 AA.
AAB55001;
11-SEP-2003 (revised)
05-MAR-2001 (first entry)
Anti-HIV peptide DP107 amino truncation peptide #31.
Long lasting fusion peptide inhibitor; viral infection; antiviral;
antifusogenic; mobile blood component; measles virus; MeV; SIV;
simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX	Human immunodeficiency virus 1.
XX	
XX	WO200069902-A1.
XX	
XX	23-NOV-2000.
XX	
XX	17-MAY-2000; 2000WO-US013651.
XX	
XX	17-MAY-1999; 99US-0134406P.
XX	
XX	10-SEP-1999; 99US-0153406P.
XX	
XX	(CONF-) CONJUCHEM INC.
XX	
XX	Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG,
XX	
XX	WPI; 2001-007496/01.
XX	
XX	A modified peptide and a reactive group which is reactive with amino
XX	groups, hydroxyl groups, or thiol groups on blood components to form
XX	stable covalent bonds useful for treatment of viral infections, e.g.
XX	human immunodeficiency virus.
XX	
XX	Disclosure; Page 139; 211pp; English.
XX	
XX	The present invention describes a modified anti-viral peptide (I)
XX	comprising a peptide that exhibits anti-viral activity and a reactive
XX	group which is reactive with amino groups, hydroxyl groups, or thiol
XX	groups on blood components to form stable covalent bonds. (I) has anti-
XX	viral and anti-fusogenic activities. (I) inhibits viral infection of
XX	cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX	the level of membrane fusion events between two or more entities, e.g.,
XX	virus-cell or cell-cell, relative to the level of membrane fusion that
XX	occurs in the absence of the peptide. (I) is useful in the treatment of
XX	patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX	MeV, and SIV. (I) may be administered prophylactically to previously
XX	uninfected individuals. This is useful in cases where an individual has
XX	been subjected to a high risk of exposure to a virus. By bonding of long-
XX	lived components of the blood, such as immunoglobulin, serum albumin, red
XX	blood cells and platelets the activity is extended for days to weeks.
XX	This is due to improved stability in vivo and a reduced susceptibility to
XX	peptidase or protease degradation. This minimises the need for more
XX	frequent, or even continual, administration of the peptides. AAB54784 to
XX	AAB55431 represent peptides used in the exemplification of the present
XX	invention. (Updated on 11-SEP-2003 to standardise OS field)
XX	
XX	Sequence 34 AA;
XX	
XX	Query Match 97.7%; Score 167; DB 4; Length 34;
XX	Best Local Similarity 100.0%; Pred. No. 5.8e-15;
XX	Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
XX	2 RAIEAQHLLQLTWQIKOLARILAVRRYKDD 35
XX	1 RAIEAQHLLQLTWQIKOLARILAVRRYKDD 34
XX	
XX	RESULT 16
XX	AAB14705
XX	ID AAB14705 standard; peptide; 37 AA.
XX	
XX	AAB14705;
XX	
XX	12-SEP-2003 (revised)
XX	DT 24-NOV-2000 (first entry)
XX	
XX	HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
XX	
XX	HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX	core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX	humoral response; broad spectrum vaccine; anti-HIV;
XX	envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX	isolate LAI.
XX	

OS		Human immunodeficiency virus 1.
PX		
PN		WO200040616-A1.
PX		
PD		13-JUL-2000.
PX		
PF		10-JAN-2000; 2000MO-USO00456.
PX		
PR		08-JAN-1999; 99US-0115404P.
PX		07-JAN-2000; 2000US-00480336.
PA		(WILD/) WILD C T.
PA		(WEISS/) WEISS C D.
PX		
PI		Wild CT, Weiss CD;
PX		
DR		WPI; 2000-465959/40.
PX		
PT		Raising neutralizing antibody response to human immunodeficiency virus,
PT		comprises administering a polypeptide capable of forming a stable coiled-
PT		coil solution structure.
PX		
PS		Disclosure; Page 36; 97p; English.
PX		
CC		Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC		domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC		isolate LM1. The invention relates to raising a neutralising antibody
CC		response to a broad spectrum of HIV (human immunodeficiency virus)
CC		strains and isolates, comprising the administration of a peptide which
CC		corresponds to or mimics highly conserved portions of gp41 which are
CC		important in mediating the process of viral entry into host cells. Such
CC		peptides can correspond to or mimic the coiled coil solution structure of
CC		the N-helical domain (the heptad repeat region), or can correspond or
CC		mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC		helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC		interaction of the N- and C-helical domains of three gp41 proteins. The
CC		peptides can be administered either singly or as a combination
CC		(particularly a combination of N-helical and C-helical peptides) and can
CC		be multimerised. For example, N- and C-helical domain peptides can be
CC		alternately linked together to form a peptide which mimics the core 6-
CC		helix bundle. Administration of the peptide(s) generates a humoral
CC		response, with the production of antibodies against gp41 structures
CC		involved in viral entry. As these portions of gp41 are well conserved,
CC		such antibodies may be effective against a broad range of HIV strains and
CC		isolates. The peptide compositions may be administered as a prophylactic
CC		or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC		ability of HIV to infect uninfected cells. A composition comprising
CC		polyclonal or monoclonal antibodies can be administered to reduce HIV
CC		infection of uninfected cells. Antibodies raised against entry-relevant
CC		gp41 structures may also be used therapeutically and as tools to further
CC		elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC		standardise OS field)
PX		
SQ		Sequence 37 AA:
	Query Match	97.1%; Score 166; DB 3; Length 37;
	Best Local Similarity	100.0%; Pred. No. 8.ee-15;
	Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		1 LRAIEAQCHLQLTWVQIKQLQARILAVERTLKD 34
DB		4 LRAIEAQCHLQLTWVQIKQLQARILAVERTLKD 37
RESULT 17		
ID	AAB54969 standard; peptide; 37 AA.	
XX		
AC	AAB54969;	
XX		
DT	11-SEP-2003 (revised)	
DT	05-MAR-2001 (first entry)	
XX		

DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; MeV; SIV;
KM simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX Human immunodeficiency virus 1.
XX WO200069902-A1.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US013651.
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI WPI; 2001-007496/01.
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX Disclosure; Page 137; 21pp; English.
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPiV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 37 AA;
Query Match 97.1%; Score 166; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. NO. 8.e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKD 34
Db 4 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKD 37
RESULT 18
AAB52783
ID AAB52783 standard; peptide; 35 AA.
XX AAB52783;
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX T21/DP107 peptide fragment #65.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX Human immunodeficiency virus 1.
XX WO200066622-A1.
XX 09-NOV-2000.
XX 05-MAY-2000; 2000WO-US012371.
XX 05-MAY-1999; 99US-0132686P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
PI WPI; 2000-656493/63.
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX Claim 12; Page 29; 149pp; English.
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 35 AA;
Query Match 95.9%; Score 164; DB 3; Length 35;
Best Local Similarity 97.1%; Pred. NO. 1.5e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKDQ 35
Db 1 LRAIEAQOHLLQLTWQIKOLQARIILAVERYLKDQ 35
RESULT 19
AAB52784
ID AAB52784 standard; peptide; 36 AA.
XX AAB52784;
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX T21/DP107 peptide fragment #66.
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX Human immunodeficiency virus 1.
XX WO200066622-A1.
XX 09-NOV-2000.
XX 05-MAY-2000; 2000WO-US012371.
XX 05-MAY-1999; 99US-0132686P.
XX

PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX	
DR	WPI; 2000-656493/63.
XX	
PT	Administration of peptide agents with a sequence corresponding to a
PT	partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor antagonist
PT	is used to modulate inflammation.
XX	
PS	Claim 12; Page 29; 148pp; English.
XX	
CC	The present sequence is a peptide fragment of T21/DPI07. T21/DPI07 is a
CC	helical segment of the ectodomain of HIV-1 protein gp41. T21/DPI07 is
CC	located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC	critical role in the fusion of HIV-1 and host cell membranes. T21/DPI07
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemoattractant and activator of human peripheral blood phagocytes (but
CC	not T cells). The present peptide can be used to modulate an inflammatory
CC	response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
CC	
SQ	Sequence 36 AA;
Query Match	95.9%; Score 164; DB 3; Length 36;
Best Local Similarity	97.1%; Pred. No. 1.5e-14;
Matches 34; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 LRATFAOQHLLQLFTWVQIKQIARLTAVERLYKDG 35 2 LRATFAOQHLLQLFTWVGIKIQIARLTAVERYLYKDG 36
Db	
RESULT 20	
AAB52785	
ID	AAB52785 standard; peptide; 37 AA.
XX	
AC	AAB52785;
XX	
DT	12-SEP-2003 (revised)
DT	23-FEB-2001 (first entry)
XX	
DE	T21/DPI07 peptide fragment #67.
XX	
KX	Antiinflammatory; T21/DPI07; gp41 ectodomain; HIV-1 fusion;
KW	formyl peptide receptor family; FPR; inflammatory response up-regulation;
KW	chemoattractant.
XX	
OS	Human immunodeficiency virus 1.
OS	
PN	WO20006622-A1.
PD	
PD	09-NOV-2000.
XX	
PF	05-MAY-2000; 2000WO-US012371.
XX	
PR	05-MAY-1999; 99US-0132686P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX	
DR	WPI; 2000-656493/63.
XX	
PT	Administration of peptide agents with a sequence corresponding to a
PT	partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor antagonist
PT	is used to modulate inflammation.
XX	
PS	Claim 12; Page 29; 148pp; English.
XX	
CC	The present sequence is a peptide fragment of T21/DPI07. T21/DPI07 is a
CC	helical segment of the ectodomain of HIV-1 protein gp41. T21/DPI07 is a
CC	located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC	critical role in the fusion of HIV-1 and host cell membranes. T21/DPI07
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemoattractant and activator of human peripheral blood phagocytes (but
CC	not T cells). The present peptide can be used to modulate an inflammatory
CC	response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
CC	
SQ	Sequence 36 AA;

CC	critical role in the fusion of HIV-1 and host cell membranes. T21/Dp107
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemoattractant and activator of human peripheral blood phagocytes (but
CC	not T cells). The present peptide can be used to modulate an inflammatory
CC	response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX	
XX	
SQ	Sequence 37 AA:
Query Match	95.9%; Score 164; DB 3; Length 37;
Best Local Similarity	97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 LRAIEAQOHLLQLTWGIKOLARILAVERYLKDDQ 35 Db 3 LRAIEAQOHLLQLTWGIKOLARILAVERYLKDDQ 37
RESULT 21	
AARS5635	AARS5635 standard; peptide; 38 AA.
XX	
AC	AARS5635;
XX	
DT	25-MAR-2003 (revised)
DT	25-JUL-1994 (first entry)
XX	
DE	DP-139 - DP-107 analogue.
XX	
KW	Leucine zipper; HIV-1; human immunodeficiency virus;
KM	transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM	antiviral; gp41.
XX	
OS	Synthetic.
XX	
PN	MO9402505-AI.
XX	
PD	03-FEB-1994.
XX	
PF	19-JUL-1993; 93WO-US006769.
XX	
PR	20-JUL-1992; 92US-00916540.
PR	07-AUG-1992; 92US-00927532.
XX	
PA	(UYDU-) UNIV DUKE.
XX	
P1	Wild CT, Matthews TJ, Bolognesi DP;
XX	
DR	WPI; 1994-048790/06.
XX	
PT	New peptides corresponding to HIV transmembrane protein - used for
PT	inhibiting infection of cells by an enveloped virus, partic. for
PT	inhibiting HIV-induced cell fusion.
XX	
E8	Disclosure; Page 25; 38pp; English.
XX	
CC	Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC	of forming a heterodimer with DP-107; or a multimer of these peptides can
CC	be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC	fusion. DP-107 is based on a highly conserved region in the transmembrane
CC	protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC	amphipathic alpha-helix with structural analogues in the TM proteins of
CC	several fusogenic viruses. Other peptides studied and DP-107 analogues
CC	are given in AARS52839-48 and AARS5633-37. (Updated on 25-MAR-2003 to
CC	correct PN field.)
XX	
SQ	Sequence 38 AA:
Query Match	95.9%; Score 164; DB 2; Length 38;
Best Local Similarity	97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 LRAIEAQOHLLQLTWGIKOLARILAVERYLKDDQ 35

Db 4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 22

AAK55636 standard; peptide; 38 AA.

AC AAR55636;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-140 - DP-107 analogue.

Leucine zipper; HIV-1; human immunodeficiency virus;

transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

antiviral; gp41.

Synthetic.

MO9402505-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93MO-US006769.

PR 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

PA (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

PT New peptides corresponding to HIV transmembrane protein - used for

inhibiting infection of cells by an enveloped virus, partic. for

inhibiting HIV-induced cell fusion.

PS Disclosure; Page 25; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

of forming a heterodimer with DP-107; or a multimer of these peptides can

be contacted with an HIV-infected cell to inhibit HIV- induced cell

fusion. DP-107 is based on a highly conserved region in the transmembrane

protein (TM) of HIV-1 (gp41) which was predicted to form an extended

amphipathic alpha-helix with structural analogues in the TM proteins of

several fusogenic viruses. Other peptides studied and DP-107 analogues

are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to

correct PN field.)

XX Sequence 38 AA;

XX Query Match 95.9%; Score 164; DB 2; Length 38;

XX Best Local Similarity 97.1%; Pred. No. 1.6e-14;

XX Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 35

4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 23

AAK47216 standard; peptide; 38 AA.

AC AAR47216;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (558-595).

XX Leucine zipper; HIV-1; human immunodeficiency virus;

KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

KM antiviral; gp41.

XX Synthetic.

XX MO9402505-A1.

XX PD 03-FEB-1994.

XX PF 19-JUL-1993; 93MO-US006769.

XX PR 20-JUL-1992; 92US-00916540.

XX PR 07-AUG-1992; 92US-00927532.

XX PA (UYDU-) UNIV DUKE.

XX PI Wild CT, Matthews TJ, Bolognesi DP;

XX DR WPI; 1994-048790/06.

XX PT New peptides corresponding to HIV transmembrane protein - used for

inhibiting infection of cells by an enveloped virus, partic. for

inhibiting HIV-induced cell fusion.

XX Claim 1; Page 27; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

of forming a heterodimer with DP-107; or a multimer of these peptides can

be contacted with an HIV-infected cell to inhibit HIV- induced cell

fusion. DP-107 is based on a highly conserved region in the transmembrane

protein (TM) of HIV-1 (gp41) which was predicted to form an extended

amphipathic alpha-helix with structural analogues in the TM proteins of

several fusogenic viruses. Other peptides studied and DP-107 analogues

are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to

correct PN field.)

XX Sequence 38 AA;

XX Query Match 95.9%; Score 164; DB 2; Length 38;

XX Best Local Similarity 97.1%; Pred. No. 1.6e-14;

XX Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 35

4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 24

AAW27614 standard; peptide; 38 AA.

AC AAW27614;

DT 25-MAR-2003 (revised)

DT 22-DEC-1997 (first entry)

DE Human immunodeficiency virus gp41 derived peptide DP-107.

XX Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;

KW inhibition; induction; cell fusion; transmission; type 1.

XX Human immunodeficiency virus.

XX US5656480-A.

XX 12-AUG-1997.

Query Match	95.9%	Score 164	DB 2	Length 38
Best Local Similarity	97.1%	Pred. No. 1,6e-14		
Matches	34	Conservative	0	Mismatches 1, Indels 0, Gaps 0
Qy	1	LRAIEAQGHLLQITWQIKOLQARLLAVERRYKQ	35	
Db	4	LRAIEAQGHLLQITWQIKOLQARLLAVERRYKQ	38	

Query Match	Score 164;	DB 3;	Length 38;
Best Local Similarity	97.1%;	Pred. No. 1.6e-14;	
Matches	34;	Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	1	LRATACQHTLTQVWQIKQCARLAVERYIKDQ	35
Db	4	LRATACQHTLTQVWQIKQCARLAVERYIKDQ	38

RESULT	26
AA58730	
ID	AA58730 standard; peptide; 38 AA.
XX	
AC	AA58730;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	Core polypeptide fragment T No. 85.
XX	
KW	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW	anti-tumorigenic; differentiation factor; interleukin; interferon;
KM	colony stimulating factor; hormone; angiogenic factor.
XX	
OS	Unidentified.
XX	
PN	W09959615-A1.
XX	
PD	25-NOV-1999.
XX	
PF	20-MAY-1999; 99WO-US011219.
XX	
PR	20-MAY-1998; 98US-00082279.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX	
DR	WPI, 2000-136792/12.
XX	
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
XX	
PS	comprises enhancer sequence.
XX	
PS	Disclosure; Page 22; 124pp; English.
XX	
CC	The invention relates to hybrid polypeptides comprising enhancer peptide
CC	sequence linked to core polypeptides. The enhancer polypeptides are
CC	derived from various retroviral envelope (gp41) protein sequences, and
CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC	pharmacokinetic properties thereof as increasing the half-life of any core
CC	polypeptide that they are linked to. The core polypeptides are any
CC	polypeptide that may be introduced into a living system and that can
CC	function as a pharmacologically useful peptide for the treatment or
CC	prevention of a disease. The core polypeptides are bioactive peptides
CC	selected from a growth factor, cytokine, differentiation factor,
CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 4 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 27

AAV8731
ID AAV8731 standard; peptide; 38 AA.

AC AAV8731;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 86.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO9959615-A1.

XX 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

PT WPI; 2000-136792/12.

PS A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.

XX Disclosure; Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;

Best Local Similarity 97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 4 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 28

AAV89145
ID AAV89145 standard; peptide; 38 AA.

AC AAV89145;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 583.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO9959615-A1.

XX 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

PT WPI; 2000-136792/12.

PS A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.

XX Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 4 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 29

AAV89146
ID AAV89146 standard; peptide; 38 AA.
XX
AC AAV89146;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 583.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
XX WO953615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
PS Disclosure; Page 30; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAV8651-Y9005 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
XX
Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 35
Db 4 LRAIEAQOHLQLTWGICIKQLQARILAVERYLKDQ 38
XX
RESULT 30
AAV89243
ID AAV89243 standard; peptide; 38 AA.
XX
AC AAV89243;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 681.
XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
XX WO953615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
PS Disclosure; Page 32; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAV8651-Y9005 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
XX
Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.6e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 35
Db 4 LRAIEAQOHLQLTWGICIKQLQARILAVERYLKDQ 38
XX

Search completed: June 2, 2004, 11:41:44
Job time : 43.8451 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 9.51087 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336a-181
Perfect score: 171
Sequence: 1 LRAIEAQHILQITWVQIKQLQARILAVERYLKQ 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	95.9	357	2 S21996	envelope protein g
2	164	95.9	851	2 S33985	env polypotein -
3	164	95.9	853	2 S54384	envelope polypote
4	164	95.9	854	2 S13288	env protein - huma
5	164	95.9	855	1 VCLJZR	env polypotein pr
6	164	95.9	856	1 VCLJH3	env polypotein pr
7	164	95.9	856	1 VCLJVL	env polypotein pr
8	164	95.9	861	1 VCLJLV	env polypotein pr
9	163	95.3	357	2 S22006	envelope protein g
10	163	95.3	357	2 S21994	envelope protein g
11	163	95.3	357	2 S22004	envelope protein g
12	163	95.3	358	2 S22002	envelope protein g
13	163	95.3	358	2 S22000	envelope protein g
14	163	95.3	358	2 S70417	envelope protein g
15	161	94.2	357	2 S21990	envelope protein g
16	161	94.2	357	2 S21992	envelope protein g
17	161	94.2	357	2 S21992	envelope protein g
18	160	93.6	443	2 C41621	env polypotein pr
19	160	93.6	443	2 A41621	env polypotein pr
20	160	93.6	444	2 B41621	env polypotein pr
21	160	93.6	729	1 VCLJLK	env polypotein pr
22	160	93.6	843	1 H44001	env polypotein pr
23	160	93.6	846	1 VCLJND	env polypotein pr
24	160	93.6	852	2 T12016	envelope glycoprot
25	160	93.6	855	1 VCLJAZ	env polypotein pr
26	160	93.6	856	1 VCLJAZ	env polypotein pr
27	160	93.6	856	1 A44933	env polypotein pr
28	160	93.6	861	1 VCLJKB	env polypotein pr
29	160	93.6	861	1 VCLJSC	env polypotein pr

30	160	93.6	868	1 VCLJTH4	env polypotein -
31	159	93.0	859	2 T01672	envelope polypote
32	156	91.2	358	2 S21998	envelope protein g
33	152	88.9	852	1 VCLJBR	env polypotein -
34	149	87.1	854	1 VCLJST	env polypotein pr
35	146	85.4	847	2 T09448	envelope glycoprot
36	146	85.4	847	2 S13289	env protein - huma
37	146	85.4	847	2 S52930	env polypotein -
38	145	67.3	104	2 VCLJSA	env polypotein -
39	135	67.3	877	2 C46356	env polypotein -
40	133	66.1	877	2 S49197	envelope protein p
41	111	64.3	366	2 B41565	env polypotein -
42	110	64.3	732	2 S46352	env polypotein -
43	109	63.7	712	1 VCLJSA4	env polypotein pr
44	109	63.7	851	2 S12159	env protein - huma
45	109	63.7	852	1 VCLJST	env polypotein pr
46	109	63.7	859	1 VCLJST	env polypotein pr
47	109	63.7	859	1 S24571	env protein - huma
48	109	63.7	869	2 S53098	envelope polypote
49	108	63.2	859	1 VCLJCT	env polypotein pr
50	107	62.6	151	2 S30458	env protein - huma
51	107	62.6	855	2 A45713	env transmembrane
52	107	62.6	858	1 VCLJG2	env polypotein pr
53	107	62.6	881	2 S03068	env protein - huma
54	107	62.6	885	2 S04322	env polypotein -
55	107	62.6	886	2 T11555	env protein - siml
56	106	62.0	881	1 VCLJG3	env polypotein -
57	105	61.4	151	2 S30448	env protein - huma
58	105	61.4	151	2 S30453	env protein - huma
59	105	61.4	151	2 S30452	env protein - huma
60	105	61.4	151	2 S30450	env protein - huma
61	105	61.4	151	2 S30451	env protein - huma
62	105	61.4	863	2 A53034	env polypotein -
63	105	61.4	869	2 A47665	env protein gpi20 (
64	104	60.8	880	1 VCLJ82	env polypotein pr
65	103	60.2	151	2 S30459	env protein - huma
66	103	60.2	151	2 S30457	env protein - huma
67	103	60.2	151	2 S30457	env protein - huma
68	103	60.2	151	2 S30456	env protein - huma
69	103	60.2	151	2 S30455	env protein - huma
70	103	60.2	151	2 S30454	env protein - huma
71	103	60.2	786	2 S28084	env polypotein -
72	102	59.6	889	1 VCLJG5	env polypotein -
73	81	47.4	68	2 T11566	envelope glycoprot
74	81	47.4	68	2 S60695	env protein - huma
75	81	47.4	68	2 S60696	env protein - huma
76	81	47.4	68	2 S60705	env protein - huma
77	81	47.4	68	2 S60707	env protein - huma
78	81	47.4	68	2 S60694	env protein - huma
79	81	47.4	68	2 S60687	env protein - huma
80	81	47.4	69	2 S60706	env protein - huma
81	79	46.2	68	2 S60692	env protein - huma
82	82	42.7	68	2 S60688	env protein - huma
83	70	40.9	69	2 S60690	env protein - huma
84	70	40.9	69	2 S60689	env protein - huma
85	70	40.9	69	2 S60691	env protein - huma
86	66	38.6	294	2 S60525	envelope polypote
87	66	38.6	297	2 S60538	envelope polypote
88	65	38.0	372	2 S46344	env polypotein -
89	65	38.0	375	2 S46345	env polypotein -
90	62	36.3	294	2 S60545	envelope polypote

ALIGNMENTS

RESULT 1
S21996
envelope protein gpi20/gp41 - human immunodeficiency virus type 1 (patient 27L)
C;Species: human immunodeficiency virus type 1; HIV-1
C;Date: 20-Feb-1995 #sequence_rev1995 #text_change 26-Aug-1999
C;Accession: S70422; S21996
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <S72>
A/Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129
A/Experimental source: patient 27L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type B retrovirus env polyprotein

Query Match 95.9%; Score 164; DB 2; Length 357;
Best Local Similarity 97.1%; Pred. No. 8.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 35
Db 57 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 91

RESULT 2

S33985
env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C/Accession: S33985
R/Carlini, F.
Submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33985
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-851 <CAR>
A/Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199
C/Superfamily: type B retrovirus env polyprotein

Query Match 95.9%; Score 164; DB 2; Length 851;
Best Local Similarity 97.1%; Pred. No. 2.2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 35
Db 551 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 585

RESULT 3

S54384
envelope polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <THE>
A/Cross-references: EMBL:M22639; NID:G329377; PIDN:AAA45370.1; PID:G329385
C/Superfamily: type B retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 95.9%; Score 164; DB 2; Length 853;
Best Local Similarity 97.1%; Pred. No. 2.2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 35
Db 553 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 587

RESULT 4

S13288
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C/Accession: S13288
R/O'Brien, W.A.; Koyangi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; MUID:91043044; PMID:2172833
A/Accession: S13288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OBR>
C/Superfamily: type B retrovirus env polyprotein

Query Match 95.9%; Score 164; DB 2; Length 854;
Best Local Similarity 97.1%; Pred. No. 2.2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 35
Db 554 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 588

RESULT 5

VCLJLR
env polyprotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <SRI>
A/Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403
C/Genetics:
A/Gene: env
C/Superfamily: type B retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-855/Product: env polyprotein #status predicted <MAT>
F/501-855/Product: transmembrane glycoprotein #status predicted <TM>
F/87,129,140,145,154,158,166,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,
F/87,129,140,145,154,158,166,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 95.9%; Score 164; DB 1; Length 855;
Best Local Similarity 97.1%; Pred. No. 2.2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 35
Db 555 LRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 589

RESULT 6

VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03973
R/Retner, D.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93353; MUID:85111123; PMID:2578615
A/Accession: A03973
A/Molecule type: DNA

A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2,2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 35
Db 556 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 590
RESULT 7
VCLUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, W.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Tasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A:Reference number: A93355; MUID:8511157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MOE>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2,2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 35
Db 556 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 590
RESULT 8
VCLUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:8509933; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:

A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 95.9%; Score 164; DB 1; Length 861;
Best Local Similarity 97.1%; Pred. No. 2,2e-14;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 35
Db 561 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 595
RESULT 9
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A:Experimental source: patient L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein
Query Match 95.3%; Score 163; DB 2; Length 357;
Best Local Similarity 94.3%; Pred. No. 1,2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 35
Db 57 LRAIEAQHLLQLTWGIKQARILAVERYLKQ 91
RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein
Query Match 95.3%; Score 163; DB 2; Length 357;

Best Local Similarity 94.3%; Pred. No. 1.2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 57 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 11

S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 48
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43616.1; PID:g60189
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:g60188
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 357;
Best Local Similarity 94.3%; Pred. No. 1.2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 57 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 12

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:g60186
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 1.2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 35
Db 58 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 13

S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 1.2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 58 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 14

S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.3%; Score 163; DB 2; Length 358;
Best Local Similarity 94.3%; Pred. No. 1.2e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 58 LRAIEAQHLLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 15

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A;Reference number: S70417; MUID:92144209; PMID:11736940
A;Accession: S70423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332; X, 334-357 <STE2>
A;Cross-references: EMBL:X61357; NID:960175; PIDN:CMA43626.1; PID:960176
C;Superfamily: type E retrovirus env polyprotein

Query Match 94.2%; Score 161; DB 2; Length 357;
Best Local Similarity 91.4%; Pred. No. 2.2e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 35
Db 57 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 91

RESULT 16
S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S70424; S21992
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A;Reference number: S70417; MUID:92144209; PMID:11736940
A;Accession: S70424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <S2>
A;Cross-references: EMBL:X61358; NID:960177; PIDN:CMA43628.1; PID:960178
A;Experimental source: patient 22
A;Note: Submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein

Query Match 94.2%; Score 161; DB 2; Length 357;
Best Local Similarity 91.4%; Pred. No. 2.2e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 35
Db 57 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 91

RESULT 17
env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: A28922
R;Garg, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, B.; Farrell, K.; Wong-Staal, G.
Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Accession: A28922
A;Molecule type: DNA
A;Residues: 1-859 <GUR>
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein; 1-29/DNA: signal sequence #status predicted <SIG>
F;1-29/DNA: signal sequence #status predicted <SIG>
F;30-859/Product: env polyprotein #status predicted <EP>
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.2%; Score 161; DB 1; Length 859;
Best Local Similarity 91.4%; Pred. No. 5.6e-14;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 35
Db 560 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 594

RESULT 18
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: C41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
A;Accession: C41621
A;Molecule type: DNA
A;Residues: 1-443 <BUR>
A;Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015
A;Note: this virus was isolated from the mother's sexual partner
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein; 1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;424-443/DNA: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: car

Query Match 93.6%; Score 160; DB 2; Length 443;
Best Local Similarity 91.4%; Pred. No. 3.7e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 35
Db 296 LRAIEAQOHMLQLTWGIKQARVLAVERYLKQ 330

RESULT 19
A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: A41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
A;Accession: A41621
A;Molecule type: DNA
A;Residues: 1-445 <BUR>
A;Cross-references: GB:M77228; NID:9328627; PIDN:AAB03790.1; PID:9555013
A;Note: this virus was isolated from the mother
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein; 1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/DNA: transmembrane #status predicted <TMN>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 93.6%; Score 160; DB 2; Length 445;
Best Local Similarity 91.4%; Pred. No. 3.8e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db      298 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 332

RESULT 20
env polypeptide D - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C:Accession: B41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Guila, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:11763038
A:Accession: B41621
A:Molecule type: DNA
A:Residues: 1-454 <BUR>
A:Cross-references: GB:M77279
A:Note: this virus was isolated from the daughter
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:435-454/Domain: transmembrane #status predicted <TM>
F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo
Query Match      93.6%; Score 160; DB 2; Length 454;
Best Local Similarity 91.4%; Pred. No. 3,8e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db      307 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 341

RESULT 21
env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polypeptide
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted <CP1>
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted <CP2>
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted <CP2>
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-729/Domain: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414
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Query Match      93.6%; Score 160; DB 1; Length 729;
Best Local Similarity 91.4%; Pred. No. 6.4e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db      562 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 596

RESULT 22
env polypeptide precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polypeptide
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <LTY>
A:Cross-references: GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TM>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,
Query Match      93.6%; Score 160; DB 1; Length 843;
Best Local Similarity 91.4%; Pred. No. 7.5e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db      543 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 577

RESULT 23
env polypeptide precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polypeptide
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Gallibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-NDK: a highly cytopathic strain of the human immunoc
A:Reference number: J00065; MUID:90034200; PMID:2806917
A:Accession: J00066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polypept
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
```

F;502-846/Product: coat protein gp41 #status predicted <CP2>
F;502-820/Domain: transmembrane #status predicted <TM>
F;674-692/Domain: transmembrane #status predicted <TM>
F;87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 93.6%; Score 160; DB 1; Length 846;
Best Local Similarity 91.4%; Pred. No. 7.6e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 35
546 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 580

RESULT 24

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T12016

R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A/Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A/Reference number: Z17379; PMID:98178716; PMID:9519894

A/Accession: T12016

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-852 <MCC>

A/Cross-references: EMBL:U90934; NID:G2351783; PIDN:AAC59271.1; PID:G2351784

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

Query Match 93.6%; Score 160; DB 2; Length 852;
Best Local Similarity 91.4%; Pred. No. 7.6e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 35
552 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 586

RESULT 25

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
VCLJ2
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03976

R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-St
Science 227, 484-492, 1985

A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A/Reference number: A04003; PMID:8509453; PMID:2578227

A/Accession: A03976

A/Molecule type: DNA

A/Residues: 1-855 <SAN>

A/Cross-references: GB:K02007; NID:G328658; PIDN:AAB59882.1; PID:G328666

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT>

F;510-855/Product: transmembrane glycoprotein #status predicted <TM>

F;87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458

F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.6%; Score 160; DB 1; Length 855;
Best Local Similarity 91.4%; Pred. No. 7.7e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 35

555 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 589

RESULT 26

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WM1)
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C/Accession: A24774

R;Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986

A/Title: Identification and characterization of conserved and variable regions in the env

A/Reference number: A24774; PMID:86218077; PMID:2423250

A/Accession: A24774

A/Molecule type: DNA

A/Residues: 1-856 <STA>

A/Cross-references: GB:K03455; GB:M38432; NID:G1906382

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-501/Product: coat protein gp120 #status predicted <GP1>

F;502-847/Product: coat protein gp41 #status predicted <GP2>
F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 93.6%; Score 160; DB 1; Length 856;
Best Local Similarity 91.4%; Pred. No. 7.7e-14;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 35
556 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 590

RESULT 27

env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
A44963
N/Alternate names: coat polyprotein
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
C/Accession: A44963

R;Strinvaasen, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J

AIDS Res. Hum. Retroviruses 5, 121-129, 1989

A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976; nuc

A/Reference number: A44963; PMID:89228766; PMID:2713163

A/Accession: A44963

A/Molecule type: DNA

A/Residues: 1-856 <SRI>

A/Cross-references: GB:M15896; NID:G329392; PIDN:AAB5948.1; PID:G329394

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-520/Product: coat protein gp120 #status predicted <GP1>

F;521-856/Product: coat protein gp41 #status predicted <GP2>

F;64-705/Domain: transmembrane #status predicted <TM>
F;87,133,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 93.6%; Score 160; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 7.7e-14;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 35
556 LRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 590

RESULT 28

VCLJKB

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A/Reference number: A42995; MUID:92351552; PMID:1322587

A/Accession: A42995

A/Molecule type: mRNA

A/Residues: 1-861 <SH1>

A/Cross-references: GB:541266; GB:D01206

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domain: extracellular #status predicted <EXT>

F:1-333/Domain: signal sequence #status predicted <SIG>

F:1-333/Region: hydrophobic #status predicted <CP1>

F:34-517/Region: cleavage processing #status predicted <CP2>

F:518-661/Product: coat protein gp41 #status predicted <CP2>

F:518-534/Region: hydrophobic #status predicted <TM1>

F:680-711/Domain: transmembrane #status predicted <INT>

F:712-861/Domain: intracellular #status predicted <INT>

F:756-772/Region: hydrophobic #status predicted

F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.6%; Score 160; DB 1; Length 861;

Best Local Similarity 91.4%; Pred. No. 7.7e-14;

Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 562 LRAIEAQOHLQLTWGIKQIARILAVERYLKQ 596

RESULT 29

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C/Accession: B28922

R/Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Ste

Virology 164, 531-536, 1988

A/Title: Envelope sequences of two new United States HIV-1 isolates.

A/Reference number: A28922; MUID:86219542; PMID:3369091

A/Accession: B28922

A/Molecule type: DNA

A/Residues: 1-861 <GUR>

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-861/Product: env polyprotein #status predicted <EPP>

F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 93.6%; Score 160; DB 1; Length 861;

Best Local Similarity 91.4%; Pred. No. 7.7e-14;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 561 LRAIEAQOHLQLTWGIKQIARILAVERYLKQ 595

RESULT 30

VCLJH4

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: C25523

R/Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A/Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human i

A/Reference number: A94136; MUID:87041461; PMID:3490666

A/Accession: C25523

A/Molecule type: DNA

A/Residues: 1-868 <DES>

A/Cross-references: GB:M13137; NID:G326460; PIDN:AAA44311.1; PID:G326467

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei

F:1-521/Product: coat protein gp120 #status predicted <GP1>

F:522-868/Product: coat protein gp41 #status predicted <GP2>

F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match 93.6%; Score 160; DB 1; Length 868;

Best Local Similarity 94.3%; Pred. No. 7.8e-14;

Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 568 LRAIEAQOHLQLTWGIKQIARILAVERYLKQ 602

Search completed: June 2, 2004, 11:50:10

Job time : 9.51087 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 / Search time 5.70652 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-181
Perfect score: 171
Sequence: 1 LRAIEAQHLLQLTWQIKQIQARILAVERYLKQ 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	164	95.9	853	1	ENV_HV1EL
2	164	95.9	853	1	ENV_HV1MP
3	164	95.9	853	1	ENV_HV122
4	164	95.9	855	1	ENV_HV126
5	164	95.9	856	1	ENV_HV1B1
6	164	95.9	856	1	ENV_HV1H2
7	164	95.9	856	1	ENV_HV1H3
8	164	95.9	856	1	ENV_HV1H4
9	164	95.9	856	1	ENV_HV1H5
10	164	95.9	856	1	ENV_HV1H6
11	164	95.9	856	1	ENV_HV1H7
12	163	95.3	855	1	ENV_HV1H8
13	163	95.3	855	1	ENV_HV1H9
14	161	94.2	848	1	ENV_HV1H10
15	160	93.6	843	1	ENV_HV1H11
16	160	93.6	846	1	ENV_HV1H12
17	160	93.6	851	1	ENV_HV1H13
18	160	93.6	852	1	ENV_HV1H14
19	160	93.6	855	1	ENV_HV1H15
20	160	93.6	856	1	ENV_HV1H16
21	160	93.6	856	1	ENV_HV1H17
22	160	93.6	856	1	ENV_HV1H18
23	160	93.6	861	1	ENV_HV1H19
24	160	93.6	865	1	ENV_HV1H20
25	160	93.6	867	1	ENV_HV1H21
26	160	93.6	868	1	ENV_HV1H22
27	159	93.0	859	1	ENV_HV1H23
28	157	91.8	863	1	ENV_HV1H24
29	155	90.6	863	1	ENV_HV1H25
30	152	88.9	852	1	ENV_HV1H26
31	149	87.1	854	1	ENV_HV1H27
32	115	67.3	865	1	ENV_HV1H28
33	115	67.3	877	1	ENV_HV1H29

34	112	65.5	854	1	ENV_HV1H30
35	109	63.7	712	1	ENV_HV1H31
36	109	63.7	851	1	ENV_HV1H32
37	109	63.7	851	1	ENV_HV1H33
38	109	63.7	856	1	ENV_HV1H34
39	109	63.7	859	1	ENV_HV1H35
40	109	63.7	859	1	ENV_HV1H36
41	108	63.2	859	1	ENV_HV1H37
42	107	62.6	858	1	ENV_HV1H38
43	107	62.6	858	1	ENV_HV1H39
44	107	62.6	858	1	ENV_HV1H40
45	106	62.0	768	1	ENV_HV1H41
46	106	62.0	882	1	ENV_HV1H42
47	106	62.0	882	1	ENV_HV1H43
48	104	60.8	821	1	ENV_HV1H44
49	103	60.2	821	1	ENV_HV1H45
50	103	60.2	846	1	ENV_HV1H46
51	103	60.2	881	1	ENV_HV1H47
52	102	59.6	857	1	ENV_HV1H48
53	102	59.6	860	1	ENV_HV1H49
54	51.5	30.1	924	1	ENV_HV1H50
55	51	29.8	2564	1	ENV_HV1H51
56	50.5	29.5	1445	1	ENV_HV1H52
57	50	29.2	445	1	ENV_HV1H53
58	49.5	28.9	581	1	ENV_HV1H54
59	49.5	28.9	581	1	ENV_HV1H55
60	49	28.7	236	1	ENV_HV1H56
61	49	28.7	1938	1	ENV_HV1H57
62	49	28.7	8797	1	ENV_HV1H58
63	48.5	28.4	790	1	ENV_HV1H59
64	48	28.1	213	1	ENV_HV1H60
65	48	28.1	305	1	ENV_HV1H61
66	48	28.1	551	1	ENV_HV1H62
67	48	28.1	702	1	ENV_HV1H63
68	48	28.1	906	1	ENV_HV1H64
69	48	28.1	906	1	ENV_HV1H65
70	48	28.1	1379	1	ENV_HV1H66
71	47.5	27.8	253	1	ENV_HV1H67
72	47.5	27.8	962	1	ENV_HV1H68
73	47.5	27.8	969	1	ENV_HV1H69
74	47.5	27.8	1955	1	ENV_HV1H70
75	47	27.5	376	1	ENV_HV1H71
76	47	27.5	380	1	ENV_HV1H72
77	47	27.5	418	1	ENV_HV1H73
78	47	27.5	851	1	ENV_HV1H74
79	47	27.5	1756	1	ENV_HV1H75
80	46.5	27.2	132	1	ENV_HV1H76
81	46.5	27.2	134	1	ENV_HV1H77
82	46.5	27.2	536	1	ENV_HV1H78
83	46.5	27.2	966	1	ENV_HV1H79
84	46.5	27.2	1093	1	ENV_HV1H80
85	46	26.9	70	1	ENV_HV1H81
86	46	26.9	286	1	ENV_HV1H82
87	46	26.9	314	1	ENV_HV1H83
88	46	26.9	358	1	ENV_HV1H84
89	46	26.9	443	1	ENV_HV1H85
90	46	26.9	1102	1	ENV_HV1H86

ALIGNMENTS

RESULT 1
ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP111)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).

CC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11689;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=66245056; PubMed=2424612;
RA	Aizoon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT	"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients."
RL	Cell 46:63-74(1986).
CC	-----
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CC	-----
DR	EMBL; K03454; AAA444329.1; -.
DR	EMBL; A07108; CAA00616.1; -.
DR	HIV; K03454; ENVSELT.
DR	InterPro; IPR000328; Env_GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120; 1.
DR	Pfam; PF00517; GP41; 1.
KM	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT	SIGNAL. 1 31 BY SIMILARITY.
FT	CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID 53 73 BY SIMILARITY.
FT	DISULFID 118 206 BY SIMILARITY.
FT	DISULFID 125 197 BY SIMILARITY.
FT	DISULFID 130 154 BY SIMILARITY.
FT	DISULFID 219 248 BY SIMILARITY.
FT	DISULFID 229 240 BY SIMILARITY.
FT	DISULFID 297 330 BY SIMILARITY.
FT	DISULFID 376 442 BY SIMILARITY.
FT	DISULFID 383 416 BY SIMILARITY.
FT	CARBOHYD 87 87 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 129 129 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 137 137 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 143 143 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 153 153 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 157 157 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 183 183 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 188 188 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 198 198 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 235 235 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 242 242 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 263 263 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 277 277 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 290 290 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 331 331 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 353 353 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 384 384 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 390 390 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 394 394 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 400 400 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 405 405 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 406 406 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 411 411 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 445 445 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 458 458 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 459 459 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 462 462 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 608 608 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 613 613 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 622 622 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 634 634 N-LINKED (GLCNAC . .) (POTENTIAL).
SQ	SEQUENCE 853 AA; 96721 MW; F9CDD64DAAD00D7A5 CRC64;
Query Match	95.9%; Score 164; DB 1; Length 853;

Bst Local Similarity	97.1%	Pred. No.	2.3e-15;			
Matches	34;	Conservative	0; Mismatches	1; Indels	0; Gaps	0;

Qy	1	LRAIEAOQHLLQLTWNOIKOLQAIIIVERTKIQ	35
Db	553	LRAIEAQOHHLLQLTWGIGIKOLQAARILAVERYLKQD	587

RESULT 2

ID	ENV_HVIMF	STANDARD;	PRT;	863 AA.
AC	P19551;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxId=11704;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90317877; PubMed=1695254;			
SA	Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C., Wasiak A.;			
RT	"Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis."			
RL	J. Virol. 64:3792-3803(1990).			
CC	-----			
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CC	-----			
DR	EMBL; M33943; AAA44850.1; -.			
DR	PDB; LAIK; I6-JUN-97.			
DR	HIV; M33943; ENVSMFA.			
DR	InterPro; IPR000328; Env GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
KW	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal; 3D-structure.			
FT	SIGNAL	1	30	
FT	CHAIN	31	509	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	510	853	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	203	BY SIMILARITY.
FT	DISULFID	126	194	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	216	245	BY SIMILARITY.
FT	DISULFID	226	237	BY SIMILARITY.
FT	DISULFID	294	329	BY SIMILARITY.
FT	DISULFID	376	443	BY SIMILARITY.
FT	DISULFID	383	416	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	232	232	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 3377893B6F22A8A CRC64;

Query Match 95.9%; Score 164; DB 1; Length 853;
 Best Local Similarity 97.1%; Pred. No. 2.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 35
 Db 554 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 588

RESULT 3
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11683;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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 CC EMBL; M22639; AAA45370.1; -.
 DR PIR; S54384; S54384.
 DR HIV; M22639; ENV52226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.

FT DISULFID 383 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 853;
 Best Local Similarity 97.1%; Pred. No. 2.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 35
 Db 553 LRAIEAQHLLQLTWQIKQLQARILAVERYLKQ 587

RESULT 4
 ID ENV_HV126 STANDARD; PRT; 855 AA.
 AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11708;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87248097; PubMed=3036660;
 RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
 RA Schuchman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
 RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from
 RT Zaire; nucleotide sequence analysis identifies conserved and variable
 RT domains in the envelope gene";
 RL Gene 52:71-82(1987).
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 CC -----

CC	EMBL; K03458; AAA45380.1; -.
DR	PIR; D26192; VCLJZR.
DR	HIV; K03458; ENV5Z6.
DR	InterPro; IPR000328; Env_GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120_1.
DR	Pfam; PF00517; GP41_1.
KM	AIR5; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
FT	SIGNAL 1 30
FT	CHAIN 31 510
FT	CHAIN 511 855
FT	DISULFID 53 73
FT	DISULFID 118 207
FT	DISULFID 125 198
FT	DISULFID 130 155
FT	DISULFID 220 249
FT	DISULFID 230 241
FT	DISULFID 298 332
FT	DISULFID 378 444
FT	DISULFID 385 417
FT	CARBOHYD 87 87
FT	CARBOHYD 129 129
FT	CARBOHYD 140 140
FT	CARBOHYD 145 145
FT	CARBOHYD 154 154
FT	CARBOHYD 158 158
FT	CARBOHYD 186 186
FT	CARBOHYD 189 189
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FT	CARBOHYD 264 264
FT	CARBOHYD 278 278
FT	CARBOHYD 291 291
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FT	CARBOHYD 333 333
FT	CARBOHYD 340 340
FT	CARBOHYD 355 355
FT	CARBOHYD 386 386
FT	CARBOHYD 392 392
FT	CARBOHYD 398 398
FT	CARBOHYD 404 404
FT	CARBOHYD 443 443
FT	CARBOHYD 447 447
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FT	CARBOHYD 461 461
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FT	CARBOHYD 624 624
FT	CARBOHYD 636 636
FT	CARBOHYD 673 673
SO	SEQUENCE 855 AA; 96971 MM; 38BD306E239C3457 CRC64;
Query Match	95.9%; Score 164; DB 1; Length 855;
Best Local Similarity	97.1%; Pred. No. 2.3e-15;
Matches 34; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 LRAIQAQHLLQLTWQIKOGLARIANRYRIKQD 35
Dd	555 LRAIEAQHLLQLTWGIGIKOLARILAVERYIKQD 589
RESULT 5	
ID ENV_HVIB1 STANDARD; PRT; 856 AA.	
AC P03375;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last annotation update)	
DT 15-JUL-1999 (Rel. 38, Last annotation update)	
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane	

[illegible]


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FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931B827 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2,3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLQARIILAVERYLKQ 35
Db 556 LRAIEAQOHLLQLTWQIKQLQARIILAVERYLKQ 590

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP MEDLINE=8729196; Pubmed=3040055;
RX Retner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN REVISIONS.
RA Retner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
CC
CC EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF038419; AAC82596.1; -
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DEB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120, 1.
DR Pfam; PF00517; GP41, 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KM 3D-structure.
FT CHAIN 1 30
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
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FT CARBOHYD 241 241
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FT CARBOHYD 276 276
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FT CARBOHYD 332 332
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FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107E0 CRC64;

Query Match 95.9%; Score 164; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2,3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLQARIILAVERYLKQ 35
Db 556 LRAIEAQOHLLQLTWQIKQLQARIILAVERYLKQ 590

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 10-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=85228248; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-III env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
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 CC -----
 DR EMBL; M14100; AAA44679.1; -;
 DR PDB; 1JAU; 17-OCT-01.
 DR PDB; 1JAU; 17-OCT-01.
 DR HIV; M14100; ENVSHXB3.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 136
 FT CARBOHYD 136 141
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
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 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
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 FT CARBOHYD 386 386
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 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;
 Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 2.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHILQITWGIKOLARILAVERYIKDO 35
 Db 556 LRAIEAQOHILQITWGIKOLARILAVERYIKDO 590
 RESULT 8
 ENV_HVILW STANDARD; PRT; 856 AA.
 ID ENV_HVILW
 AC Q70626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (TM12.3 isolate) (HIV-1).
 OS Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type 1IB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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 CC -----
 DR EMBL; U12055; AAA76690.1; -;
 DR PDB; 1IF3; 02-MAY-01.
 DR GlycoStatedB; Q70626; -;
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 136
 FT CARBOHYD 136 141
 FT CARBOHYD 141 141
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 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
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 FT CARBOHYD 241 241
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 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
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 FT CARBOHYD 339 339
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 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;
 Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 2.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 2,3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 LRAIEAQOHLLQLTWQIKOLQRIILAVERYLKQ 35
 556 LRAIEAQOHLLQLTWQIKOLQRIILAVERYLKQ 590

ENV_HV1PV STANDARD; PRT; 856 AA.

AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus.";
 RU Nature 313:450-458(1985).
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 CC -----
 CC EMBL: K02083; AAB59873.1; -;
 DR EMBL: X01762; CAA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120.1.
 DR Pfam: PF00517; GP41.1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT CHAIN 1 30
 FT CHAIN 511 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

Query Match 95.9%; Score 164; DB 1; Length 856;
 Best Local Similarity 97.1%; Pred. No. 2,3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 LRAIEAQOHLLQLTWQIKOLQRIILAVERYLKQ 35
 556 LRAIEAQOHLLQLTWQIKOLQRIILAVERYLKQ 590

ENV_HV1PV STANDARD; PRT; 861 AA.

AC P03377;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509933; PubMed=2981635;
 RA Wain-Hobson S., Sonigo P., Dancos O., Cole S., Alizon M., Cell 40:9-17(1985).
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RU -----
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 CC -----

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CC -----
DR EMBL; K02013; AAB59751.1; -.
DR EMBL; A04321; CAA00352.1; -.
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV5BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516
FT CHAIN 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88
FT CARBOHYD 136
FT CARBOHYD 141
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FT CARBOHYD 191
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FT CARBOHYD 391
FT CARBOHYD 397
FT CARBOHYD 402
FT CARBOHYD 411
FT CARBOHYD 453
FT CARBOHYD 468
FT CARBOHYD 616
FT CARBOHYD 621
FT CARBOHYD 630
FT CARBOHYD 642
FT CARBOHYD 679
FT CARBOHYD 755
FT CARBOHYD 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 95.3%; Score 164; DB 1; Length 861;
Best Local Similarity 97.1%; Pred. No. 2.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RX Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.,
RA "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RU J. Virol. 64:4390-4398(1990).
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CC -----
DR EMBL; M65024; AAA45072.1; -.
DR PDB; 1OBE; 15-MAY-97.
DR HIV; M38428; ENV5SF162.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT CHAIN 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87
FT CARBOHYD 135
FT CARBOHYD 154
FT CARBOHYD 186
FT CARBOHYD 195
FT CARBOHYD 232
FT CARBOHYD 239
FT CARBOHYD 260
FT CARBOHYD 274
FT CARBOHYD 293
FT CARBOHYD 299
FT CARBOHYD 329
FT CARBOHYD 336
FT CARBOHYD 352
FT CARBOHYD 382
FT CARBOHYD 388
FT CARBOHYD 392
FT CARBOHYD 398
FT CARBOHYD 401
FT CARBOHYD 438
FT CARBOHYD 454
FT CARBOHYD 602
FT CARBOHYD 607
FT CARBOHYD 616
FT CARBOHYD 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7F2AB CRC64;

Query Match 95.3%; Score 163; DB 1; Length 847;
Best Local Similarity 94.3%; Pred. No. 3.2e-15;
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[illegible]

FT	CARBOHYD	336	336	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	359	359	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	395	395	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	399	399	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	610	610	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. .)	(POTENTIAL).
SQ	SEQUENCE	855 AA;	97476 MM;	9CFA2A607ADD62DA CRC64;	
Query Match		95.3%;	Score 163;	DB 1;	Length 855;
Best Local Similarity		94.3%;	Pred. No. 3.2e-15;		
Matches 33;		Conservative 1;	Mismatches 15;	Indels 0;	Gaps 0;
Qy	1	LRAEAOOHLLQLTWGKIQANLAVERYLKDD	35		
Dd	555	LRAEAOOHLLQLTWGKIQANLAVERYLKDD	589		
RESULT 13					
ID	ENV_HV1JR	STANDARD;	PRT;	848 AA.	
AC	P20871;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11688;				
RN	[1]				
RP	SEQUENCE FROM N.A. Koyanagi S., Chen I.S.-Y.; Submitted (DEC-1988) to the HIV data bank.				
RL	-----				
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CC	-----				
DR	EMBL; M38429; AAB03749.1; -. PDB; 1CE4; 18-MAR-99.				
DR	HIV; M38429; ENVJURCSF.				
DR	InferPro; IPR000328; Env GP41.				
DR	InferPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.				
FT	SIGNAL	1	32		
FT	CHAIN	33	503	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	504	848	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFD	53	73	BY SIMILARITY.	
FT	DISULFD	118	203	BY SIMILARITY.	
FT	DISULFD	125	194	BY SIMILARITY.	
FT	DISULFD	130	154	BY SIMILARITY.	
FT	DISULFD	216	245	BY SIMILARITY.	
FT	DISULFD	226	237	BY SIMILARITY.	
FT	DISULFD	294	328	BY SIMILARITY.	
FT	DISULFD	374	437	BY SIMILARITY.	
FT	DISULFD	381	410	BY SIMILARITY.	
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. .)	(POTENTIAL).

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FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC33 CRC64;

Query Match 94.2%; Score 161; DB 1; Length 848;
Best Local Similarity 91.4%; Pred. No. 6.1e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLARILAVERYLKQD 35
Db 548 LRAIEAQOHLQLTWQIKOLARILAVERYLKQD 582

RESULT 14
ID ENV_HV12M STANDARD; PRT; 856 AA.
AC P05877;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gungo C., Guo H.-G., Franchini G., Aldovini A., Collalti B.,
RA Farrell K., Wong-Straal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
RL -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
PATIENT IN 1984.

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CC -----
CC EMBL; M17449; AAA44857.1; -
CC PDB; 1ACJ; 31-JUL-94.
CC PDB; 1F58; 29-DEC-99.
CC PDB; 1N1Z; 25-FEB-03.
CC PDB; 1ND0; 25-FEB-03.
CC HIV; M17449; ENVSMN.

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DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 513
FT CHAIN 514 856
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 445
FT DISULFID 388 418
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 140 140
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 336 336
FT CARBOHYD 343 343
FT CARBOHYD 359 359
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FT CARBOHYD 401 401
FT CARBOHYD 405 405
FT CARBOHYD 406 406
FT CARBOHYD 413 413
FT CARBOHYD 448 448
FT CARBOHYD 465 465
FT CARBOHYD 612 612
FT CARBOHYD 617 617
FT CARBOHYD 626 626
FT CARBOHYD 638 638
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match 94.2%; Score 161; DB 1; Length 856;
Best Local Similarity 91.4%; Pred. No. 6.1e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLARILAVERYLKQD 35
Db 557 LRAIEAQOHLQLTWQIKOLARILAVERYLKQD 591

RESULT 15
ID ENV_HV12M STANDARD; PRT; 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;

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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2E83 CRC64;

Query Match 93.6%; Score 160; DB 1; Length 846;
Best Local Similarity 91.4%; Pred. No. 8.4e-15;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Dy 1 LRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 35
Db 546 LRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 580

RESULT 17
ENV_HV1B8 STANDARD; PRT; 851 AA.
ID ENV_HV1B8
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS HIV.
SN Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP MEDLINE=5511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Lyak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Chirayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RL "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1985).
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CC -----
CC EMBL, K02011; AAA44661.1; .
DR PDB; 1DDH; 13-JAN-99.
DR PDB; 1HHG; 31-OCT-93.
DR PDB; 1QO3; 02-JAN-00.
DR PDB; 1S2T; 24-DEC-97.
DR HIV; K02011; ENV5B8.
DR Glycosylated; P04582; .
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT CHAIN 1 30
FT CHAIN 506
FT DISULFID 507 851 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 205 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.

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FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 440 BY SIMILARITY.
FT DISULFID 385 413 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 93.6%; Score 160; DB 1; Length 851;
Best Local Similarity 94.3%; Pred. No. 8.4e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dy 1 LRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 35
Db 551 LRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 585

RESULT 18
ENV_HV1S3 STANDARD; PRT; 852 AA.
ID ENV_HV1S3
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS HIV.
SN Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RA "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
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CC EMBL; AY352275; A017031.1; -

DR PDB; 1ME0; 11-DEC-02.

DR HIV; M38427; ENVSSRF3.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;

KW 3D-structure.

FT SIGNAL 1 31 BY SIMILARITY

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 852 AA; 96663 MW; E57B8F8D3C9910D CRC64;

Query Match 93.6%; Score 160; DB 1; Length 852;

Best Local Similarity 91.4%; Pred. No. 8.4e-15;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAOQHLLQTLTWOIKOLARILAVERTLKQ 35

DB 552 LRAIEAOQHLLQTLTWOIKOLARILAVERTLKQ 586

ENV_HV1A2

ID ENV_HV1A2 STANDARD; PRT; 855 AA.

AC P03378;

DT 21-JUN-1986 (Rel. 01, Created)

DT 21-JUN-1986 (Rel. 01, Last sequence update)

DT 15-JUN-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus;

OX NCBI TaxID=11685;

RN [1] -

RP SEQUENCE FROM N.A.

RX MEDLINE=65090453; PubMed=2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,

RA Stempien M.W., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)";

RT Science 227:484-492(1985).

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CC or send an email to license@lsb-sib.ch).

CC EMBL; K02007; AAB59882.1; -

DR PIR; A03976; VCLJ1A2.

DR HIV; K02007; ENVSSRF2.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW Signal.

FT SIGNAL 1 29

FT CHAIN 30 509

FT CHAIN 510 855

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 208 BY SIMILARITY.

FT DISULFID 125 199 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 221 250 BY SIMILARITY.

FT DISULFID 221 242 BY SIMILARITY.

FT DISULFID 299 333 BY SIMILARITY.

FT DISULFID 380 442 BY SIMILARITY.

FT DISULFID 387 415 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).


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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1B49C04049D9 CRC64;

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Query Match 93.6%; Score 160; DB 1; Length 856;
Best Local Similarity 91.4%; Pred. No. 8.5e-15;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 35
556 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 590

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RESULT 22
ENV_HV1ZH STANDARD; PRT; 856 AA.
AC P05881;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H3231 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11692;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89228766; PubMed=2713163;
RA Steinvaan A., York D., Butler D., Jannoun-Naer R., Getche J., McCormick J., Ou C.Y., Myers G., Smith T., Chen B.;
RT "Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence comparison to recent isolates and generation of hybrid HIV-1."
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
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CC -----
CC EMBL; M15896; AAB53948.1; -
CC PIR; A44963; A44963.
CC HIV; M15896; ENV52321.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC signal.
FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 30 511 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 512 856 BY SIMILARITY.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 153 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 379 445 BY SIMILARITY.
FT DISULFID 386 418 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;

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Query Match 93.6%; Score 160; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 8.5e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 35
556 LRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 590

RESULT 23
ENV_HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (XB-1 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.

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FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 93.6%; Score 160; DB 1; Length 865;
Best Local Similarity 91.4%; Pred. No. 8.6e-15;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 35
Db 565 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 599

RESULT 25
ENV_HV1J3 STANDARD; PRT; 867 AA.
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; Pubmed=2669897;
RA Komiyama N., Hattori N., Inoue T., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria.";
RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC -----
DR EMBL; M21138; AB03526.1; -
DR HIV; M21138; ENV5JH3.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
RT signal.
FT SIGNAL 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.

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FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA; 98399 MW; 5F23101468B8B860 CRC64;

Query Match 93.6%; Score 160; DB 1; Length 867;
Best Local Similarity 94.3%; Pred. No. 8.6e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 35
Db 567 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 601

RESULT 26
ENV_HV1C4 STANDARD; PRT; 868 AA.
AC P05879;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
GN ENV.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; Pubmed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
RN [2]
RP SEQUENCE OF 34-43.

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RX MEDLINE=90253924; PubMed=2187500;
 RA Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
 RA Davila A.L., Copeland T., Oroszlan S., Gallo R.C., Sarnagadharan M.G.;
 RT "Characterization of the secreted, native gp120 and gp160 of the human
 immunodeficiency virus type 1.";
 RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).
 CC -----
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 CC -----
 DR EMBL; M13137; AAA44311.1; -;
 DR PIR; C25523; VCLJH4.
 DR HIV; M13137; ENVSCD45.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 33
 FT DISULFID 34 522 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).
 FT DISULFID 55 75 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 120 216 BY SIMILARITY.
 FT DISULFID 127 207 BY SIMILARITY.
 FT DISULFID 132 163 BY SIMILARITY.
 FT DISULFID 229 258 BY SIMILARITY.
 FT DISULFID 239 250 BY SIMILARITY.
 FT DISULFID 307 341 BY SIMILARITY.
 FT DISULFID 387 456 BY SIMILARITY.
 FT DISULFID 394 429 BY SIMILARITY.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 SQ SEQUENCE 868 AA; 98698 MW; A11527FCS2A6F0C8 CRC64;

QY 1 LRA1EAOHILQRTWQIKOLQARILAVERYLKDQ 35
 Db 568 LRA1KAOQHLLQLTWGIKQLQARILAVERYLKDQ 602
 RESULT 27
 ENV_HV1MA STANDARD; PRT; 859 AA.
 ID ENV_HV1MA
 AC P04583;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MNL isolate) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11697;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86245056; PubMed=2424612;
 RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 RT of two isolates from African patients.";
 RL Cell 46:63-74 (1986).
 CC -----
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 CC -----
 DR EMBL; X04415; CA28016.1; -;
 DR EMBL; A07116; CA00623.1; -;
 DR PIR; T01672; T01672.
 DR HIV; K03456; ENVSMAL.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 30
 FT DISULFID 31 513 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 118 210 BY SIMILARITY.
 FT DISULFID 125 201 BY SIMILARITY.
 FT DISULFID 130 162 BY SIMILARITY.
 FT DISULFID 223 252 BY SIMILARITY.
 FT DISULFID 233 244 BY SIMILARITY.
 FT DISULFID 301 334 BY SIMILARITY.
 FT DISULFID 380 445 BY SIMILARITY.
 FT DISULFID 387 418 BY SIMILARITY.
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 SQ SEQUENCE 859 AA; 97109 MW; DBCF9A5E3ABF29 CRC64;
 Query Match 93.0%; Score 159; DB 1; Length 859;
 Best Local Similarity 91.4%; Pred. No. 1.2e-14;
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LRAIEAQHLLQTLTWGIKQLQARILAVERYLKDQ 35
 558 LRAIEAQHLLQTLTWGIKQLQARILAVERYLKDQ 592
 Db
 RESULT 28
 ENV_HV1W2 STANDARD; PRT; 847 AA.
 ID ENV_HV1W2
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP MEDLINE=6235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
 RA Salanudin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.,
 RT "Genetic variation in HIV-1/LAV over time in patients with AIDS or
 RT at risk for AIDS."
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 CC WAS PERINATALLY INFECTED BY HER MOTHER.
 CC -----
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 CC -----
 CC EMBL: M12507; AAB12990.1; -
 DR HIV; M12507; ENV; WMJ2.
 DR InterPro: IPR000328; ENV GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
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 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CD1B33D73AA5B0CAE CRC64;
 Query Match 91.8%; Score 157; DB 1; Length 847;
 Best Local Similarity 88.6%; Pred. No. 2.2e-14;
 Matches 31; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LRAIEAQHLLQTLTWGIKQLQARILAVERYLKDQ 35
 547 LRAIEAQHLLQTLTWGIKQLQARILAVERYLKDQ 581
 Db
 RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.
 ID ENV_HV1Z8
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP MEDLINE=68281278; PubMed=3395517;
 RA Yoon J., Joseph S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.,
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1."
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
 CC ZAIREAN MALE.
 CC -----
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CC -----
DR EMBL: J03653; AAA44684.1; -.
DR HIV; J03653; ENV5J1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 518 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 519 863 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 452 BY SIMILARITY.
FT DISULFID 395 425 BY SIMILARITY.
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SQ SEQUENCE 863 AA; 97743 MW; B729C85A6FAD1641 CRC64;

Query Match 90.6%; Score 155; DB 1; Length 863;
Best Local Similarity 88.6%; Pred. No. 4.4e-14;
Matches 31; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_Taxid=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2789516;
RA Mand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia.";
RT Virology 168:79-89 (1989).
CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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CC -----
CC EMBL: M21098; AAA44221.1; -.
CC PIR; A31667; VCLUR.
DR PDB; 1IM7; 23-OCT-02.
DR HIV; M21098; ENV5J1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
3D-structure.
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FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
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FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
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Query Match 88.9%; Score 152; DB 1; Length 852;
Best Local Similarity 85.7%; Pred. No. 1,1e-13;

Matches 30; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLOLTWQIKQLQARILAVERYLKDQ 35
| | | | | : | | | | | : | | | | |
Db 552 LMAIEAQOHLLELTWVGIKQLQARVLAVERYLKDQ 586

Search completed: June 2, 2004, 11:42:58
Job time : 6.70652 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 29.3886 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-181
Perfect score: 171
Sequence: 1 LRAIFAQOHLQLTWQIQKQARILAVERYLKDQ 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DE seq length: 0
Maximum DE seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	96.5	852	15	08UJ55
2	164	95.9	129	15	09YVZ1
3	164	95.9	131	15	07SM43
4	164	95.9	132	15	09OQ52
5	164	95.9	132	15	07SLZ2
6	164	95.9	143	15	07SM06
7	164	95.9	144	15	07ZCD7
8	164	95.9	144	15	07ZCD6
9	164	95.9	145	15	07ZCS2
10	164	95.9	153	15	07SM03
11	164	95.9	173	15	08JAJ9
12	164	95.9	357	15	078119
13	164	95.9	588	15	0993A8
14	164	95.9	588	15	0993A7
15	164	95.9	589	15	0993B1
16	164	95.9	590	15	0993A9

17	164	95.9	616	15	0993B0	0993B0 human immun
18	164	95.9	618	15	0993B2	0993B2 human immun
19	164	95.9	727	15	09G723	09G723 human immun
20	164	95.9	747	15	070607	070607 human immun
21	164	95.9	748	15	070605	070605 human immun
22	164	95.9	752	15	070604	070604 human immun
23	164	95.9	752	15	070605	070605 human immun
24	164	95.9	752	15	070608	070608 human immun
25	164	95.9	757	15	09G722	09G722 human immun
26	164	95.9	811	15	09DVL6	09dvl6 human immun
27	164	95.9	826	15	09DVL1	09dvl1 human immun
28	164	95.9	842	15	073341	073341 human immun
29	164	95.9	842	15	070495	070495 human immun
30	164	95.9	842	15	073340	073340 human immun
31	164	95.9	845	15	091D89	091d89 human immun
32	164	95.9	847	15	069996	069996 human immun
33	164	95.9	851	15	078243	078243 human immun
34	164	95.9	854	15	056566	056566 human immun
35	164	95.9	854	15	085582	085582 human immun
36	164	95.9	854	15	072502	072502 human immun
37	164	95.9	854	15	090178	090178 human immun
38	164	95.9	854	15	078705	078705 human immun
39	164	95.9	855	15	08AQV7	08aqv7 human immun
40	164	95.9	855	15	08ADT7	08adt7 human immun
41	164	95.9	856	15	074090	074090 human immun
42	164	95.9	856	15	092877	092877 simlan-huma
43	164	95.9	856	15	074599	074599 human immun
44	164	95.9	856	15	041772	041772 human immun
45	164	95.9	857	15	092822	092822 human immun
46	164	95.9	857	15	071013	071013 human immun
47	164	95.9	857	15	089654	089654 human immun
48	164	95.9	859	15	09WLJ1	09wlj1 human immun
49	164	95.9	864	15	09YXP3	09yxp3 human immun
50	164	95.9	864	15	07ZJC8	07zjc8 human immun
51	164	95.9	866	15	09WPZ4	09wpz4 human immun
52	164	95.9	870	15	08Q2X1	08q2x1 human immun
53	164	95.9	870	15	08Q2X0	08q2x0 human immun
54	164	95.3	113	15	07ZCES	07zces human immun
55	163	95.3	125	15	091WP9	091wp9 human immun
56	163	95.3	127	15	09YXX9	09yxx9 human immun
57	163	95.3	127	15	09YXX0	09yxx0 human immun
58	163	95.3	129	15	09YXY7	09yxy7 human immun
59	163	95.3	132	15	091WQ5	091wq5 human immun
60	163	95.3	132	15	08UQ26	08uq26 human immun
61	163	95.3	133	15	08UQ27	08uq27 human immun
62	163	95.3	133	15	08UQ28	08uq28 human immun
63	163	95.3	133	15	08UQ24	08uq24 human immun
64	163	95.3	133	15	08UQ23	08uq23 human immun
65	163	95.3	133	15	090Q20	090q20 human immun
66	163	95.3	134	15	091WQ6	091wq6 human immun
67	163	95.3	136	15	08UQ25	08uq25 human immun
68	163	95.3	137	15	09DQMO	09dqmo human immun
69	163	95.3	137	15	09DQM4	09dqm4 human immun
70	163	95.3	142	15	091WQ7	091wq7 human immun
71	163	95.3	142	15	091WQ3	091wq3 human immun
72	163	95.3	143	15	091WQ1	091wq1 human immun
73	163	95.3	143	15	07ZC46	07zc46 human immun
74	163	95.3	144	15	091WQ4	091wq4 human immun
75	163	95.3	144	15	070207	070207 human immun
76	163	95.3	144	15	07ZCE6	07zce6 human immun
77	163	95.3	144	15	07ZCD8	07zcd8 human immun
78	163	95.3	144	15	07ZCC6	07zcc6 human immun
79	163	95.3	144	15	07ZCC5	07zcc5 human immun
80	163	95.3	144	15	07ZCC2	07zcc2 human immun
81	163	95.3	144	15	07ZCB1	07zcb1 human immun
82	163	95.3	144	15	07ZCB0	07zcb0 human immun
83	163	95.3	144	15	07ZC96	07zc96 human immun
84	163	95.3	144	15	07ZC95	07zc95 human immun
85	163	95.3	144	15	07ZC89	07zc89 human immun
86	163	95.3	144	15	07ZC88	07zc88 human immun
87	163	95.3	144	15	07ZC71	07zc71 human immun
88	163	95.3	144	15	07ZC70	07zc70 human immun
89	163	95.3	144	15	07ZC45	07zc45 human immun

90 163 95.3 145 15 Q7ZC57 Q7ZC57 human immun

ALIGNMENTS

RESULT 1

Q8UL55 PRELIMINARY; PRT; 852 AA.
AC Q8UL55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp160 protein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;
RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells
RT and Herpesvirus saimiri transformed T-cells is comparable."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418531; CAD10941.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 852 AA; 96711 MW; 57D8CA06A42F377F CRC64;

Query Match 96.5%; Score 165; DB 15; Length 852;
Best Local Similarity 94.3%; Pred. No. 5.9e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 551 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 585

RESULT 2

Q9YVZ1 PRELIMINARY; PRT; 129 AA.
ID Q9YVZ1;
AC Q9YVZ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=205.586;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006896; AAD01340.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1

FT NON_TER 129 129
SQ SEQUENCE 129 AA; 15612 MW; 9CA606B58F42ADF CRC64;

Query Match 95.9%; Score 164; DB 15; Length 129;
Best Local Similarity 97.1%; Pred. No. 1.1e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 3 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 37

RESULT 3

Q7SM43 PRELIMINARY; PRT; 131 AA.
ID Q7SM43;
AC Q7SM43;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G1362;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529973; AAP87704.1; -
KM Envelope protein.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 15539 MW; C11B4FEFEBA1860F CRC64;

Query Match 95.9%; Score 164; DB 15; Length 131;
Best Local Similarity 97.1%; Pred. No. 1.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 14 LRAIEAQHLLQLTWGIKQLQARIILAVERYLKQ 48

RESULT 4

Q90Q52 PRELIMINARY; PRT; 132 AA.
ID Q90Q52;
AC Q90Q52;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MOI496;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeo N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331089; AAK92300.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.

FT NON_TER 1 1
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15708 MW; 519DB8AED574FAE CRC64;
Query Match
Best Local Similarity 97.1%; Score 164; DB 15; Length 132;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 35
Db 13 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 47

RESULT 5

ID 07SLZ2 PRELIMINARY; PRT; 132 AA.
AC 07SLZ2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT970;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530024; AAP87755.1; -
KM Envelope protein.
FT NON_TER 1 1
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;
Query Match
Best Local Similarity 97.1%; Score 164; DB 15; Length 132;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 35
Db 14 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 48

RESULT 6

ID 07SM06 PRELIMINARY; PRT; 143 AA.
AC 07SM06;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530010; AAP87741.1; -
KM Envelope protein.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BE0 CRC64;
Query Match
95.9%; Score 164; DB 15; Length 143;

Best Local Similarity 97.1%; Pred. No. 1.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 35
Db 14 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 48

RESULT 7

ID 07ZCD7 PRELIMINARY; PRT; 144 AA.
AC 07ZCD7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185383; AAO65658.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318EBE CRC64;

Query Match
Best Local Similarity 97.1%; Score 164; DB 15; Length 144;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 35
Db 27 LRAIEAQHLLQLTWGIKOLQARILAVERYLKQ 61

RESULT 8

ID 07ZCD6 PRELIMINARY; PRT; 144 AA.
AC 07ZCD6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185384; AAO65659.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 144
 SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EB CRC64;

Query Match 95.9%; Score 164; DB 15; Length 144;
 Best Local Similarity 97.1%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 35
 Db 27 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 61

RESULT 9

Q7ZCS2 PRELIMINARY; PRT; 145 AA.

AC Q7ZCS2; 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).

OS ENV.
 GN Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HRLU18;
 RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
 RA Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
 RT "Unccommon mutations at residue positions critical for enfuvirtide (T-
 RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
 RT subtype HIV-1.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF185468; AA065743.1;

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 145

SQ SEQUENCE 145 AA; 17020 MW; AC8C32E97B09D1A1 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 145;
 Best Local Similarity 97.1%; Pred. No. 1.3e-15;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 35
 Db 25 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 59

RESULT 10

Q7SMO3 PRELIMINARY; PRT; 153 AA.

AC Q7SMO3; 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GT598;

RA Gonzalez Perez M.P., Garcia Saiz A.;

RT "Epidemiological and molecular characteristics of HIV and HTLV

RT Infection in Equatorial Guinea, 1996-1998.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF530013; AA87744.1; -.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 153

SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1FFFC03 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 153;
 Best Local Similarity 97.1%; Pred. No. 1.4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 35
 Db 14 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 48

RESULT 11

Q8JAJ9 PRELIMINARY; PRT; 173 AA.

AC Q8JAJ9; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=98BRJ045;

RA Galimraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,

RA Morgado M.G.;

RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian

RT Southeastern and Southern regions.";

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF463445; AA090821.1; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON_TER 1

FT NON_TER 173

SQ SEQUENCE 173 AA; 19858 MW; 300D69C94C03AD14 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 173;
 Best Local Similarity 97.1%; Pred. No. 1.5e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 35
 Db 59 LRAIEAQHLLQLTWQIKQARILAVERYLKQ 93

RESULT 12

Q78119 PRELIMINARY; PRT; 357 AA.

AC Q78119; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
 DE Envelope protein, gp120 /gp41 (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

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RX MEDLINE=92144209; PubMed=1736940;
RA Seuler H., Storch-Hagenlocher B., Wildemann B.;
RT "distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61356; CAA43624.1; -.
DR PIR; A53591; A53591.
DR PIR; S70422; S21966.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER
FT NON_TER
SQ SEQUENCE 357 AA; 4118 MW; FE4CA7E122AB8E6 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 357;
Best Local Similarity 97.1%; Pred. No. 3.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LRAIEAQOHLLQLTWGIKQIARILAVERYLKQ 35
Db 57 LRAIEAQOHLLQLTWGIKQIARILAVERYLKQ 91

RESULT 13
ID 0993A8 PRELIMINARY; PRT; 588 AA.
AC 0993A8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA Dcosta S.S., Hurtwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240A88 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 588;
Best Local Similarity 97.1%; Pred. No. 5.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ID 0993A7 PRELIMINARY; PRT; 588 AA.
AC 0993A7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

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DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA Dcosta S.S., Hurtwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321148; AAK20296.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match 95.9%; Score 164; DB 15; Length 588;
Best Local Similarity 97.1%; Pred. No. 5.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LRAIEAQOHLLQLTWGIKQIARILAVERYLKQ 35
Db 499 LRAIEAQOHLLQLTWGIKQIARILAVERYLKQ 533

RESULT 15
ID 0993B1 PRELIMINARY; PRT; 589 AA.
AC 0993B1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RA Dcosta S.S., Hurtwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AAK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 589;
Best Local Similarity 97.1%; Pred. No. 5.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 35
DB 499 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 533

RESULT 16

Q99329 ID Q993A9 PRELIMINARY; PRT; 590 AA.
AC Q993A9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WC2;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF221146; AAK20294.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 590
FT SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;
SQ

Query Match 95.9%; Score 164; DB 15; Length 590;
Best Local Similarity 97.1%; Pred. No. 5.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 35
DB 500 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 534

RESULT 17

Q993B0 ID Q993B0 PRELIMINARY; PRT; 616 AA.
AC Q993B0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF221145; AAK20293.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 616
FT SEQUENCE 616 AA; 69189 MW; 57ABE20F9A580A4F CRC64;
SQ

Query Match 95.9%; Score 164; DB 15; Length 616;
Best Local Similarity 97.1%; Pred. No. 5.9e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 35
DB 500 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 534

RESULT 18

Q993B2 ID Q993B2 PRELIMINARY; PRT; 618 AA.
AC Q993B2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF221143; AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 618
FT SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;
SQ

Query Match 95.9%; Score 164; DB 15; Length 618;
Best Local Similarity 97.1%; Pred. No. 5.9e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 35
DB 502 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKQ 536

RESULT 19

Q90723 ID Q90723 PRELIMINARY; PRT; 727 AA.
AC Q90723;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=111Bx;


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RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL; AF189158; AAF25627.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD626D2659E66 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 727;
Best Local Similarity 97.1%; Pred. No. 7e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 551 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 585

RESULT 20
OY 070607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Raitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RX Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AAA76669.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 95.9%; Score 164; DB 15; Length 748;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 552 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 586

RESULT 22
OY 070604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

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DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 747;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 551 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 585

RESULT 21
OY 070606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RX MEDLINE=95127297; PubMed=7826699;
RA Raitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RX Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 95.9%; Score 164; DB 15; Length 748;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 35
DB 552 LRAIEAQOHLLQLTWGIKQLQARIILAVERYLKQ 586

RESULT 22
OY 070604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

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OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
RX MEDLINE=95127297; PubMed=7826699;
RC STRAIN=LW851;
RA Shaw G., Kong L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
infectd with HIV type 1 (HTLV type IIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 35
Db 556 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 590
RESULT 23
QY 070605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
RX MEDLINE=95127297; PubMed=7826699;
RC STRAIN=LW852;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
infectd with HIV type 1 (HTLV type IIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 35
Db 556 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 590
RESULT 24
QY 070608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
ON NCBI_Taxid=11676;
RX MEDLINE=95127297; PubMed=7826699;
RC STRAIN=LW87-2;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
infectd with HIV type 1 (HTLV type IIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AAA76670.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0B8F8 CRC64;
Query Match 95.9%; Score 164; DB 15; Length 752;
Best Local Similarity 97.1%; Pred. No. 7.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 35
Db 556 LRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 590
RESULT 25
QY 090722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI Taxid=11676;
[1]
RN
RC STRAIN=FROM N.A.
RA MEDLINE=99272699; PubMed=10339592;
RX Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RT "Determinants of CD4 independence for a human immunodeficiency virus
type 1 variant map outside regions required for coreceptor
specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL; AF189159; AAF25628.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
DR AIDS; Coit protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AFB8263BD2E CRC64;

Query Match 95.9%; Score 164; DB 15; Length 757;
Best Local Similarity 97.1%; Pred. No. 7.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 35
Db 551 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 585

RESULT 26
Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI Taxid=11676;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; PubMed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
group M genetic diversity in the Democratic Republic of Congo suggests
that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL; AJ401037; CAC15045.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
DR AIDS; Coit protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 811;
Best Local Similarity 97.1%; Pred. No. 7.8e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 35
Db 560 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 594

RESULT 27
Q9DVL6 PRELIMINARY; PRT; 826 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI Taxid=11676;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=97DC.KTB22;
RX MEDLINE=20499072; PubMed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RT "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
group M genetic diversity in the Democratic Republic of Congo suggests
that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL; AJ401042; CAC15050.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
DR AIDS; Coit protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 826;
Best Local Similarity 97.1%; Pred. No. 8e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 35
Db 543 LRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 577

RESULT 28
Q73341

ID Q7341 PRELIMINARY; PRT; 842 AA.
 AC Q7341;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RA MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
 RA Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization.";
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL; U39236; AAB37173.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1E9F1 CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 8.1e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
 Db 542 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 576

RESULT 29
 O70895 PRELIMINARY; PRT; 842 AA.
 AC Q70895;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope gp160.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=93br029;
 RA MEDLINE=98285725; PubMed=9621027;
 RA Gao F., Robertson D.L., Carnuthers C.D., Morrison S.G., Jian B.,
 RA Chen Y., Bare-Sinowski F., Girard M., Srinivasan A., Abimiku A.G.,
 RA Shaw G.M., Sharp P.M., Hahn B.H.;
 RT "A comprehensive panel of near-full-length clones and reference
 RT sequences for non-subtype B isolates of human immunodeficiency virus
 RT type 1.";
 RL J. Virol. 72:5680-5698(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=93br029;
 RA Gao F.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005495; AAD03179.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 842 AA; 94810 MW; F82041BD932DCAD CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 8.1e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
 Db 542 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 576

RESULT 30
 O73340 PRELIMINARY; PRT; 842 AA.
 AC Q73340;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RA MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
 RA Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization.";
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL; U39235; AAB37172.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 607B4F2A47B791EB CRC64;

Query Match 95.9%; Score 164; DB 15; Length 842;
 Best Local Similarity 97.1%; Pred. No. 8.1e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
 Db 542 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 576

Search completed: June 2, 2004, 11:48:21
 Job time : 29.3886 secs

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OM protein - protein search, using SW model

Run on: June 2, 2004, 11:33:58 ; Search time 12.9348 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-181
Perfect score: 171
Sequence: 1 LRAIEAQQHLLQLTWQIKQLQARILAVERYLKDQ 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	38 4	US-08-973-952-82	Sequence 82, App1
2	164	95.9	35 4	US-09-515-965A-1755	Sequence 1755, App
3	164	95.9	36 4	US-09-515-965A-1756	Sequence 1756, App
4	164	95.9	37 4	US-09-515-965A-1757	Sequence 1757, App
5	164	95.9	38 1	US-08-374-666-1	Sequence 1, App1
6	164	95.9	38 3	US-08-486-099-89	Sequence 89, App1
7	164	95.9	38 3	US-08-360-107A-99	Sequence 99, App1
8	164	95.9	38 3	US-08-360-107A-132	Sequence 132, App1
9	164	95.9	38 3	US-08-484-223B-89	Sequence 89, App1
10	164	95.9	38 3	US-08-919-597-89	Sequence 89, App1
11	164	95.9	38 3	US-08-475-668A-89	Sequence 89, App1
12	164	95.9	38 3	US-08-485-551A-89	Sequence 89, App1
13	164	95.9	38 3	US-08-471-913A-89	Sequence 89, App1
14	164	95.9	38 3	US-08-485-264A-89	Sequence 89, App1
15	164	95.9	38 3	US-08-082-279B-16	Sequence 16, App1
16	164	95.9	38 3	US-08-082-279B-507	Sequence 507, App
17	164	95.9	38 3	US-08-082-279B-604	Sequence 604, App
18	164	95.9	38 3	US-08-082-279B-658	Sequence 658, App
19	164	95.9	38 3	US-09-082-279B-659	Sequence 659, App
20	164	95.9	38 3	US-09-082-279B-660	Sequence 660, App
21	164	95.9	38 4	US-08-474-349A-89	Sequence 89, App1
22	164	95.9	38 4	US-08-474-349A-441	Sequence 441, App
23	164	95.9	38 4	US-09-315-304B-16	Sequence 16, App1
24	164	95.9	38 4	US-09-315-304B-507	Sequence 507, App
25	164	95.9	38 4	US-09-315-304B-604	Sequence 604, App
26	164	95.9	38 4	US-09-315-304B-658	Sequence 658, App
27	164	95.9	38 4	US-09-315-304B-659	Sequence 659, App

28	164	95.9	38 4	US-09-315-304B-660	Sequence 660, App
29	164	95.9	38 4	US-08-255-208A-25	Sequence 25, App1
30	164	95.9	38 4	US-08-470-896-89	Sequence 89, App1
31	164	95.9	38 4	US-08-485-546A-89	Sequence 89, App1
32	164	95.9	38 4	US-09-796-202-11	Sequence 11, App1
33	164	95.9	38 4	US-09-834-784-16	Sequence 16, App1
34	164	95.9	38 4	US-09-834-784-507	Sequence 507, App
35	164	95.9	38 4	US-09-834-784-604	Sequence 604, App
36	164	95.9	38 4	US-09-834-784-658	Sequence 658, App
37	164	95.9	38 4	US-09-834-784-659	Sequence 659, App
38	164	95.9	38 4	US-09-834-784-660	Sequence 660, App
39	164	95.9	38 4	US-08-464-003-1	Sequence 1, App1
40	164	95.9	38 4	US-09-779-451-2	Sequence 2, App1
41	164	95.9	38 4	US-09-515-965A-16	Sequence 16, App1
42	164	95.9	38 4	US-09-515-965A-507	Sequence 507, App
43	164	95.9	38 4	US-09-515-965A-604	Sequence 604, App
44	164	95.9	38 4	US-09-515-965A-658	Sequence 658, App
45	164	95.9	38 4	US-09-515-965A-659	Sequence 659, App
46	164	95.9	38 4	US-09-515-965A-660	Sequence 660, App
47	164	95.9	38 4	US-09-350-641C-16	Sequence 16, App1
48	164	95.9	38 4	US-09-350-641C-507	Sequence 507, App
49	164	95.9	38 4	US-09-350-641C-604	Sequence 604, App
50	164	95.9	38 4	US-09-350-641C-658	Sequence 658, App
51	164	95.9	38 4	US-09-350-641C-659	Sequence 659, App
52	164	95.9	38 4	US-09-350-641C-660	Sequence 660, App
53	164	95.9	41 1	US-08-073-028-8	Sequence 8, App1
54	164	95.9	41 1	US-08-374-666-3	Sequence 3, App1
55	164	95.9	41 1	US-08-374-666-9	Sequence 9, App1
56	164	95.9	41 3	US-08-486-099-8	Sequence 8, App1
57	164	95.9	41 3	US-08-360-107A-8	Sequence 8, App1
58	164	95.9	41 3	US-08-484-223B-8	Sequence 8, App1
59	164	95.9	41 3	US-08-484-223B-242	Sequence 242, App
60	164	95.9	41 3	US-08-484-223B-243	Sequence 243, App
61	164	95.9	41 3	US-08-919-597-8	Sequence 8, App1
62	164	95.9	41 3	US-08-475-668A-8	Sequence 8, App1
63	164	95.9	41 3	US-08-485-551A-8	Sequence 8, App1
64	164	95.9	41 3	US-08-471-913A-8	Sequence 8, App1
65	164	95.9	41 3	US-08-554-616-8	Sequence 8, App1
66	164	95.9	41 3	US-08-485-264A-8	Sequence 8, App1
67	164	95.9	41 3	US-09-082-279B-496	Sequence 496, App
68	164	95.9	41 3	US-09-082-279B-601	Sequence 601, App
69	164	95.9	41 3	US-09-082-279B-633	Sequence 633, App
70	164	95.9	41 3	US-09-082-279B-1163	Sequence 1163, App
71	164	95.9	41 4	US-08-474-349A-8	Sequence 8, App1
72	164	95.9	41 4	US-09-315-304B-496	Sequence 496, App
73	164	95.9	41 4	US-09-315-304B-601	Sequence 601, App
74	164	95.9	41 4	US-09-315-304B-633	Sequence 633, App
75	164	95.9	41 4	US-09-315-304B-1163	Sequence 1163, App
76	164	95.9	41 4	US-08-255-208A-8	Sequence 8, App1
77	164	95.9	41 4	US-08-973-952-8	Sequence 8, App1
78	164	95.9	41 4	US-08-470-896-8	Sequence 8, App1
79	164	95.9	41 4	US-08-485-546A-8	Sequence 8, App1
80	164	95.9	41 4	US-09-834-784-496	Sequence 496, App
81	164	95.9	41 4	US-09-834-784-601	Sequence 601, App
82	164	95.9	41 4	US-09-834-784-633	Sequence 633, App
83	164	95.9	41 4	US-09-834-784-1163	Sequence 1163, App
84	164	95.9	41 4	US-08-464-003-3	Sequence 3, App1
85	164	95.9	41 4	US-08-464-003-9	Sequence 9, App1
86	164	95.9	41 4	US-09-515-965A-496	Sequence 496, App
87	164	95.9	41 4	US-09-515-965A-601	Sequence 601, App
88	164	95.9	41 4	US-09-515-965A-633	Sequence 633, App
89	164	95.9	41 4	US-09-515-965A-1163	Sequence 1163, App
90	164	95.9	41 4	US-09-350-641C-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 100.0%; Score 171; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,8e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 2
US-09-515-965A-1755
Sequence 1755, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1755
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1755

Query Match 95.9%; Score 164; DB 4; Length 35;
Best Local Similarity 97.1%; Pred. No. 1,6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35
DB 1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35

RESULT 3
US-09-515-965A-1756
Sequence 1756, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.

APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1756
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1756

Query Match 95.9%; Score 164; DB 4; Length 36;
Best Local Similarity 97.1%; Pred. No. 1,6e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35
DB 2 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 36

RESULT 4
US-09-515-965A-1757
Sequence 1757, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1757
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1757

Query Match 95.9%; Score 164; DB 4; Length 37;
Best Local Similarity 97.1%; Pred. No. 1,7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 35
DB 3 LRAIEAQOHLQLTWQIKQARILAVERYLKQ 37

RESULT 5
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.

APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1

Query Match 95.9%; Score 164; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWTWQIKOLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWTWQIKOLQARIILAVERYLKQ 38

RESULT 6
US-08-486-099-89
Sequence 89, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWTWQIKOLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWTWQIKOLQARIILAVERYLKQ 38

RESULT 7
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 38

RESULT 8
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 149
TRANSMISSION
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 38

RESULT 9
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 245
TRANSMISSION
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWGIKQIOLARILAVERYLKQ 38

RESULT 10
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQCHLLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQCHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 11
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQCHLLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQCHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 12
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 13

US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 14
US-08-485-264A-89

Sequence 89, Application US/08485264A
Patent No. 6228983

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING

TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,264A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-021

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-485-264A-89

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 15

US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 38

RESULT 16
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082.279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 38

RESULT 17
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082.279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 38

RESULT 18
US-09-082-279B-658
Sequence 658, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082.279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 658
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-658

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGKIQKQARILAVERYLKQ 35

RESULT 19
US-09-082-279B-659
Sequence 659, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082.279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 659
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-659

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 2 LRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 36
|||||

RESULT 20
US-09-082-279B-660
Sequence 660, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthe, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 660
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-660

Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 3 LRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 37
|||||

RESULT 21
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
|||||
Db 4 LRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38
|||||

RESULT 22
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-474..349A-441

Query Match	95.9%;	Score 164;	DB 4;	Length 38;
Best Local Similarity	97.1%;	Pred. No. 1.7e-16;		
Matches 34;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	LRAIEAQGHLLQTVWQIKQIARILAVERYLKQD	35
		:	
Db	4	LRAIEAQGNLLQTVWQIKQIARILAVERYLKQD	38

RESULT 23
US-09-315

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US-09-315-304B-16
; Sequence 16, Application US/09315304B
; Patent No. 6348568
;
; GENERAL INFORMATION:
;
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
;
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
;
; FILE REFERENCE: 7872-052
;
; CURRENT APPLICATION NUMBER: US/09/315,304B
;
; CURRENT FILING DATE: 1999-05-20
;
; PRIOR APPLICATION NUMBER: 09/082,279
;
; PRIOR FILING DATE: 1998-05-20
;
; NUMBER OF SEQ ID NOS: 1667
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 16
;
; LENGTH: 38
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Core polypeptide
;
US-09-315-304B-16

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Query Match	95.9%;	Score 164;	DB 4;	Length 38;
Best Local Similarity	97.1%;	Pred. No. 1.7e-16;		
Matches 34; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	LR	IA	EQ	QH	LQ	LT	WQ	IK	QI	QAR	IL	AV	ER	YL	KD	Q	35
Db	4	LR <td>IA <td>EQ <td>QH <td>LQ <td>LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	IA <td>EQ <td>QH <td>LQ <td>LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	EQ <td>QH <td>LQ <td>LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	QH <td>LQ <td>LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td></td></td>	LQ <td>LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td></td>	LT <td>WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td></td>	WQ <td>IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td></td>	IK <td>QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td></td>	QI <td>QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td></td>	QAR <td>IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td></td>	IL <td>AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td></td>	AV <td>ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td></td>	ER <td>YL <td>KD <td>Q <td>38</td> </td></td></td>	YL <td>KD <td>Q <td>38</td> </td></td>	KD <td>Q <td>38</td> </td>	Q <td>38</td>	38

```

RESULT 24
US-09-315-304B-507
; Sequence 507, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ. ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-507

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Query Match	95.9%	Score 164	DB 4	Length 38
Best Local Similarity	97.1%	Pred. No. 1.7e-16		
Matches 34	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY 1 LRAIEAQGHLLQLTWGICIKQLARILAVERYLKQD 35
DB 4 LRAIEAQGHLLQLTWGICIKQLARILAVERYLKQD 38

US-09-315

```

Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthe, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

```

Query Match	95.9%	Score 164;	DB 4;	Length 38;
Best Local Similarity	97.1%;	Pred. No. 1.7e-16;		
Matches 34; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY 1 LRAIEAQGHLLQTLTWGICKQLQARILAVERYLKDQ 35
 |||||
Db 4 LRAIEAQGHLLQTLTWGICKQLQARILAVERYLKDQ 38

```

RESULT 26
US-09-315-304B-658
; Sequence 658, Application US/09315304B
; Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Murtka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315.304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 658
LENGTH: 38
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-658

```

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
DB 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35

RESULT 27

US-09-315-304B-659
; Sequence 659, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Metucka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 659
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-659

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
DB 2 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 36

RESULT 28

US-09-315-304B-660
; Sequence 660, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Metucka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 660
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-660

Query Match 95.9%; Score 164; DB 4; Length 38;

Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
DB 3 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 37

RESULT 29

US-08-255-208A-25
; Sequence 25, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; FILE REFERENCE: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 95.9%; Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 30

US-08-470-896-89
; Sequence 89, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.

APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-396-89

Query March 95.9% Score 164; DB 4; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LRAIEAQOHLLQTLTWQIKQLARILAVERYLKQ 35
Db 4 LRAIEAQOHLLQTLTWGIGIKQLARILAVERYLKQ 38

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OM protein - protein search, using sw model

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(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-181
Perfect score: 171
Sequence: 1 LRAIEAQOHILQLTWQIKQLQARILAVERYLKDQ 35

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

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11: /cgnt2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgnt2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep:*
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18: /cgnt2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	164	95.9	35	15	US-10-005-305-162
3	164	95.9	36	15	US-10-005-305-163
4	164	95.9	37	15	US-10-005-305-164
5	164	95.9	38	9	US-09-796-202-11
6	164	95.9	38	9	US-09-779-451-2
7	164	95.9	38	10	US-09-493-346-2
8	164	95.9	38	12	US-10-267-682-89
9	164	95.9	38	12	US-10-267-748-89
10	164	95.9	38	12	US-09-809-060-6
11	164	95.9	38	12	US-10-663-589-3
12	164	95.9	38	12	US-10-681-879-2
13	164	95.9	38	12	US-10-681-879-2
14	164	95.9	38	12	US-09-828-615-2
15	164	95.9	38	14	US-10-116-797-2

16	164	95.9	38	14	US-10-323-314-11	Sequence 11, Appl
17	164	95.9	38	14	US-10-414-192-1	Sequence 1, Appl
18	164	95.9	38	14	US-10-351-641-16	Sequence 16, Appl
19	164	95.9	38	14	US-10-351-641-507	Sequence 507, Appl
20	164	95.9	38	14	US-10-351-641-604	Sequence 604, Appl
21	164	95.9	38	14	US-10-351-641-658	Sequence 658, Appl
22	164	95.9	38	14	US-10-351-641-659	Sequence 659, Appl
23	164	95.9	38	14	US-10-351-641-660	Sequence 660, Appl
24	164	95.9	38	15	US-10-005-305-165	Sequence 165, Appl
25	164	95.9	38	15	US-10-005-305-202	Sequence 202, Appl
26	164	95.9	38	15	US-10-005-305-203	Sequence 203, Appl
27	164	95.9	38	15	US-10-420-194-1234	Sequence 1234, Ap
28	164	95.9	38	16	US-10-664-021-2	Sequence 2, Appl
29	164	95.9	38	16	US-10-671-316-2	Sequence 8, Appl
30	164	95.9	41	12	US-10-267-682-8	Sequence 8, Appl
31	164	95.9	41	12	US-10-267-748-8	Sequence 8, Appl
32	164	95.9	41	12	US-10-663-589-30	Sequence 30, Appl
33	164	95.9	41	12	US-10-663-589-33	Sequence 33, Appl
34	164	95.9	41	12	US-10-663-589-35	Sequence 35, Appl
35	164	95.9	41	14	US-10-252-136-8	Sequence 8, Appl
36	164	95.9	41	14	US-10-414-192-3	Sequence 9, Appl
37	164	95.9	41	14	US-10-414-192-9	Sequence 9, Appl
38	164	95.9	41	14	US-10-351-641-486	Sequence 486, Appl
39	164	95.9	41	14	US-10-351-641-601	Sequence 601, Appl
40	164	95.9	41	14	US-10-351-641-633	Sequence 633, Appl
41	164	95.9	41	14	US-10-351-641-1163	Sequence 1163, Ap
42	164	95.9	41	16	US-10-664-021-27	Sequence 27, Appl
43	164	95.9	41	16	US-10-671-316-27	Sequence 27, Appl
44	164	95.9	44	12	US-10-663-589-36	Sequence 36, Appl
45	164	95.9	44	14	US-10-414-192-10	Sequence 10, Appl
46	164	95.9	45	9	US-09-779-451-9	Sequence 9, Appl
47	164	95.9	45	12	US-09-809-060-50	Sequence 50, Appl
48	164	95.9	45	12	US-10-663-589-29	Sequence 29, Appl
49	164	95.9	45	14	US-10-351-641-1164	Sequence 1164, Ap
50	164	95.9	45	16	US-10-664-021-26	Sequence 26, Appl
51	164	95.9	45	16	US-10-671-316-26	Sequence 26, Appl
52	164	95.9	49	9	US-09-796-202-3	Sequence 3, Appl
53	164	95.9	49	14	US-10-323-314-3	Sequence 3, Appl
54	164	95.9	51	12	US-10-663-589-27	Sequence 27, Appl
55	164	95.9	51	14	US-10-351-641-745	Sequence 745, Appl
56	164	95.9	51	16	US-10-664-021-24	Sequence 24, Appl
57	164	95.9	51	16	US-10-671-316-24	Sequence 24, Appl
58	164	95.9	52	14	US-10-351-641-1119	Sequence 1119, Ap
59	164	95.9	53	14	US-10-351-641-955	Sequence 955, Appl
60	164	95.9	53	14	US-10-351-641-1062	Sequence 1062, Ap
61	164	95.9	55	9	US-09-779-451-1	Sequence 1, Appl
62	164	95.9	55	12	US-09-809-060-14	Sequence 14, Appl
63	164	95.9	57	15	US-10-438-691-1	Sequence 1, Appl
64	164	95.9	59	16	US-10-664-021-1	Sequence 1, Appl
65	164	95.9	59	16	US-10-664-021-1	Sequence 1, Appl
66	164	95.9	60	12	US-10-663-589-1	Sequence 1, Appl
67	164	95.9	63	12	US-10-267-682-201	Sequence 201, Appl
68	164	95.9	63	12	US-10-267-748-201	Sequence 201, Appl
69	164	95.9	63	14	US-10-252-136-54	Sequence 54, Appl
70	164	95.9	103	15	US-10-438-691-3	Sequence 29, Appl
71	164	95.9	103	15	US-10-263-816-17	Sequence 3, Appl
72	164	95.9	113	15	US-10-438-691-4	Sequence 4, Appl
73	164	95.9	177	14	US-10-040-349B-2	Sequence 2, Appl
74	164	95.9	188	9	US-09-854-816-88	Sequence 88, Appl
75	164	95.9	188	9	US-09-854-816-89	Sequence 89, Appl
76	164	95.9	200	14	US-10-263-103-25	Sequence 25, Appl
77	164	95.9	200	15	US-10-438-691-8	Sequence 8, Appl
78	164	95.9	232	14	US-10-059-271-81	Sequence 81, Appl
79	164	95.9	254	14	US-10-059-271-82	Sequence 82, Appl
80	164	95.9	256	14	US-10-059-271-97	Sequence 97, Appl
81	164	95.9	268	9	US-09-854-816-16	Sequence 16, Appl
82	164	95.9	268	9	US-09-854-816-17	Sequence 17, Appl
83	164	95.9	268	9	US-09-854-816-18	Sequence 18, Appl
84	164	95.9	268	9	US-09-854-816-19	Sequence 19, Appl
85	164	95.9	329	9	US-09-854-816-43	Sequence 43, Appl
86	164	95.9	338	12	US-10-267-682-90	Sequence 90, Appl
87	164	95.9	338	12	US-10-267-748-90	Sequence 90, Appl
88	164	95.9	344	14	US-10-040-349B-1	Sequence 1, Appl

89 164 95.9 345 9 US-09-779-451-8
90 164 95.9 345 14 US-10-026-741-49

ALIGNMENTS

Sequence 8, Appl1
Sequence 49, Appl1

RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 171; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 2
US-10-005-305-162
; Sequence 162, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-162

Query Match 95.9%; Score 164; DB 15; Length 35;
Best Local Similarity 97.1%; Pred. No. 1.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35

RESULT 3
US-10-005-305-163
; Sequence 163, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-163

Query Match 95.9%; Score 164; DB 15; Length 36;
Best Local Similarity 97.1%; Pred. No. 1.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db 2 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 36

RESULT 4
US-10-005-305-164
; Sequence 164, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-164

Query Match 95.9%; Score 164; DB 15; Length 37;
Best Local Similarity 97.1%; Pred. No. 1.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 35
Db 3 LRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 37

RESULT 5
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUPPLEMENTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 95.9%; Score 164; DB 9; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 6
US-09-779-451-2
; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 95.9%; Score 164; DB 9; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 7
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1

; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 95.9%; Score 164; DB 10; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 8
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 9
US-10-267-748-89

Sequence 89, Application US/10267748
Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.
Matthews, Thomas J.
Wild, Carl T.

Barney, Shawn O.
Lambert, Dennis M.
Peteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 10
US-09-809-060-6

Sequence 6, Application US/09809060
Publication No. US20020010317A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies against Fusion-Active

TITLE OF INVENTION: Regions of HIV Envelope Proteins

FILE REFERENCE: 1900.0260001

CURRENT APPLICATION NUMBER: US/09/809,060

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: US 60/189,981

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patent version 3.0

SEQ ID NO 6

LENGTH: 38

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-809-060-6

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 11
US-09-809-060-7

Sequence 7, Application US/09809060
Publication No. US20020010317A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies against Fusion-Active

TITLE OF INVENTION: Regions of HIV Envelope Proteins

FILE REFERENCE: 1900.0260001

CURRENT APPLICATION NUMBER: US/09/809,060

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: US 60/189,981

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patent version 3.0

SEQ ID NO 7

LENGTH: 38

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-809-060-7

Query Match 95.9%; Score 164; DB 12; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 12
US-10-663-589-3

Sequence 3, Application US/10663589
Publication No. US20040063637A1

GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
gp11-derived peptides, and its use in therapy

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FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIORITY APPLICATION NUMBER: US 60/414,441
PRIORITY FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match
Best Local Similarity 95.9%; Score 164; DB 12; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 38

RESULT 13
US-10-681-879-2
Sequence 2, Application US/10681879
Publication No. US20040062767A1
GENERAL INFORMATION:
APPLICANT: Olson, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/10/681,879
CURRENT FILING DATE: 2003-10-09
PRIORITY APPLICATION NUMBER: US/09/493,346
PRIORITY FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match
Best Local Similarity 95.9%; Score 164; DB 12; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 38

RESULT 14
US-09-828-615-2
Sequence 2, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
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ORGANISM: Homo sapiens
US-09-828-615-2

Query Match
Best Local Similarity 95.9%; Score 164; DB 12; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 38

RESULT 15
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US2003004441A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match
Best Local Similarity 95.9%; Score 164; DB 14; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 38

RESULT 16
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match
Best Local Similarity 95.9%; Score 164; DB 14; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGKIKQLQARIILAVERYLKQ 38

RESULT 17
```

US-10-414-192-1
; Sequence 1, Application US/10414192
; Publication No. US20030181382A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; Bolognesi, Daniel P.
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/414,192
; FILING DATE: 15-Apr-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1
Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 38
RESULT 18
US-10-351-641-16
; Sequence 16, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-16
Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 38
RESULT 19
US-10-351-641-507
; Sequence 507, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-507
Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 35
DB 4 LRAIEAQOHLQLTWGIKQLQARIILAVERYLKQ 38
RESULT 20
US-10-351-641-604
; Sequence 604, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641

;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 604
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35
DB 4 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 21
US-10-351-641-658

;; Sequence 658, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Amwer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 658
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-658

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35
DB 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35

RESULT 22

US-10-351-641-659
;; Sequence 659, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.

;; APPLICANT: Merutka, G.
;; APPLICANT: Amwer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 659
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-659

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35
DB 2 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 36

RESULT 23

US-10-351-641-660
;; Sequence 660, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthrie, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Amwer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 660
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-10-351-641-660

Query Match 95.9%; Score 164; DB 14; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 35
DB 3 LRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 24
US-10-005-305-165
; Sequence 165, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 25
US-10-005-305-202
; Sequence 202, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 26

US-10-005-305-203
; Sequence 203, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 1,5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 35
Db 4 LRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 27
US-10-420-194-1234
; Sequence 1234, Application US/10420194
; Publication No. US20040006035A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; APPLICANT: Biact, Larry
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
; TITLE OF INVENTION: Interactions
; FILE REFERENCE: MBH02-305-A (400/011)
; CURRENT APPLICATION NUMBER: US/10/420,194
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: PCT/US 03/05190
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/398,036
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/374,722
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1234
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1234

LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match 95.9%; Score 164; DB 15; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 28
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US20040076637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
TITLE OF INVENTION: Immunodeficiency Virus
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 95.9%; Score 164; DB 16; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 29
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: Peptides, and trimers formed therefrom
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized

US-10-671-316-2

Query Match 95.9%; Score 164; DB 16; Length 38;
Best Local Similarity 97.1%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 35
DB 4 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 30
US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-682-8

Query Match 95.9%; Score 164; DB 12; Length 41;
Best Local Similarity 97.1%; Pred. No. 1.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 35
DB 7 LRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 41

Wed Jun 2 13:47:12 2004

us-09-657-336a-181.rpb

Page 10

Search completed: June 2, 2004, 12:29:26
Job time : 33.2418 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 47.6033 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-542
Perfect score: 185
Sequence: 1 SNLRAIEAQHILQITWQIKQIQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jun04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	182	98.4	38 2 AAR98408	AAR98408 DP107 cor
2	182	98.4	38 2 AAB54785	AAB54785 HIV anti-HIV
3	182	98.4	38 4 AAB55005	AAB55005 Anti-HIV
4	182	98.4	38 4 AAB54970	AAB54970 Anti-HIV
5	182	98.4	38 4 AAB52244	AAB52244 Virus rel
6	182	98.4	38 4 AAB92244	AAB92244 Virus rel
7	182	98.4	38 5 AAB14011	AAB14011 DP107 pep
8	181	97.8	37 3 AAB14739	AAB14739 HIV-1 iso
9	181	97.8	37 4 AAB55004	AAB55004 Anti-HIV
10	178	96.2	866 3 AAY79020	AAY79020 HIV-1 env
11	177	95.7	37 3 AAB14705	AAB14705 HIV-1 iso
12	177	95.7	37 4 AAB54969	AAB54969 Anti-HIV
13	177	95.7	38 2 AAY22902	AAY22902 SEQ ID NO
14	177	95.7	198 2 AAY22905	AAY22905 SEQ ID NO
15	177	95.7	198 2 AAY22901	AAY22901 SEQ ID NO
16	177	95.7	198 5 AAB68372	AAB68372 Envelope
17	177	95.7	198 5 AAB68373	AAB68373 Envelope
18	177	95.7	198 5 AAB68376	AAB68376 Envelope
19	177	95.7	198 6 AAB57783	AAB57783 Human imm
20	177	95.7	198 6 AAB57780	AAB57780 Human imm
21	177	95.7	198 6 AAB57779	AAB57779 Human imm
22	177	95.7	268 5 AAY22843	AAY22843 SEQ ID NO
23	177	95.7	268 5 AAB68314	AAB68314 Envelope
24	177	95.7	268 6 AAB57721	AAB57721 Human imm
25	177	95.7	269 2 AAY22828	AAY22828 SEQ ID NO

26	177	95.7	269 2 AAY22900	AAY22900 SEQ ID NO
27	177	95.7	269 5 AAB68371	AAB68371 Consensus
28	177	95.7	269 5 AAB68299	AAB68299 Envelope
29	177	95.7	269 6 AAB57778	AAB57778 Human imm
30	177	95.7	269 6 AAB57706	AAB57706 Human imm
31	177	95.7	651 5 AAB68397	AAB68397 HIV ENV C
32	177	95.7	845 3 AAB69349	AAB69349 HIV-1 non
33	177	95.7	846 3 AAB69345	AAB69345 HIV-1 non
34	175	94.6	36 3 AAB14738	AAB14738 HIV-1 iso
35	175	94.6	36 3 AAB55003	AAB55003 Anti-HIV
36	175	94.6	38 2 AAB55635	AAB55635 DP-139 -
37	175	94.6	38 2 AAB55636	AAB55636 DP-140 -
38	175	94.6	38 2 AAB55637	AAB55637 DP-107 -
39	175	94.6	38 2 AAB55638	AAB55638 DP-107 -
40	175	94.6	38 2 AAB55639	AAB55639 DP-107 -
41	175	94.6	38 3 AAB55640	AAB55640 DP-107 -
42	175	94.6	38 3 AAB55641	AAB55641 DP-107 -
43	175	94.6	38 3 AAB55642	AAB55642 DP-107 -
44	175	94.6	38 3 AAB55643	AAB55643 DP-107 -
45	175	94.6	38 3 AAB55644	AAB55644 DP-107 -
46	175	94.6	38 3 AAB55645	AAB55645 DP-107 -
47	175	94.6	38 3 AAB55646	AAB55646 DP-107 -
48	175	94.6	38 3 AAB55647	AAB55647 DP-107 -
49	175	94.6	38 3 AAB55648	AAB55648 DP-107 -
50	175	94.6	38 3 AAB55649	AAB55649 DP-107 -
51	175	94.6	38 3 AAB55650	AAB55650 DP-107 -
52	175	94.6	38 3 AAB55651	AAB55651 DP-107 -
53	175	94.6	38 3 AAB55652	AAB55652 DP-107 -
54	175	94.6	38 3 AAB55653	AAB55653 DP-107 -
55	175	94.6	38 3 AAB55654	AAB55654 DP-107 -
56	175	94.6	38 3 AAB55655	AAB55655 DP-107 -
57	175	94.6	38 3 AAB55656	AAB55656 DP-107 -
58	175	94.6	38 3 AAB55657	AAB55657 DP-107 -
59	175	94.6	38 3 AAB55658	AAB55658 DP-107 -
60	175	94.6	38 3 AAB55659	AAB55659 DP-107 -
61	175	94.6	38 3 AAB55660	AAB55660 DP-107 -
62	175	94.6	38 3 AAB55661	AAB55661 DP-107 -
63	175	94.6	38 3 AAB55662	AAB55662 DP-107 -
64	175	94.6	38 3 AAB55663	AAB55663 DP-107 -
65	175	94.6	38 3 AAB55664	AAB55664 DP-107 -
66	175	94.6	38 3 AAB55665	AAB55665 DP-107 -
67	175	94.6	38 3 AAB55666	AAB55666 DP-107 -
68	175	94.6	38 3 AAB55667	AAB55667 DP-107 -
69	175	94.6	38 3 AAB55668	AAB55668 DP-107 -
70	175	94.6	38 3 AAB55669	AAB55669 DP-107 -
71	175	94.6	38 3 AAB55670	AAB55670 DP-107 -
72	175	94.6	38 3 AAB55671	AAB55671 DP-107 -
73	175	94.6	38 3 AAB55672	AAB55672 DP-107 -
74	175	94.6	38 3 AAB55673	AAB55673 DP-107 -
75	175	94.6	38 3 AAB55674	AAB55674 DP-107 -
76	175	94.6	38 3 AAB55675	AAB55675 DP-107 -
77	175	94.6	38 3 AAB55676	AAB55676 DP-107 -
78	175	94.6	38 3 AAB55677	AAB55677 DP-107 -
79	175	94.6	38 3 AAB55678	AAB55678 DP-107 -
80	175	94.6	38 3 AAB55679	AAB55679 DP-107 -
81	175	94.6	38 3 AAB55680	AAB55680 DP-107 -
82	175	94.6	38 3 AAB55681	AAB55681 DP-107 -
83	175	94.6	38 3 AAB55682	AAB55682 DP-107 -
84	175	94.6	38 3 AAB55683	AAB55683 DP-107 -
85	175	94.6	38 3 AAB55684	AAB55684 DP-107 -
86	175	94.6	38 3 AAB55685	AAB55685 DP-107 -
87	175	94.6	38 3 AAB55686	AAB55686 DP-107 -
88	175	94.6	38 3 AAB55687	AAB55687 DP-107 -
89	175	94.6	38 3 AAB55688	AAB55688 DP-107 -
90	175	94.6	38 3 AAB55689	AAB55689 DP-107 -

ALIGNMENTS

RESULT 1
AAR98408
AAR98408 standard; peptide; 38 AA.

XX AC AAR98408;
 XX PN 16-OCT-2003 (revised)
 XX DT 17-FEB-1997 (first entry)
 XX DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.
 XX Anti-fusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM Influenza virus; hepatitis B virus.
 XX OS Human immunodeficiency virus 1.
 XX PN WO9619495-A1.
 XX PD 27-JUN-1996.
 XX PF 20-DEC-1995; 95WO-US016733.
 XX PR 20-DEC-1994; 94US-00360107.
 XX PR 06-JUN-1995; 95US-00470896.
 XX PA (TUDU-) UNIV DUKE.
 XX PA (TRIM-) TRIMERIS INC.
 XX PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
 XX PI Petteway SR, Langlois AJ;
 XX DR WPI; 1996-309517/31.
 XX PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 XX PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence
 XX PT search motif.
 XX PS Disclosure; Page 30; 471pp; English.
 XX CC The sequences given in AAR98398-408 represent peptides which exhibit
 XX CC anti-fusogenic activity, antiviral capability and/or the ability to
 XX CC modulate intracellular processes involving coiled-coil peptide
 XX CC structures. These peptides are recognised by the ALLMOT15, 107x178x4 and
 XX CC PLZIP search motifs. These peptides may be used to inhibit the
 XX CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 XX CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 38 AA;
 XX
 XX Query Match 98.4%; Score 182; DB 2; Length 38;
 XX Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 XX Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNLLRAIEAOQHLLQTLTWQIKQLQARILAVERYLKQD 38
 Db 1 NNLLRAIEAOQHLLQTLTWQIKQLQARILAVERYLKQD 38
 XX
 XX RESULT 2
 XX ID AAB54785
 XX AC AAB54785;
 XX DT 11-SEP-2003 (revised)
 XX DT 05-MAR-2001 (first entry)
 XX DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.
 XX KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 XX KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
 XX KM simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
 XX KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX OS Human immunodeficiency virus 1.

XX XX WO200069902-A1.
 XX XX 23-NOV-2000.
 XX XX 17-MAY-2000; 2000WO-US013651.
 XX XX 17-MAY-1999; 99US-0134406P.
 XX PR 10-SEP-1999; 99US-0153406P.
 XX PA (CONU-) CONJUCHEM INC.
 XX PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX DR WPI; 2001-007496/01.
 XX PT A modified peptide and a reactive group which is reactive with amino
 XX PT groups, hydroxyl groups, or thiol groups on blood components to form
 XX PT stable covalent bonds useful for treatment of viral infections, e.g.
 XX PT human immunodeficiency virus.
 XX PS Claim 6; Page 173; 211pp; English.
 XX CC The present invention describes a modified anti-viral peptide (I)
 XX CC comprising a peptide that exhibits anti-viral activity and a reactive
 XX CC group which is reactive with amino groups, hydroxyl groups, or thiol
 XX CC groups on blood components to form stable covalent bonds. (I) has anti-
 XX CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 XX CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 XX CC the level of membrane fusion events between two or more entities, e.g.,
 XX CC virus-cell or cell-cell, relative to the level of membrane fusion that
 XX CC occurs in the absence of the peptide. (I) is useful in the treatment of
 XX CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 XX CC MeV, and SIV. (I) may be administered prophylactically to previously
 XX CC uninfected individuals. This is useful in cases where an individual has
 XX CC been subjected to a high risk of exposure to a virus. By bonding of long-
 XX CC lived components of the blood, such as immunoglobulin, serum albumin, red
 XX CC blood cells and platelets the activity is extended for days to weeks.
 XX CC This is due to improved stability in vivo and a reduced susceptibility to
 XX CC peptidase or protease degradation. This minimises the need for more
 XX CC frequent, or even continual, administration of the peptides. AAB54784 to
 XX CC AAB5531 represent peptides used in the exemplification of the present
 XX CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 38 AA;
 XX
 XX Query Match 98.4%; Score 182; DB 4; Length 38;
 XX Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 XX Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNLLRAIEAOQHLLQTLTWQIKQLQARILAVERYLKQD 38
 Db 1 NNLLRAIEAOQHLLQTLTWQIKQLQARILAVERYLKQD 38
 XX
 XX RESULT 3
 XX ID AAB55005
 XX AC AAB55005;
 XX DT 11-SEP-2003 (revised)
 XX DT 05-MAR-2001 (first entry)
 XX DE Anti-HIV peptide DP107 amino truncation peptide #35.
 XX KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 XX KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
 XX KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 XX KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX OS Human immunodeficiency virus 1.

PN WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX Disclosure; Page 139; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MEV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX AAB55431 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 38 AA;
SQ
Query Match 98.4%; Score 182; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NMLLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
RESULT 4
AAB54970
ID AAB54970 standard; peptide; 38 AA.
XX
XX AAB54970;
XX
XX 11-SEP-2003 (revised)
XX 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #35.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX anti-fusogenic; mobile blood component; measles virus; MEV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200069902-A1.
XX
XX

XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX Disclosure; Page 137; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MEV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX AAB55431 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 38 AA;
SQ
Query Match 98.4%; Score 182; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NMLLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
RESULT 5
AAB92244
ID AAB92244 standard; peptide; 38 AA.
XX
XX AAB92244;
XX
XX 22-JUN-2001 (first entry)
XX
XX Virus related peptide SEQ ID NO:1420.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidy; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX

XX	PF	17-MAY-2000; 2000MO-USO13576.
XX	PR	17-MAY-1999; 99US-0134406P.
XX	PR	10-SEP-1999; 99US-0153406P.
XX	PR	15-OCT-1999; 99US-0159783P.
XX	PA	(CONJ-) CONJUCHEM INC.
XX	PI	Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudau K;
XX	DR	WPI; 2001-112059/12..
XX	PT	Modifying and attaching therapeutic peptides to albumin prevents
XX	PT	peptidase degradation, useful for increasing length of in vivo activity.
XX	PS	Disclosure; Page 662; 73pp; English.
XX	CC	The present invention describes a modified therapeutic peptide (I)
XX	CC	comprising a therapeutically active amino acid region (III) and a
XX	CC	reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
XX	CC	a less therapeutically active amino acid region (IV), which covalently
XX	CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
XX	CC	peptide stabilised therapeutic peptide composed of 3-50 amino acids.
XX	CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX	CC	factors and neurotransmitters, to protect them from peptidase activity in
XX	CC	vivo for the treatment of various disorders. Endogenous therapeutic
XX	CC	peptides are not suitable as drug candidates as they require frequent
XX	CC	administration due to rapid degradation by peptidases in the body.
XX	CC	Modifying and attaching therapeutic peptides to albumin prevents or
XX	CC	reduces the action of peptidases to increase length of activity (half
XX	CC	life) and specifically as bonding to large molecules decreases
XX	CC	intracellular uptake and interference with physiological processes.
XX	CC	AAB90829 to AAB92441 represent peptides which can be used in the
XX	CC	exemplification of the present invention
XX	SQ	Sequence 38 AA:
OY	Query Match	98.4%; Score 182; DB 4; Length 38;
D8	Best Local Similarity	97.4%; Pred. No. 1,7e-16;
	Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0,	
OY	1 SNLRRAEAQQHLLQLTWQIKQKOLARILAVRYLKDQ 38	
	:	
D8	1 NNLRRAEAQQHLLQLTWQIKQKOLARILAVRYLKDQ 38	
RESULT 6		
ID	AAU14011 standard; peptide; 38 AA.	
XX	AC	AAU14011;
XX	DT	11-SEP-2003 (revised)
XX	DT	21-NOV-2001 (first entry)
DE	DP107 peptide from HIV-1 transmembrane protein gp41.	
XX	KW	Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX	KW	antifusogenic; antiviral; HIV transmission.
XX	OS	Human immunodeficiency virus 1; isolate LAI.
XX	Key	Location/Qualifiers
FT	Misc-difference 1..35	/note= "Amino acids 1-35 can be optionally and serially
FT	deleted from the N-terminus"	deleted from the N-terminus"
FT	Misc-difference 4..38	/note= "Amino acids 4-38 can be optionally and serially
FT	deleted from the C-terminus"	deleted from the C-terminus"
XX	WO200151673-A2.	

PD		19-JUL-2001.	
XX			
PF	05-JUL-2000;	2000OWO-US035727.	
XX			
PR	09-JUL-1999;	99US-00350841.	
XX			
PA	(TRIM-) TRIMERIS INC.		
XX			
PI	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;		
DR	WPI; 2001-442157/47.		
XX			
PT	Identifying a compound that inhibits the formation of or disrupts a		
XX	Dp107/Dp178 complex, especially compounds with antifeedant, antiviral		
PT	or intracellular modulatory activity, by detecting the formation of a		
XX	Dp107/Dp178 complex.		
XX			
PS	Disclosure; Page 33; 259pp; English.		
XX			
CC	The present invention relates to peptides which exhibit anti-retroviral		
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise		
CC	Dp178-like and Dp107-like peptides. The Dp178 peptide corresponds to		
CC	amino acids 639-673 of the transmembrane protein gp41 from human		
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The Dp107 peptide		
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention		
CC	also relates to a method of identifying compounds that inhibit the		
CC	formation of or disrupts a Dp107/Dp178 complex. The method comprises		
CC	detecting the formation of a Dp107/Dp178 complex, both in the presence or		
CC	absence of a test compound, in a reaction mixture containing Dp107 and		
CC	Dp178 peptides. The method is useful for identifying compounds, including		
CC	small molecule compounds, which may themselves exhibit antifusogenic,		
CC	antiviral or intracellular modulatory activity. The Dp178-like/Dp107-like		
CC	peptides are useful to inhibit human and non-human retroviral,		
CC	particularly HIV, transmission to uninfected cells. The present sequence		
CC	represents the Dp107 peptide. (Updated on 11-SEP-2003 to standardise OS		
CC	field)		
XX			
SQ	Sequence 38 AA;		
	Query Match	98.4%; Score 182; DB 4; Length 38;	
	Best Local Similarity	97.4%; Pred. No. 1.7e-16;	
	Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
CY	1 SNTLRATEAOCHLTQLTWVQKCOLQARPLAVERYLKDQ 38		
	:		
DB	1 NNLLRAIEAQGHLLQLTWVQIKQLQARLAVERYLKDQ 38		
RESULT 7			
AA018771	AA018771 standard; peptide; 38 AA.		
AC	AA018771;		
DT	29-OCT-2002 (first entry)		
DE	HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.		
KW	Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;		
OS	gp41.		
PN	Human immunodeficiency virus.		
PD	WO200256902-A2.		
PF	25-JUL-2002.		
PR	17-DEC-2001; 2001WO-US048802.		
RR	19-DEC-2000; 2000US-0256657P.		
SCHE	(SCHE) SCHERING CORP.		

PI Baroudy BM;
 XX
 DR WPI; 2002-636513/68.
 XX
 PT Treatment of HIV infection in an individual involves administration of a
 PT combination of chemokine co-receptor five antagonist and a specified HIV
 PT envelope polypeptide.
 XX
 PS Disclosure; Page 34; 52pp; English.
 XX
 CC The present invention relates to a method of treating an HIV infection in
 CC an individual, which involves administering in combination a chemokine co-
 CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
 CC derivative. Other viral infections can also be treated using the method.
 CC The present sequence is a peptide derived from HIV and useful in the
 CC method of the invention
 XX
 SQ Sequence 38 AA;
 Query Match 98.4%; Score 182; DB 5; Length 38;
 Best Local Similarity 97.4%; Pred. No. 1,7e-16;
 Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNLRATIAEQOHLLQLTWMOIKQLQARILAVERYLKQ 38
 1 NNLRAITAEAOQHLLQLTWMOIKQLQARILAVERYLKQ 38
 Db
 RESULT 8
 AAB14739 AAB14739 standard; peptide; 37 AA.
 XX
 AC AAB14739;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 PI WILD CT, Weiss CD;
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Disclosure; Page 38; 97pp; English.
 XX
 CC Sequences AAB1472-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralising antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)

CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 37 AA;
 Query Match 97.8%; Score 181; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLRATIAEQOHLLQLTWMOIKQLQARILAVERYLKQ 38
 1 NLRATIAEQOHLLQLTWMOIKQLQARILAVERYLKQ 37
 Db
 RESULT 9
 AAB55004 AAB55004 standard; peptide; 37 AA.
 XX
 AC AAB55004;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #34.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONU-) CONUICHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 DR WPI; 2001-007496/01.
 XX
 CC A modified peptide and a reactive group which is reactive with amino
 CC groups, hydroxyl groups, or thiol groups on blood components to form
 CC stable covalent bonds useful for treatment of viral infections, e.g.
 CC human immunodeficiency virus.

XX Disclosure; Page 139; 211pp; English.
PS
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 37 AA;
Query Match 97.8%; Score 181; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,2e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 37
RESULT 10
AAY79020
ID AAY79020 standard; protein; 866 AA.
XX
AC AAY79020;
XX
DT 12-SEP-2003 (revised)
DT 05-JUN-2000 (first entry)
XX
DE HIV-1 envelope protein amino acid sequence.
XX
KM HIV-1; envelope protein; env; cross reactive anti-serum; antibody;
KM vaccine; antibody; detect.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200007631-A1.
XX
PD 17-FEB-2000.
XX
PF 04-AUG-1999; 99WO-US017596.
XX
PR 04-AUG-1998; 98US-0095267P.
XX
PA (JACK-) JACKSON FOUND HENRY M.
XX
PI Quinan GV, Zhang PF;
XX
PI WPI; 2000-205578/18.
XX
XX Human immunodeficiency virus-1 envelope protein, useful as a vaccine or
PT immunogenic preparation against HIV-1 infection induces the production of
PT broadly cross-reactive neutralizing anti-serum.
XX
PS Claim 2; Page 33; 54pp; English.
XX This sequence represents a human immunodeficiency virus type 1 (HIV-1)
CC envelope (env) protein amino acid sequence. The invention relates to the

CC HIV-1 env protein or its fragments, which when administered to a mammal,
CC induces the production of broadly cross-reactive neutralizing anti-serum
CC against multiple strains of HIV-1. The HIV-1 env protein and its
CC fragments are useful as vaccines, immunogenic compositions or diagnostic
CC reagents. They can also be used to detect anti-HIV-1/HIV-1 neutralizing
CC antibodies in a sample. The amino acid sequence and its fragments or mRNA
CC sequence are useful for generating antibodies in a mammal. In addition, a
CC recombinant delivery vector containing the env amino acid sequence may
CC also be used as a vaccine. (Updated on 12-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 866 AA;
Query Match 96.2%; Score 178; DB 3; Length 866;
Best Local Similarity 97.4%; Pred. No. 1.6e-14;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 562 SNLRRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 599
RESULT 11
AAB14705
ID AAB14705 standard; peptide; 37 AA.
XX
AC AAB14705;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
XX
OS Human immunodeficiency virus 1.
XX
PN WO2000040616-A1.
XX
PD 13-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US000456.
XX
PR 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
PA (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
PI WILD CT, Weiss CD;
XX
PI WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX
PS Disclosure; Page 36; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralizing antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-

CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)

SQ Sequence 37 AA;

Query Match 95.7%; Score 177; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. No. 7.2e-16;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARIILAVERYLKD 37
:|||||
Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARIILAVERYLKD 37

RESULT 12

AAB54969 standard; peptide; 37 AA.

AAB54969;

DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 carboxy truncation peptide #34.

KW Long laeeting fusion peptide inhibitor; viral infection; antiviral;
KW antitumorogenic; mobile blood component; measles virus; MeV; SIV;
KW simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.

PN WO200069902-A1.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013651.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

(CONT-) CONJUCHEM INC.

PI Bridon DE, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

PS Disclosure; Page 137; 21pp; English.

CC The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol

CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPiV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB54783 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 37 AA;

Query Match 95.7%; Score 177; DB 4; Length 37;
Best Local Similarity 97.3%; Pred. No. 7.2e-16;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARIILAVERYLKD 37
:|||||
Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARIILAVERYLKD 37

RESULT 13

AAV22902 standard; protein; 198 AA.

AAV22902;

DT 19-AUG-1999 (first entry)

DE SEQ ID NO. 98 from WO9820036.

KW HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
KW antibody; viral membrane fusion; viral infectivity;
KW ligand affinity purification; protein A replacement;
KW immunoglobulin purification; epitope mimic.

OS Human immunodeficiency virus.

PN WO9820036-A1.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US020069.

PR 06-NOV-1996; 96US-00743698.

PR 16-JUN-1997; 97US-00876698.

(GENTH) GENENTECH INC.

PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA,

PI Wells JA;

WPI; 1998-28686/25.

PT Production of constrained helical peptide(s) by linking side chains on
PT termini of octapeptide - derived from human immunodeficiency virus gp41
PT protein, useful in vaccines for treatment and prevention of infection.
XX Claim 11, Page 226; 279pp; English.

CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins of
CC known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and
CC AAV22903 represent consensus sequences of various sections of the gp41
CC protein). Sequences derived from the peptides are used to produce

CC constrained helical peptides of the invention. The constrained helical
CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds. The
CC constrained helical peptides are used to treat or prevent HIV infection,
CC especially as vaccines that generate antibodies that prevent viral
CC membrane fusion or infectivity. Vaccines may contain constrained helical
CC peptides derived from several different strains of HIV. The antibodies
CC are also useful for diagnosing HIV infection. Other uses for the
CC constrained helical peptides are in affinity purification of ligands
CC (particularly where complete binding protein is not readily available,
CC e.g. replacements for protein A in immunoglobulin purification); as
CC epitope mimics for antibody production; for isolation of synthetic
CC antibody clones from phage display libraries, or as stable forms of
CC "floppy" peptides or proteins

XX
SQ Sequence 198 AA;

Query Match 95.7%; Score 177; DB 2; Length 198;
Best Local Similarity 94.7%; Pred. No. 4,4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 120

RESULT 14
AAV22905
ID AAV22905 standard; protein: 198 AA.
XX
AC AAV22905;
XX
DT 19-AUG-1999 (first entry)
XX
DE SEQ ID NO. 101 from W09820036.
XX
KM HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
XX antibody; viral membrane fusion; viral infectivity;
XX ligand affinity purification; protein A replacement;
XX immunoglobulin purification; epitope mimic.
XX
OS Human immunodeficiency virus.
XX
PN W09820036-A1.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020069.
XX
PR 06-NOV-1996; 96US-00743698.
XX 16-JUN-1997; 97US-00876698.
XX
PA (GETH) GENENTECH INC.
XX
PI Braisted A, Judice JK, McDowell RS, Pheelan JC, Starovaenik MA;
PI Wells JA;
XX
DR WPI; 1998-286866/25.
XX
PT Production of constrained helical peptide(s) by linking side chains on
PT termini of octapeptide - derived from human immunodeficiency virus gp41
PT protein, useful in vaccines for treatment and prevention of infection.
XX
PS Claim 11; Page 228-229; 279pp; English.

XX
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus
XX (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins of
XX known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and
XX AAV22903 represent consensus sequences of various sections of the gp41
XX protein). Sequences derived from the peptides are used to produce
XX constrained helical peptides of the invention. The constrained helical

CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds. The
CC constrained helical peptides are used to treat or prevent HIV infection,
CC especially as vaccines that generate antibodies that prevent viral
CC membrane fusion or infectivity. Vaccines may contain constrained helical
CC peptides derived from several different strains of HIV. The antibodies
CC are also useful for diagnosing HIV infection. Other uses for the
CC constrained helical peptides are in affinity purification of ligands
CC (particularly where complete binding protein is not readily available,
CC e.g. replacements for protein A in immunoglobulin purification); as
CC epitope mimics for antibody production; for isolation of synthetic
CC antibody clones from phage display libraries, or as stable forms of
CC "floppy" peptides or proteins

XX
SQ Sequence 198 AA;

Query Match 95.7%; Score 177; DB 2; Length 198;
Best Local Similarity 94.7%; Pred. No. 4,4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 120

RESULT 15
AAV22901
ID AAV22901 standard; protein: 198 AA.
XX
AC AAV22901;
XX
DT 19-AUG-1999 (first entry)
XX
DE SEQ ID NO. 97 from W09820036.
XX
KM HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
XX antibody; viral membrane fusion; viral infectivity;
XX ligand affinity purification; protein A replacement;
XX immunoglobulin purification; epitope mimic.
XX
OS Human immunodeficiency virus.
XX
PN W09820036-A1.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020069.
XX
PR 06-NOV-1996; 96US-00743698.
XX 16-JUN-1997; 97US-00876698.
XX
PA (GETH) GENENTECH INC.
XX
PI Braisted A, Judice JK, McDowell RS, Pheelan JC, Starovaenik MA;
PI Wells JA;
XX
DR WPI; 1998-286866/25.
XX
PT Production of constrained helical peptide(s) by linking side chains on
PT termini of octapeptide - derived from human immunodeficiency virus gp41
PT protein, useful in vaccines for treatment and prevention of infection.
XX
PS Claim 11; Page 225-226; 279pp; English.

XX
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus
XX (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins of
XX known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and
XX AAV22903 represent consensus sequences of various sections of the gp41
XX protein). Sequences derived from the peptides are used to produce
XX constrained helical peptides of the invention. The constrained helical
XX peptide is produced by synthesizing an octapeptide in which both terminal

CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds. The
CC constrained helical peptides are used to treat or prevent HIV infection,
CC especially as vaccines that generate antibodies that prevent viral
CC membrane fusion or infectivity. Vaccines may contain constrained helical
CC peptides derived from several different strains of HIV. The antibodies
CC are also useful for diagnosing HIV infection. Other uses for the
CC constrained helical peptides are in affinity purification of ligands
CC (particularly where complete binding protein is not readily available,
CC e.g. replacements for protein A in immunoglobulin purification), as
CC epitope mimics for antibody production, for isolation of synthetic
CC antibody clones from phage display libraries, or as stable forms of
CC "floppy" peptides or proteins
XX
SQ Sequence 198 AA;
Query Match 95.7%; Score 177; DB 2; Length 198;
Best Local Similarity 94.7%; Pred. No. 4.4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 83 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 120
RESULT 16
ABG68372
ID ABG68372 standard; protein; 198 AA.
AC ABG68372;
XX
DT 29-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX
DE Envelope protein gp41 from HIV clade E strain #1.
XX
KM HIV; glycoprotein; gp41; antigen; helical conformation;
KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
KM viral envelope protein; vaccine; virucide; anti-HIV.
XX
OS Human immunodeficiency virus 1; clade E.
XX
PN US6271198-B1.
XX
PD 07-AUG-2001.
XX
PF 05-NOV-1997; 97US-00965056.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
XX
PA (GETH) GENENTECH INC.
XX
PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2002-487624/52.
XX
PT New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have alpha-
PT helical conformation.
XX
PS Disclosure; Col 257-258; 175pp; English.
XX
XX The invention relates to cyclic peptides (A) with a constrained helical
XX conformation, derived from gp41 (glycoprotein 41, a viral envelope
XX protein) protein of human immunodeficiency virus (HIV). The cyclic
XX peptides have formulas given in the specification part of which are
XX derived from a consensus sequence of gp41 derived from HIV clades A, B,
XX C, D, E or O. The peptides are used to cause induction of a specific
XX immune response, resulting in antibodies that prevent virus-induced

CC membrane fusion. The peptides are used to treat subjects with, or at risk
CC of, HIV infection, either as antifuison/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular HIV
CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
CC 2003 to standardise OS field)
XX
SQ Sequence 198 AA;
Query Match 95.7%; Score 177; DB 5; Length 198;
Best Local Similarity 94.7%; Pred. No. 4.4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 83 SNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 120
RESULT 17
ABG68373
ID ABG68373 standard; protein; 198 AA.
AC ABG68373;
XX
DT 29-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX
DE Envelope protein gp41 from HIV clade E strain #2.
XX
KM HIV; glycoprotein; gp41; antigen; helical conformation;
KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
KM viral envelope protein; vaccine; virucide; anti-HIV.
XX
OS Human immunodeficiency virus 1; clade E.
XX
PN US6271198-B1.
XX
PD 07-AUG-2001.
XX
PF 05-NOV-1997; 97US-00965056.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
XX
PA (GETH) GENENTECH INC.
XX
PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2002-487624/52.
XX
PT New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have alpha-
PT helical conformation.
XX
PS Disclosure; Col 257-260; 175pp; English.
XX
XX The invention relates to cyclic peptides (A) with a constrained helical
XX conformation, derived from gp41 (glycoprotein 41, a viral envelope
XX protein) protein of human immunodeficiency virus (HIV). The cyclic
XX peptides have formulas given in the specification part of which are
XX derived from a consensus sequence of gp41 derived from HIV clades A, B,
XX C, D, E or O. The peptides are used to cause induction of a specific
XX immune response, resulting in antibodies that prevent virus-induced
XX membrane fusion. The peptides are used to treat subjects with, or at risk
XX of, HIV infection, either as antifuison/anti-infection agents or,

CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular HIV
CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX Sequence 198 AA:

Query Match 95.7%; Score 177; DB 5; Length 198;
Best Local Similarity 94.7%; Pred. No. 4.4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARVLAVERYLKDQ 120

RESULT 18

ABG68376 standard; protein; 198 AA.

XX ABG68376;

XX 29-AUG-2003 (revised)

DT 07-OCT-2002 (first entry)

DE Envelope protein gp41 from HIV clade E strain #5.

XX HIV; glycoprotein; gp41; antigen; helical conformation;

KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;

KM viral envelope protein; vaccine; virucide; anti-HIV.

XX Human immunodeficiency virus 1; clade E.

OS US6271198-B1.

XX 07-AUG-2001.

XX 05-NOV-1997; 97US-00865056.

XX 06-NOV-1996; 96US-00743698.

PR 16-JUN-1997; 97US-0049787P.

PR 16-JUN-1997; 97US-00876698.

XX (GERTH) GENENTECH INC.

XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;

PI Wells JA;

DR WPI; 2002-487624/52.

XX New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have alpha-
PT helical conformation.

PS Disclosure; Col 261-264; 175pp; English.

XX The invention relates to cyclic peptides (A) with a constrained helical
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
CC protein) of human immunodeficiency virus (HIV). The cyclic
CC peptides have formulas given in the specification part of which are
CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
CC C, D, E or O. The peptides are used to cause induction of a specific
CC immune response, resulting in antibodies that prevent virus-induced
CC membrane fusion. The peptides are used to treat subjects with, or at risk
CC of, HIV infection, either as antifusion/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or

CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular HIV
CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX Sequence 198 AA:

Query Match 95.7%; Score 177; DB 5; Length 198;
Best Local Similarity 94.7%; Pred. No. 4.4e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARVLAVERYLKDQ 120

RESULT 19

ABU57783 standard; protein; 198 AA.

XX ABU57783;

XX 10-APR-2003 (first entry)

DE Human immunodeficiency virus (HIV) envelope protein gp41 #92.

XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;

KM viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;

KM envelope protein.

XX Human immunodeficiency virus.

OS US2002151473-A1.

XX 17-OCT-2002.

XX 15-MAY-2001; 2001US-00854816.

XX 06-NOV-1996; 96US-00743698.

PR 16-JUN-1997; 97US-0049787P.

PR 16-JUN-1997; 97US-00876698.

PR 05-NOV-1997; 97US-00865056.

XX (BRAI/) BRAISTED A C.

PA (JUDI/) JUDICE J K.

PA (MCDO/) MCDOWELL R S.

PA (PHEL/) PHELAN J C.

PA (STAR/) STAROVASNIK M A.

PA (WELL/) WELLS J A.

XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;

PI Wells JA;

DR WPI; 2003-182525/18.

XX Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.

PS Disclosure; Fig 16; 180pp; English.

XX The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as happens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that

CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinant in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41, fragments of which are used in the creation of
CC locked helix peptides
XX
SQ Sequence 198 AA;

Query Match 95.7%; Score 177; DB 6; Length 198;
Best Local Similarity 94.7%; Pred. No. 4,4e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 120

RESULT 20
ABU57780
XX ABU57780 standard; protein; 198 AA.
XX
AC ABU57780;
XX
DT 10-APR-2003 (first entry)
XX
DE Human immunodeficiency virus (HIV) envelope protein gp41 #89.
XX
XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KM viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KM envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A. C.
PA (JUDI/) JUDICE J. K.
PA (MCDO/) MCDOWELL R. S.
PA (PHEL/) PHELAN J. C.
PA (STAR/) STAROVASNIK M. A.
PA (WELL/) WELLS J. A.
PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
XX MPI; 2003-182525/18.
XX
XX Novel constrained helical peptide compound useful for prophylactically or
XX therapeutically treating mammal at risk for or infected with human
XX immunodeficiency virus.
XX
XX Disclosure; Fig 16; 180pp; English.
XX
PS

XX The invention describes a constrained helical peptide compound (1)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.a.s) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.a.s, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (1) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinant in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41, fragments of which are used in the creation of
CC locked helix peptides
XX
SQ Sequence 198 AA;

Query Match 95.7%; Score 177; DB 6; Length 198;
Best Local Similarity 94.7%; Pred. No. 4,4e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 120

RESULT 21
ABU57779
XX ABU57779 standard; protein; 198 AA.
XX
AC ABU57779;
XX
DT 10-APR-2003 (first entry)
XX
DE Human immunodeficiency virus (HIV) envelope protein gp41 #88.
XX
XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KM viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KM envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A. C.
PA (JUDI/) JUDICE J. K.
PA (MCDO/) MCDOWELL R. S.
PA (PHEL/) PHELAN J. C.
PA (STAR/) STAROVASNIK M. A.
PA (WELL/) WELLS J. A.
PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
XX MPI; 2003-182525/18.
XX
XX Novel constrained helical peptide compound useful for prophylactically or
XX therapeutically treating mammal at risk for or infected with human
XX immunodeficiency virus.
XX
XX Disclosure; Fig 16; 180pp; English.
XX
PS

PI Wells JA;
 XX WPI; 2003-182525/18.
 XX
 PT Novel constrained helical peptide compound useful for prophylactically or
 PT therapeutically treating mammal at risk for or infected with human
 PT immunodeficiency virus.
 PS Disclosure; Fig 16; 180pp; English.
 XX
 CC The invention describes a constrained helical peptide compound (I)
 CC comprising a first constrained helical peptide comprising a sequence of 8
 CC amino acids (a.as) having a first and second terminal residue both
 CC flanking an internal sequence of 6 a.as, where the terminal residues have
 CC a side chain that are linked to each other forming a locking group to
 CC form a constrained helical peptide. (I) is useful for preparing
 CC antibodies that prevent viral membrane fusion, as hapten, preferably
 CC attached to a carrier, for use as an immunogen to raise antibodies that
 CC have a diagnostic use, as a vaccine for treatment of patients at risk of
 CC or infected with HIV, to create combinatorial constrained helical peptide
 CC libraries that are useful in chemical selection systems, to isolate the
 CC binding determinants from alpha-helical binding domains of known
 CC proteins, for determining whether a binding determinate in an alpha-
 CC helical binding domain of a known protein can serve as a structural model
 CC for the design of peptidomimetics, to replace intact binding proteins or
 CC protein binding domains in the affinity purification of ligands, to mimic
 CC epitopes in proteins to selectively raise polyclonal or monoclonal
 CC antibodies against such individual epitopes for isolating synthetic
 CC antibody clones with a selected binding activity from phage display
 CC combinatorial libraries, to provide conformationally stable variants of
 CC peptides or proteins which exhibit floppy or unstable alpha-helical
 CC secondary structure at one or more sites in unrestrained form under
 CC conditions of interest. This is the amino acid sequence of an HIV
 CC envelope protein gp41, fragments of which are used in the creation of
 CC locked helix peptides
 XX
 SQ Sequence 198 AA;
 Query Match 95.7%; Score 177; DB 6; Length 198;
 Best Local Similarity 94.7%; Pred. No. 4.4e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SNLRRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 83 SNLRRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 120
 RESULT 22
 AAY22843
 ID AAY22843 standard; protein; 268 AA.
 XX
 AC AAY22843;
 XX
 DT 19-AUG-1999 (first entry)
 XX
 DE SEQ ID NO. 39 from WO9820036.
 XX
 KW HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KW antibody; viral membrane fusion; viral infectivity;
 KW ligand affinity purification; protein A replacement;
 KW immunoglobulin purification; epitope mimic.
 OS Human immunodeficiency virus.
 XX
 PN WO9820036-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 05-NOV-1997; 97WO-US020069.
 XX
 PR 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-00876698.
 XX

PA (GETH) GENENTECH INC.
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX WPI; 1998-286866/25.
 DR
 XX
 PT Production of constrained helical peptide(s) by linking side chains on
 PT termini of octa-peptide - derived from human immunodeficiency virus gp41
 PT protein, useful in vaccines for treatment and prevention of infection.
 PS Claim 11; Page 180-181; 279pp; English.
 XX
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
 CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification), as
 CC epitope mimics for antibody production, for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 XX
 SQ Sequence 268 AA;
 Query Match 95.7%; Score 177; DB 2; Length 268;
 Best Local Similarity 94.7%; Pred. No. 6e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SNLRRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 83 SNLRRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 120
 RESULT 23
 ABG68314
 ID ABG68314 standard; protein; 268 AA.
 XX
 AC ABG68314;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Envelope protein gp41 from HIV clade B strain #33.
 XX
 KW HIV; glycoprotein; gp41; antigen; helical conformation;
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
 KW viral envelope protein; vaccine; virucide; anti-HIV.
 OS Human immunodeficiency virus 1; clade B.
 XX
 PN US6271198-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 05-NOV-1997; 97US-00965056.
 XX
 PR 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-0049787P.
 PR 16-JUN-1997; 97US-00876698.
 XX

PA (GETH) GENENTECH INC.
 XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX WPI; 2002-487624/52.
 DR
 PT New cyclic peptides from human immune deficiency virus gp41, useful for
 PT treatment or prevention of HIV infection, are constrained to have alpha-
 PT helical conformation.
 XX
 PS Disclosure; Col 189-192; 175pp; English.
 XX
 CC The invention relates to cyclic peptides (A) with a constrained helical
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
 CC protein) of human immunodeficiency virus (HIV). The cyclic
 CC peptides have formulae given in the specification part of which are
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
 CC C, D, E or O. The peptides are used to cause induction of a specific
 CC immune response, resulting in antibodies that prevent virus-induced
 CC membrane fusion. The peptides are used to treat subjects with, or at risk
 CC of, HIV infection, either as anti-fusion/anti-infection agents or,
 CC preferably where associated with a carrier, as an immunogen (including as
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
 CC cases of health care accidents. The peptides can be based on specific HIV
 CC strains, e.g. breakthrough isolates of HIV that have developed during
 CC vaccine trials, so a combination of them should cover a wide range of
 CC protection. The present sequence is gp41 protein from a particular HIV
 CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 268 AA:
 QY
 Db 1 SNLLRAIEAQOHLLQLTWGIKQLQARVLAVERYLKQD 38
 83 SNLLRAIEAQOHLLQLTWGIKQLQARVLAVERYLKQD 120
 Query Match 95.7%; Score 177; DB 5; Length 268;
 Best Local Similarity 94.7%; Pred. No. 6e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 24
 ABUS7721
 ID ABUS7721 standard; protein; 268 AA.
 XX
 AC ABUS7721;
 DT 10-APR-2003 (first entry)
 XX
 DE Human immunodeficiency virus (HIV) envelope protein gp41 #33.
 XX
 KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
 KM viral membrane fusion; hapten; immunogen; pepidomimetic; gp41;
 KM envelope protein.
 XX
 OS Human immunodeficiency virus.
 PN US2002151473-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 15-MAY-2001; 2001US-00854816.
 XX
 PR 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-0049787P.
 PR 16-JUN-1997; 97US-00876698.
 PR 05-NOV-1997; 97US-00965056.
 XX
 XX (BRAI/) BRAISTED A C.
 PA (JUDI/) JUDICE J K.

PA (MCDO/) MCDOWELL R S.
 PA (PHEL/) PHELAN J C.
 PA (STAR/) STAROVASNIK M A.
 PA (WELL/) WELLS J A.
 XX
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX WPI; 2003-182525/18.
 DR
 PT Novel constrained helical peptide compound useful for prophylactically or
 PT therapeutically treating mammal at risk for or infected with human
 PT immunodeficiency virus.
 XX
 PS Disclosure; Fig 16; 180pp; English.
 XX
 CC The invention describes a constrained helical peptide compound (1)
 CC comprising a first constrained helical peptide comprising a sequence of 8
 CC amino acids (a.as) having a first and second terminal residue both
 CC flanking an internal sequence of 6 a.as, where the terminal residues have
 CC a side chain that are linked to each other forming a locking group to
 CC form a constrained helical peptide. (1) is useful for preparing
 CC antibodies that prevent viral membrane fusion, as happens, preferably
 CC attached to a carrier, for use as an immunogen to raise antibodies that
 CC have a diagnostic use, as a vaccine for treatment of patients at risk of
 CC or infected with HIV, to create combinatorial constrained helical peptide
 CC libraries that are useful in chemical selection systems, to isolate the
 CC binding determinants from alpha-helical binding domains of known
 CC proteins, for determining whether a binding determinate in an alpha-
 CC helical binding domain of a known protein can serve as a structural model
 CC for the design of pepidomimetics, to replace intact binding proteins or
 CC protein binding domains in the affinity purification of ligands, to mimic
 CC epitopes in proteins to selectively raise polyclonal or monoclonal
 CC antibodies against such individual epitopes for isolating synthetic
 CC antibody clones with a selected binding activity from phage display
 CC combinatorial libraries, to provide conformationally stable variants of
 CC peptides or proteins which exhibit floppy or unstable alpha-helical
 CC secondary structure at one or more sites in unstrained form under
 CC conditions of interest. This is the amino acid sequence of an HIV
 CC envelope protein gp41, fragments of which are used in the creation of
 CC locked helix peptides
 XX
 SQ Sequence 268 AA:
 QY
 Db 1 SNLLRAIEAQOHLLQLTWGIKQLQARVLAVERYLKQD 38
 83 SNLLRAIEAQOHLLQLTWGIKQLQARVLAVERYLKQD 120
 Query Match 95.7%; Score 177; DB 6; Length 268;
 Best Local Similarity 94.7%; Pred. No. 6e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 25
 AAY22828
 ID AAY22828 standard; protein; 269 AA.
 XX
 AC AAY22828;
 DT 19-AUG-1999 (first entry)
 XX
 DE SEQ ID NO. 24 from WO9820036.
 XX
 KW HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KM antibody; viral membrane fusion; viral infectivity;
 KM ligand affinity purification; protein A replacement;
 KM immunoglobulin purification; epitope mimic.
 XX
 OS Human immunodeficiency virus.
 PN WO9820036-A1.
 XX
 PD 14-MAY-1998.

```

PE 05-NOV-1997; 97WO-US020069.
XX
XX 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-00876698.
PA (GETH ) GENENTECH INC.
XX
PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
XX WPI; 1998-286866/25.
DR
XX
XX Production of constrained helical peptide(s) by linking side chains on
PT terminl of octa-peptide - derived from human immunodeficiency virus gp41
PT protein, useful in vaccines for treatment and prevention of infection.
PS
PS Claim 11; Page 164-165; 279pp; English.
XX
XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
CC AAY22903 represent consensus sequences of various sections of the gp41
CC protein). Sequences derived from the peptides are used to produce
CC constrained helical peptides of the invention. The constrained helical
CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds. The
CC constrained helical peptides are used to treat or prevent HIV infection,
CC especially as vaccines that generate antibodies that prevent viral
CC membrane fusion or infectivity. Vaccines may contain constrained helical
CC peptides derived from several different strains of HIV. The antibodies
CC are also useful for diagnosing HIV infection. Other uses for the
CC constrained helical peptides are in affinity purification of ligands
CC (particularly where complete binding protein is not readily available,
CC e.g. replacements for protein A in immunoglobulin purification), as
CC epitope mimics for antibody production; for isolation of synthetic
CC antibody clones from phage display libraries, or as stable forms of
XX "floppy" peptides or proteins
XX
SQ Sequence 269 AA;
XX
XX Query Match 95.7%; Score 177; DB 2; Length 269;
XX Best Local Similarity 94.7%; Pred. No. 6.1e-15;
XX Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRATRAOQHLLQLTWVGKQLQARLTAVERVRYKD 38
XX |||||||||||||||||||||||||||||||
Db 84 SNLRATRAOQHLLQLTWVGKQLQARLTAVERVRYKD 121
XX
RESULT 26
XX ID AAY22900 standard; protein; 269 AA.
XX
XX AAY22900;
XX
XX 19-AUG-1999 (first entry)
XX
XX SEQ ID NO. 96 from WO9820036.
XX
XX HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
KW antibody; viral membrane fusion; viral infectivity;
KW ligand affinity purification; protein A replacement;
KW immunoglobulin purification; epitope mimic.
XX
XX Human immunodeficiency virus.
XX
XX WO9820036-A1.
XX
XX 14-MAY-1998.
XX

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[illegible]

XX 06-NCV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
XX (GETH) GENENTECH INC.
XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX WPI; 2002-487624/52.
XX
XX New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have alpha-
PT helical conformation.
XX
XX Disclosure; Col 255-256; 175pp; English.
XX
XX The invention relates to cyclic peptides (A) with a constrained helical
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
CC protein) protein of human immunodeficiency virus (HIV). The cyclic
CC peptides have formulas given in the specification part of which are
CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
CC C, D, E or O. The peptides are used to cause induction of a specific
CC immune response, resulting in antibodies that prevent virus-induced
CC membrane fusion. The peptides are used to treat subjects with, or at risk
CC of, HIV infection, either as antitumor/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is a consensus sequence of gp41 from a
CC particular HIV clade
XX
XX
SQ Sequence 269 AA:
Query Match 95.7%; Score 177; DB 5; Length 269;
Best Local Similarity 94.7%; Pred. No. 6.1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
DB 84 SNLLRAIEAQOHLLQTLTWGKIQOLARVLAVERYLKQ 121
RESULT 28
ABG68299
ID ABG68299 standard; protein; 269 AA.
XX
XX ABG68299;
AC
XX 29-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX
XX Envelope protein gp41 from HIV clade B strain #18.
DE
XX HIV; glycoprotein; gp41; antigen; helical conformation;
KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
KM viral envelope protein; vaccine; virucide; anti-HIV.
XX
XX Human immunodeficiency virus 1; clade B.
OS
XX US6271198-B1.
PN
XX 07-AUG-2001.
PD
XX
XX 05-NOV-1997; 97US-00965056.
PF
XX 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
XX

PR 16-JUN-1997; 97US-00876698.
XX
XX (GETH) GENENTECH INC.
XX
XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX WPI; 2002-487624/52.
XX
XX New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have alpha-
PT helical conformation.
XX
XX Disclosure; Col 165-168; 175pp; English.
XX
XX The invention relates to cyclic peptides (A) with a constrained helical
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
CC protein) protein of human immunodeficiency virus (HIV). The cyclic
CC peptides have formulas given in the specification part of which are
CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
CC C, D, E or O. The peptides are used to cause induction of a specific
CC immune response, resulting in antibodies that prevent virus-induced
CC membrane fusion. The peptides are used to treat subjects with, or at risk
CC of, HIV infection, either as antitumor/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular HIV
CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
XX 2003 to standardise OS field)
XX
XX
SQ Sequence 269 AA:
Query Match 95.7%; Score 177; DB 5; Length 269;
Best Local Similarity 94.7%; Pred. No. 6.1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
DB 84 SNLLRAIEAQOHLLQTLTWGKIQOLARVLAVERYLKQ 121
RESULT 29
ABU57778
ID ABU57778 standard; protein; 269 AA.
XX
XX ABU57778;
AC
XX 10-APR-2003 (first entry)
DT
XX Human immunodeficiency virus (HIV) gp41 consensus sequence #4.
DE
XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KM viral membrane fusion; haptens; immunogen; peptidomimetic; gp41;
KM envelope protein; consensus sequence.
XX
XX Human immunodeficiency virus.
OS
XX US2002151473-A1.
PN
XX 17-OCT-2002.
PD
XX
XX 15-MAY-2001; 2001US-00854816.
PF
XX 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
XX 05-NOV-1997; 97US-00965056.
XX

PA (BRAI/) BRAISTED A C.
PA (JUDI/) JUDICE J K.
PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVANSNIK M A.
PA (WELL/) WELLS J A.
PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovansnik MA;
PI Wells JA;
PI WPI: 2003-182525/18.
XX
XX
XX Novel constrained helical peptide compound useful for prophylactically or
XX therapeutically treating mammal at risk for or infected with human
XX immunodeficiency virus.
XX
XX
XX Disclosure; Fig 16; 180pp; English.
XX
XX The invention describes a constrained helical peptide compound (I)
XX comprising a first constrained helical peptide comprising a sequence of 8
XX amino acids (a.as) having a first and second terminal residue both
XX flanking an internal sequence of 6 a.as, where the terminal residues have
XX a side chain that are linked to each other forming a locking group to
XX form a constrained helical peptide. (I) is useful for preparing
XX antibodies that prevent viral membrane fusion, as haptens, preferably
XX attached to a carrier, for use as an immunogen to raise antibodies that
XX have a diagnostic use, as a vaccine for treatment of patients at risk of
XX or infected with HIV, to create combinatorial constrained helical peptide
XX libraries that are useful in chemical selection systems, to isolate the
XX binding determinants from alpha-helical binding domains of known
XX proteins, for determining whether a binding determinate in an alpha-
XX helical binding domain of a known protein can serve as a structural model
XX for the design of peptidomimetics, to replace intact binding proteins or
XX protein binding domains in the affinity purification of ligands, to mimic
XX epitopes in proteins to selectively raise polyclonal or monoclonal
XX antibodies against such individual epitopes for isolating synthetic
XX antibody clones with a selected binding activity from phage display
XX combinatorial libraries, to provide conformationally stable variants of
XX peptides or proteins which exhibit floppy or unstable alpha-helical
XX secondary structure at one or more sites in unrestrained form under
XX conditions of interest. This is the amino acid sequence of a consensus
XX sequence derived from envelope protein gp41
XX
XX Sequence 269 AA;
XX
XX
XX Query Match 95.7%; Score 177; DB 6; Length 269;
XX Best Local Similarity 94.7%; Pred. No. 6,1e-15;
XX Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 38
DB 84 SNLLRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 121
RESULT 30
ABUS7706
ID ABUS7706 standard; protein; 269 AA.
XX
XX ABUS7706;
XX
XX 10-APR-2003 (first entry)
XX
XX Human immunodeficiency virus (HIV) envelope protein gp41 #18.
XX
XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
XX viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
XX envelope protein.
XX
XX Human immunodeficiency virus.
XX
XX US2002151473-A1.
XX
XX 17-OCT-2002.
PD

XX
XX 15-MAY-2001; 2001US-00854816.
XX
XX 06-NOV-1996; 96US-00743698.
XX 16-JUN-1997; 97US-0049787P.
XX 16-JUN-1997; 97US-00876698.
XX 05-NOV-1997; 97US-00965056.
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XX (BRAI/) BRAISTED A C.
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PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovansnik MA;
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XX comprising a first constrained helical peptide comprising a sequence of 8
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XX flanking an internal sequence of 6 a.as, where the terminal residues have
XX a side chain that are linked to each other forming a locking group to
XX form a constrained helical peptide. (I) is useful for preparing
XX antibodies that prevent viral membrane fusion, as haptens, preferably
XX attached to a carrier, for use as an immunogen to raise antibodies that
XX have a diagnostic use, as a vaccine for treatment of patients at risk of
XX or infected with HIV, to create combinatorial constrained helical peptide
XX libraries that are useful in chemical selection systems, to isolate the
XX binding determinants from alpha-helical binding domains of known
XX proteins, for determining whether a binding determinate in an alpha-
XX helical binding domain of a known protein can serve as a structural model
XX for the design of peptidomimetics, to replace intact binding proteins or
XX protein binding domains in the affinity purification of ligands, to mimic
XX epitopes in proteins to selectively raise polyclonal or monoclonal
XX antibodies against such individual epitopes for isolating synthetic
XX antibody clones with a selected binding activity from phage display
XX combinatorial libraries, to provide conformationally stable variants of
XX peptides or proteins which exhibit floppy or unstable alpha-helical
XX secondary structure at one or more sites in unrestrained form under
XX conditions of interest. This is the amino acid sequence of an HIV
XX envelope protein gp41, fragments of which are used in the creation of
XX locked helix peptides
XX
XX Sequence 269 AA;
XX
XX
XX Query Match 95.7%; Score 177; DB 6; Length 269;
XX Best Local Similarity 94.7%; Pred. No. 6,1e-15;
XX Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 38
DB 84 SNLLRAIEAQOHLQLTWQIKOLARILAVERYLKDQ 121
Search completed: June 2, 2004, 11:41:45
Job time : 48.6033 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.3261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336A-542

Perfect score: 185

Sequence: 1 SNLLRAIEAQHLQLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	94.6	357	2 S21996	env polypeptide g
2	175	94.6	851	2 S31985	env polypeptide g
3	175	94.6	853	2 S54384	env polypeptide g
4	175	94.6	854	2 S13288	env polypeptide g
5	175	94.6	855	1 VCLJ2R	env polypeptide pr
6	175	94.6	856	1 VCLJH3	env polypeptide pr
7	175	94.6	856	1 VCLJVL	env polypeptide pr
8	175	94.6	861	1 VCLJIV	env polypeptide pr
9	174	94.1	357	2 S22006	env polypeptide g
10	174	94.1	357	2 S21994	env polypeptide g
11	174	94.1	357	2 S22004	env polypeptide g
12	174	94.1	358	2 S22002	env polypeptide g
13	174	94.1	358	2 S22000	env polypeptide g
14	174	94.1	358	2 S70417	env polypeptide g
15	172	93.0	357	2 S21990	env polypeptide g
16	172	93.0	859	1 VCLJMN	env polypeptide pr
17	171	92.4	357	2 S21992	env polypeptide pr
18	171	92.4	443	2 C41621	env polypeptide p
19	171	92.4	445	2 A41621	env polypeptide M
20	171	92.4	454	2 B41621	env polypeptide D
21	171	92.4	729	1 VCLJXK	env polypeptide pr
22	171	92.4	843	1 H44001	env polypeptide pr
23	171	92.4	846	1 VCLJND	env polypeptide pr
24	171	92.4	852	2 T12016	env polypeptide pr
25	171	92.4	855	1 VCLJAZ	env polypeptide pr
26	171	92.4	856	1 VCLJZW	env polypeptide pr
27	171	92.4	856	1 A44993	env polypeptide pr
28	171	92.4	861	1 VCLJXB	env polypeptide pr
29	171	92.4	861	1 VCLJSC	env polypeptide pr

30	171	92.4	868	1 VCLJHA	env polypeptide -
31	170	91.9	358	2 T01672	env polypeptide
32	167	90.3	358	2 S21998	env polypeptide g
33	163	88.1	852	1 VCLJBR	env polypeptide -
34	160	86.5	854	1 VCLJST	env polypeptide pr
35	157	84.9	847	2 T09448	env polypeptide pr
36	157	84.9	847	2 S13289	env polypeptide -
37	126	68.1	104	2 S52930	env polypeptide -
38	125	67.6	877	2 C46356	env polypeptide -
39	125	67.6	877	2 C46356	env polypeptide -
40	123	66.5	877	2 S49197	env polypeptide p
41	120	64.9	732	2 S46352	env polypeptide -
42	115	62.2	366	2 B41565	env polypeptide -
43	115	62.2	863	2 A53034	env polypeptide -
44	113	61.1	712	1 VCLJSA	env polypeptide pr
45	113	61.1	851	2 S12159	env polypeptide -
46	113	61.1	852	1 VCLJGG	env polypeptide pr
47	113	61.1	859	1 VCLJST	env polypeptide pr
48	113	61.1	859	2 S53098	env polypeptide pr
49	112	60.5	859	1 VCLJCT	env polypeptide pr
50	111	60.0	855	2 A45713	env polypeptide pr
51	111	60.0	881	2 VCLJG2	env polypeptide pr
52	111	60.0	881	2 S03068	env polypeptide -
53	111	60.0	885	2 S04322	env polypeptide -
54	111	60.0	886	2 T11555	env polypeptide -
55	110	59.5	881	1 VCLJG3	env polypeptide -
56	109	58.9	859	2 S24571	env polypeptide -
57	109	58.9	869	2 A47655	env polypeptide pr
58	108	58.4	880	1 VCLJG2	env polypeptide pr
59	107	57.8	151	2 S30458	env polypeptide -
60	107	57.8	766	2 S28084	env polypeptide -
61	107	57.8	889	1 VCLJG5	env polypeptide -
62	106	57.3	887	2 T11566	env polypeptide -
63	105	56.8	151	2 S30448	env polypeptide -
64	105	56.8	151	2 S30453	env polypeptide -
65	105	56.8	151	2 S30452	env polypeptide -
66	105	56.8	151	2 S30450	env polypeptide -
67	105	56.8	151	2 S30451	env polypeptide -
68	103	55.7	151	2 S30459	env polypeptide -
69	103	55.7	151	2 S30457	env polypeptide -
70	103	55.7	151	2 S30456	env polypeptide -
71	103	55.7	151	2 S30455	env polypeptide -
72	103	55.7	151	2 S30454	env polypeptide -
73	95	51.4	68	2 S60693	env polypeptide -
74	95	51.4	68	2 S60687	env polypeptide -
75	93	50.3	68	2 S60692	env polypeptide -
76	92	49.7	68	2 S60695	env polypeptide -
77	92	49.7	68	2 S60696	env polypeptide -
78	92	49.7	68	2 S60705	env polypeptide -
79	92	49.7	68	2 S60707	env polypeptide -
80	92	49.7	68	2 S60694	env polypeptide -
81	92	49.7	68	2 S60706	env polypeptide -
82	84	45.4	69	2 S60688	env polypeptide -
83	81	43.8	69	2 S60690	env polypeptide -
84	81	43.8	69	2 S60689	env polypeptide -
85	81	43.8	69	2 S60691	env polypeptide -
86	77	41.6	294	2 S60525	env polypeptide
87	77	41.6	294	2 S60538	env polypeptide
88	76	41.1	294	2 S60545	env polypeptide
89	76	41.1	294	2 S60524	env polypeptide
90	76	41.1	296	2 S60535	env polypeptide

ALIGNMENTS

RESULT 1
S21996
env polypeptide gpi20/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A/Reference number: S70417; PMID:1736940

A/Accession: S70422

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-357 <ST2>

A/Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129

A/Experimental source: patient 27L

A/Note: submitted to the EMBL Data Library, July 1991

C/Superfamily: type E retrovirus env polyprotein

Query Match 94.6%; Score 175; DB 2; Length 357;

Best Local Similarity 94.7%; Pred. No. 1e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 38

54 NNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 91

RESULT 2

S33985

env polyprotein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C/Accession: S33985

R/Carlini, F.

Submitted to the EMBL Data Library, November 1991

A/Reference number: S33979

A/Accession: S33985

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-851 <CAR>

A/Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199

C/Superfamily: type E retrovirus env polyprotein

Query Match 94.6%; Score 175; DB 2; Length 851;

Best Local Similarity 94.7%; Pred. No. 2.6e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 38

548 NNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 585

RESULT 3

S54384

envelope polyprotein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C/Accession: S54384

R/Theodore, T.; Buckler-White, A.J.

Submitted to the EMBL Data Library, July 1988

A/Reference number: S54377

A/Accession: S54384

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-853 <THE>

A/Cross-references: EMBL:M26639; NID:G329377; PIDN:AAA45370.1; PID:G329385

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: polyprotein

Query Match 94.6%; Score 175; DB 2; Length 853;

Best Local Similarity 94.7%; Pred. No. 2.6e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 38

550 NNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 587

RESULT 4

S13288

env protein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C/Accession: S13288

R/O'Brien, W.A.; Koyanagi, Y.; Nemaize, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A/Reference number: S13288; PMID:91043044; PMID:2172833

A/Accession: S13288

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-854 <OBR>

C/Superfamily: type E retrovirus env polyprotein

Query Match 94.6%; Score 175; DB 2; Length 854;

Best Local Similarity 94.7%; Pred. No. 2.6e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 38

551 NNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 588

RESULT 5

VCLVZR

env polyprotein precursor - human immunodeficiency virus Zr-6

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus Zr-6

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C/Accession: D26192

R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic

A/Reference number: A26192; PMID:87248097; PMID:3036660

A/Accession: D26192

A/Molecule type: DNA

A/Residues: 1-855 <SRI>

A/Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403

C/Genetics: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F:1-19/DNA: signal sequence #status predicted <SIG>

F:20-85/Product: env polyprotein #status predicted <MAT>

F:87-129/Product: transmembrane glycoprotein #status predicted <TM>

F:130-855/Product: transmembrane glycoprotein #status predicted <TM>

Query Match 94.6%; Score 175; DB 1; Length 855;

Best Local Similarity 94.7%; Pred. No. 2.6e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 38

552 NNLLRAIEAQQHLLQTLTWGKIQKQARILAVERYLKQ 589

RESULT 6

VCLVZR

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N/Alternate names: coat polyprotein

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C/Accession: A03973

R/Retner, U.; Haseltine, W.; Patarca, R.; Livak, K.J.; Scarich, B.; Josephs, S.F.; Dorar

berger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A/Reference number: A93353; PMID:85111123; PMID:2578615

A/Accession: A03973

A/Molecule type: DNA

A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.6%; Score 175; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 2.6e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKQ 38
DB 553 NNLLRAIEAQOHLLQTLTWGIKOLQARILAVERYLKQ 590

RESULT 7
VCUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:/Nesting: M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lesky, L.A.; Capon, D.J.
R:/Nature 313, 450-458, 1985
A:/Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A:/Reference number: A93355; MUID:8511157; PMID:2982104
A:/Accession: A03974
A:/Molecule type: DNA
A:/Residues: 1-856 <MOE>
A:/Cross-references: GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559
C:Genetics:
A:Gene: env
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:/611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.6%; Score 175; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 2.6e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKQ 38
DB 553 NNLLRAIEAQOHLLQTLTWGIKOLQARILAVERYLKQ 590

RESULT 8
VCUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:/Nesting: S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
R:/Cell 40, 9-17, 1985
A:/Title: Nucleotide sequence of the AIDS virus, LAV.
A:/Reference number: A90866; MUID:8509333; PMID:2981635
A:/Accession: A03975
A:/Molecule type: DNA
A:/Residues: 1-861 <MAI>
A:/Cross-references: GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C:Genetics:

A:Gene: env
C:Superfamily: type B retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:/1-30/Domain: signal sequence #status predicted <SIG>
F:/31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:/517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:/88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F:/616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 94.6%; Score 175; DB 1; Length 861;
Best Local Similarity 94.7%; Pred. No. 2.6e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKQ 38
DB 558 NNLLRAIEAQOHLLQTLTWGIKOLQARILAVERYLKQ 595

RESULT 9
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:/AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:/Reference number: S70417; MUID:92144209; PMID:1736940
A:/Accession: S70420
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-357 <ST2>
A:/Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
A:/Experimental source: patient L
A:/Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type B retrovirus env polyprotein
Query Match 94.1%; Score 174; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLKQ 38
DB 54 NNLLRAIEAQOHLLQTLTWGIKOLQARILAVERYLKQ 91

RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:/Variety: isolate 27B
C:/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:/Accession: S21994; S70421
R:/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:/submitted to the EMBL Data Library, July 1991
A:/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A:/Reference number: S21990
A:/Accession: S21994
A:/Molecule type: DNA
A:/Residues: 1-357 <STB1>
A:/Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R:/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:/AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:/Reference number: S70417; MUID:92144209; PMID:1736940
A:/Accession: S70421
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-140, 'X', 142-312, 'X', 314-357 <STB2>
A:/Cross-references: EMBL:X61355; NID:G60179
C:Superfamily: type B retrovirus env polyprotein
Query Match 94.1%; Score 174; DB 2; Length 357;

Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
DB 54 NNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 48
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
A/Accession: S22004; S70419
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:G60188; PIDN:CAA43618.1; PID:G60189
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:G60188
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 174; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
DB 54 NNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 91

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
A/Accession: S22002; S70418
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:G60186
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 174; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
DB 55 NNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
A/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 174; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
DB 55 NNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
A/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined
A/Reference number: S70417; PMID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 174; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
DB 55 NNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 92

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
A/Accession: S21990; S70423
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 334-357 <STR2>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polypeptide

Query Match 93.0%; Score 172; DB 2; Length 357;
Best Local Similarity 89.5%; Pred. No. 2.5e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 91

RESULT 16

env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: A28922
R;Girgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, G.; Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <GUR>
C:Gene: env
C:Genetics:

C:Superfamily: type B retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-859/Product: env polypeptide #status predicted <ERP>
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 93.0%; Score 172; DB 1; Length 859;
Best Local Similarity 89.5%; Pred. No. 6.5e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 38
Db 557 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 594

RESULT 17

env polypeptide protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70424; S21992
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70424
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STR2>
A:Cross-references: EMBL:X61358; NID:960177; PIDN:CAA43628.1; PID:960178
A:Experimental source: patient 22
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type B retrovirus env polypeptide

Query Match 92.4%; Score 171; DB 2; Length 357;
Best Local Similarity 91.9%; Pred. No. 3.4e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 38
Db 55 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 91

RESULT 18

env polypeptide P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:9328631; PIDN:AB03792.1; PID:9555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:

C:Superfamily: type B retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: car

Query Match 92.4%; Score 171; DB 2; Length 443;
Best Local Similarity 89.5%; Pred. No. 4.3e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 38
Db 293 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKQ 330

RESULT 19

env polypeptide M - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: A41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: A41621
A:Molecule type: DNA
A:Residues: 1-445 <BUR>
A:Cross-references: GB:M77228; NID:9328627; PIDN:AB03790.1; PID:9555013
A:Note: this virus was isolated from the mother
C:Genetics:

C:Superfamily: type B retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:426-445/Domain: transmembrane #status predicted <TMN>
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site: car

Query Match 92.4%; Score 171; DB 2; Length 445;
Best Local Similarity 89.5%; Pred. No. 4.3e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 92.4%; Score 171; DB 1; Length 846;
Best Local Similarity 89.5%; Pred. No. 8.7e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 38
Db 543 NNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 580

RESULT 24

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12016

R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.

A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S

A:Reference number: Z17379; MUID:98178716; PMID:9519894

A:Accession: T12016

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1852 <MCC>

A:Cross-references: EMBL:U90934; NID:G2351783; PIDN:AAC5271.1; PID:G2351784

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

Query Match 92.4%; Score 171; DB 2; Length 852;
Best Local Similarity 89.5%; Pred. No. 8.7e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 38
Db 549 NNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 586

RESULT 25

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

VCLJAJ2

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-S

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:8509453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <SAN>

A:Cross-references: GB:K02007; NID:G328658; PIDN:AAB59882.1; PID:G328666

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:31-509/Product: signal sequence #status predicted <SIG>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,204,244,255,298,304,334,341,358,364,388,394,400,408,445,458

F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.4%; Score 171; DB 1; Length 855;
Best Local Similarity 89.5%; Pred. No. 8.8e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 38

Db 552 NNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 589

RESULT 26

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

C:Accession: A24774

R:Scarich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.

Cell 45, 637-648, 1986

A:Title: Identification and characterization of conserved and variable regions in the env

A:Reference number: A24774; MUID:86218077; PMID:2423250

A:Accession: A24774

A:Molecule type: DNA

A:Residues: 1-856 <STA>

A:Cross-references: GB:K03455; GB:M38432; NID:G1906382

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-501/Product: coat protein gp120 #status predicted <GP1>

F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 92.4%; Score 171; DB 1; Length 856;
Best Local Similarity 89.5%; Pred. No. 8.8e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 38
Db 553 NNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 590

RESULT 27

env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)

A44963

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999

C:Accession: A44963

R:Stinvaasen, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J

Aids Res. Hum. Retroviruses 5, 121-129, 1989

A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc

A:Reference number: A44963; MUID:89228766; PMID:2713163

A:Accession: A44963

A:Molecule type: DNA

A:Residues: 1-856 <SRI>

A:Cross-references: GB:M15896; NID:G329392; PIDN:AAB53948.1; PID:G329394

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-520/Product: coat protein gp120 #status predicted <GP1>

F:521-856/Product: coat protein gp41 #status predicted <GP2>

F:64-705/Domain: transmembrane #status predicted <TM>

F:87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 92.4%; Score 171; DB 1; Length 856;
Best Local Similarity 92.1%; Pred. No. 8.8e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 SNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 38
Db 553 NNLLRAIEAQOHLTLTWQIKOLQARILAVERYLKQ 590

RESULT 28

VCLJKB

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-GP41)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A>Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A/Reference number: A42995; MUID:92351552; PMID:1322587

A/Accession: A42995

A/Molecule type: mRNA

A/Residues: 1-861 <SH1>

A/Cross-references: GB:S41266; GB:D01206

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domain: extracellular #status predicted <EXT>

F:1-33/Domain: signal sequence #status predicted <SIG>

F:1-33/Region: hydrophobic #status predicted

F:34-517/Product: coat protein gp120 #status predicted <CP1>

F:514-517/Region: cleavage processing #status predicted

F:518-561/Product: coat protein gp41 #status predicted <CP2>

F:518-534/Region: hydrophobic #status predicted

F:690-711/Domain: transmembrane #status predicted <TM1>

F:712-861/Domain: intracellular #status predicted <INT>

F:756-772/Region: hydrophobic #status predicted

F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 92.4%; Score 171; DB 1; Length 861;

Best Local Similarity 89.5%; Pred. No. 8.8e-15;

Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRATEAQQHLLQLTWQIKQLQARILAVERYLKDO 38

Db 559 NNLRRAIDAAQHHLLQLTWQIKQLQARILAVERYLKDO 596

RESULT 29

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C/Accession: B28922

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta

Virology 164, 531-536, 1988

A>Title: Envelope sequences of two new United States HIV-1 isolates.

A/Reference number: A28922; MUID:88219542; PMID:3369091

A/Accession: B28922

A/Molecule type: DNA

A/Residues: 1-861 <GUR>

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-861/Product: env polyprotein #status predicted <EPP>

F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 92.4%; Score 171; DB 1; Length 861;

Best Local Similarity 89.5%; Pred. No. 8.8e-15;

Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRATEAQQHLLQLTWQIKQLQARILAVERYLKDO 38

Db 558 NNLRRAIDAAQHHLLQLTWQIKQLQARILAVERYLKDO 595

RESULT 30

VCLJHA

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: C23523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S.

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A>Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A/Reference number: A9436; MUID:87041461; PMID:3490666

A/Accession: C23523

A/Molecule type: DNA

A/Residues: 1-868 <DES>

A/Cross-references: GB:M13137; NID:g326460; PIDN:AAA4431.1; PID:g326467

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F:1-521/Product: coat protein gp120 #status predicted <GP1>

F:522-868/Product: coat protein gp41 #status predicted <GP2>

F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match 92.4%; Score 171; DB 1; Length 868;

Best Local Similarity 92.1%; Pred. No. 8.9e-15;

Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRATEAQQHLLQLTWQIKQLQARILAVERYLKDO 38

Db 565 NNLRRAIDAAQHHLLQLTWQIKQLQARILAVERYLKDO 602

Search completed: June 2, 2004, 11:50:11
Job time: 11.3261 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 6.19565 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-542
Perfect score: 185
Sequence: 1 SNLRAIEAQOHLLQTLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	175	94.6	853	1	ENV_HV1EL
2	175	94.6	853	1	ENV_HV1MF
3	175	94.6	853	1	ENV_HV122
4	175	94.6	855	1	ENV_HV126
5	175	94.6	856	1	ENV_HV181
6	175	94.6	856	1	ENV_HV182
7	175	94.6	856	1	ENV_HV183
8	175	94.6	856	1	ENV_HV184
9	175	94.6	856	1	ENV_HV185
10	175	94.6	856	1	ENV_HV186
11	174	94.1	855	1	ENV_HV187
12	174	94.1	855	1	ENV_HV188
13	172	93.0	848	1	ENV_HV189
14	172	93.0	848	1	ENV_HV190
15	171	92.4	843	1	ENV_HV191
16	171	92.4	846	1	ENV_HV192
17	171	92.4	851	1	ENV_HV193
18	171	92.4	852	1	ENV_HV194
19	171	92.4	855	1	ENV_HV195
20	171	92.4	856	1	ENV_HV196
21	171	92.4	856	1	ENV_HV197
22	171	92.4	856	1	ENV_HV198
23	171	92.4	861	1	ENV_HV199
24	171	92.4	865	1	ENV_HV200
25	171	92.4	867	1	ENV_HV201
26	171	92.4	868	1	ENV_HV202
27	170	91.9	847	1	ENV_HV203
28	168	90.8	847	1	ENV_HV204
29	166	89.7	863	1	ENV_HV205
30	163	88.1	852	1	ENV_HV206
31	160	86.5	854	1	ENV_HV207
32	125	67.6	865	1	ENV_HV208
33	125	67.6	877	1	ENV_HV209

34	122	65.9	854	1	ENV_SIVAI	Q02837 simian immu
35	116	62.7	768	1	ENV_SIVAI	P27757 simian immu
36	113	61.1	712	1	ENV_HV2S2	P32536 human immu
37	113	61.1	851	1	ENV_HV2D1	P17755 human immu
38	113	61.1	851	1	ENV_HV2G1	P18040 human immu
39	113	61.1	856	1	ENV_HV2NZ	P05883 human immu
40	113	60.5	859	1	ENV_HV2ST	P20872 human immu
41	112	60.1	859	1	ENV_HV2CA	P24105 human immu
42	111	60.0	380	1	ENV_SIVM2	P08810 simian immu
43	111	60.0	858	1	ENV_HV2RO	P04577 human immu
44	111	60.0	885	1	ENV_SIVS4	P12492 simian immu
45	111	60.0	889	1	ENV_SIVS4	P19503 simian immu
46	110	59.5	882	1	ENV_SIVM1	P05885 simian immu
47	109	58.9	859	1	ENV_HV2D2	P15831 human immu
48	108	58.4	880	1	ENV_SIVM1	P11267 simian immu
49	107	57.8	821	1	ENV_SIVGB	P22380 simian immu
50	107	57.8	846	1	ENV_HV2SB	P12449 human immu
51	107	57.8	861	1	ENV_SIVMK	P05884 simian immu
52	106	57.3	857	1	ENV_HV2KR	Q74126 human immu
53	106	57.3	860	1	ENV_HV2BE	P18094 human immu
54	56	30.3	2564	1	SPCO_HUMAN	Q9h254 homo sapien
55	54	29.2	1938	1	MYH4_RABIT	Q28641 oryctolagus
56	53	28.6	1938	1	MY5_ABOIR	P24733 aequipecten
57	53	28.6	1939	1	MYH4_HUMAN	Q9y623 homo sapien
58	51.5	27.8	924	1	HXK3_RAT	P27926 rattus norv
59	51	27.6	1935	1	MY58_CYPCA	Q90339 cyprinus ca
60	50.5	27.3	445	1	EX7L_STRAH	Q99C40 staphylococ
61	50.5	27.3	1411	1	EEA1_HUMAN	Q15075 homo sapien
62	50	27.0	1941	1	MYH2_HUMAN	Q9ukx2 homo sapien
63	49.5	26.8	581	1	FRIZ_DROME	P18537 drosophila
64	49.5	26.8	583	1	FRIZ_DROVI	Q24760 drosophila
65	49.5	26.8	962	1	ARVC_HUMAN	Q00192 homo sapien
66	49.5	26.8	969	1	ARVC_MOUSE	P98203 mus musculu
67	49	26.5	236	1	GT6_SCHEMA	P46435 schistosoma
68	49	26.5	1102	1	MYSC_CHICK	P29616 gallus gall
69	49	26.5	1756	1	PEPL_HUMAN	Q60437 homo sapien
70	49	26.5	4349	1	DYHC_FUSSO	P78716 fusarium so
71	49	26.5	8797	1	SNB1_HUMAN	Q8nf91 homo sapien
72	48.5	26.2	790	1	EEA1_MOUSE	Q8b166 mus musculu
73	48.5	26.2	1955	1	PUMA_PARIN	Q61308 parascaris
74	48	25.9	213	1	Y914_THRMA	Q9x016 thermococ
75	48	25.9	305	1	OTC_STNP7	Q93574 synechococ
76	48	25.9	314	1	SEHL_HUMAN	Q9h418 homo sapien
77	48	25.9	479	1	ACH9_HUMAN	Q9ugul homo sapien
78	48	25.9	551	1	YD25_YEAST	Q07657 saccharomyc
79	48	25.9	702	1	ATT1_VARV	P34011 varicella vir
80	48	25.9	906	1	CTN1_HUMAN	P35221 homo sapien
81	48	25.9	906	1	CTN1_MOUSE	P26231 mus musculu
82	48	25.9	1379	1	M3K5_MOUSE	Q35039 mus musculu
83	48	25.9	1937	1	MYH8_HUMAN	P13535 homo sapien
84	47.5	25.7	253	1	CYSH_VIBCH	Q9kux2 vibrio chol
85	47.5	25.7	1319	1	SOS1_MOUSE	Q62245 mus musculu
86	47.5	25.7	1333	1	SOS1_HUMAN	Q07889 homo sapien
87	47	25.4	376	1	O43A_DROME	P81917 drosophila
88	47	25.4	380	1	OXA4_MYCLE	Q50205 mycobacteri
89	47	25.4	418	1	DADI_RHIL0	Q98FE8 rhicobium 1
90	47	25.4	851	1	STAA2_HUMAN	P52630 homo sapien

ALIGNMENTS

RESULT 1
ENV_HV1EL
ID ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane
glycoprotein (GP120), Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (BLI isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP MEDLINE=6245056; PubMed=2424612;
 RA Alizon M., Main-Hobson S., Montegnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 of two isolates from African patients";
 RL Cell 46:63-74(1986).
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 CC -----
 CC EMBL; K03454; AAA44329.1; -;
 DR EMBL; A07108; CAA00616.1; -;
 DR HIV; K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDs; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 31 BY SIMILARITY.
 FT SIGNAL 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MM; PSCD64DAA007075 CRC64;

Best Local Similarity 94.6%; Pred. No. 2,2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SNLRAIEAQHLLQTLTWQIKOLQARILAVERYLQD 38
 Db 550 NNLRALIEAQHLLQTLTWQIKOLQARILAVERYLQD 587
 RESULT 2
 ENV_HVLMF ID ENV_HVLMF STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
 RA Maslak A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1
 RT variants diminished in the ability to induce syncytium-independent
 RT cytolysis";
 RL J. Virol. 64:3792-3803(1990).
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 CC -----
 CC EMBL; M33943; AAA44850.1; -;
 DR PDB; 1A1K; 16-JUN-97.
 DR HIV; M33843; ENVSMFA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDs; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 329 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match

94.6%; Score 175; DB 1; Length 853;

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FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 94.6%; Score 175; DB 1; Length 853;
Best Local Similarity 94.7%; Pred. No. 2,2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 551 NNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKDQ 588

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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CC -----
CC EMBL; M22639; AAA45370.1; -.
DR PIR; S54384; S54384.
DR HIV; M22639; ENV52226.
DR InterPro; IPR000328; ENV GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KM Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTREME MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 BY SIMILARITY.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.

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FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B0B8CBAFF7008 CRC64;

Query Match 94.6%; Score 175; DB 1; Length 853;
Best Local Similarity 94.7%; Pred. No. 2,2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 550 NNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKDQ 587

RESULT 4
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126
AC P04560;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire; nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82(1987).
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CC or send an email to license@isb-sib.ch).
CC -----

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[illegible]

DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)).	
EN	ENV.	
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11678;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=8511123; PubMed=2576615;	
RA	Ratner L., Haseltine W., Patarca R., Lyaak K.J., Starcich B.R.,	
RA	Joseph S.F., Dotan E.R., Rafelski J.A., Whitehorn E.A.,	
RA	Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,	
RA	Lattemeier J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,	
RA	Wong-Staal F.;	
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";	
RL	Nature 313:277-284(1985).	
RL	[2]	
RN	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.	
RP	MEDLINE=90285159; PubMed=235006;	
RX	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,	
RA	Gregory T.J.;	
RT	"Assignment of intrachain disulfide bonds and characterization of	
RT	potential glycosylation sites of the type 1 recombinant human	
RT	immunodeficiency virus envelope glycoprotein (gp120) expressed in	
RT	Chinese hamster ovary cells.";	
RL	J. Biol. Chem. 265:10373-10382(1990).	
CC	-----	
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CC	entities requires a license agreement (See http://www.iesb.ch/announce/	
CC	or send an email to license@ib-eb.ch).	
CC	-----	
DR	EMBL; M15654; AAA44205.1; -.	
DR	PIR; A03973; VCLJH3.	
DR	HIV; M15654; ENVSBH102.	
DR	InterPro; IPR000328; Env GP41.	
DR	InterPro; IPR00777; GP120.	
DR	Pfam; PF00516; GP120, 1.	
DR	Pfam; PF00517; GP41, 1.	
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;	
KW	Signal.	
FT	1 30	
FT	SIGNAL	
FT	CHAIN	
FT	512 856	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	TRANSMEMBRANE GLYCOPROTEIN.
FT	54 74	
FT	DISULFID	
FT	119 205	
FT	DISULFID	
FT	126 196	
FT	DISULFID	
FT	131 157	
FT	DISULFID	
FT	218 247	
FT	DISULFID	
FT	228 239	
FT	DISULFID	
FT	296 331	
FT	DISULFID	
FT	378 445	
FT	DISULFID	
FT	385 418	
FT	DISULFID	
FT	CARBOHYD	
FT	88 88	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	136 136	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	141 141	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	156 156	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	160 160	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	186 186	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	197 197	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	230 230	N-LINKED (GLCNAC. . .)
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FT	234 234	N-LINKED (GLCNAC. . .)
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FT	241 241	N-LINKED (GLCNAC. . .)
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FT	262 262	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	276 276	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	289 289	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	295 295	N-LINKED (GLCNAC. . .)
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FT	301 301	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	332 332	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	339 339	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	
FT	356 356	N-LINKED (GLCNAC. . .)

FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
 SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931B27 CRC64;

Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2, 2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 38
 :|||||
 Db 553 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 590

RESULT 6
 ENV_HV1H2 STANDARD; PRT; 856 AA.

AC P04573: 009779;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11706;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8729196; Pubmed=3040055;
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS virus."
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 RN [2]
 REVISIONS.
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
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 CC -----
 CC EMBL: K03455; AAB50262.1; -
 DR EMBL: AF038399; AAB99976.1; -
 DR EMBL: AF03819; AAC82596.1; -
 DR PDB: 1DF4: 26-JAN-00.
 DR PDB: 1DF5: 26-JAN-00.
 DR PDB: 1DWB: 02-APR-00.
 DR PDB: 1G9M: 27-DEC-00.
 DR PDB: 1GCI: 19-AUG-98.
 DR PDB: 1GZL: 10-OCT-02.
 DR PDB: 1K33: 10-OCT-01.
 DR PDB: 1K34: 10-OCT-01.
 DR HIV: K03455; ENVSHXB2.
 DR Interfero: IPR000328; ENV_GP41.
 DR Interfero: IPR000777; GP120.

DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT STGNAL 1 30
 FT CHAIN 31 511
 FT 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97212 MW; 6FA16AF85107E0 CRC64;

Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2, 2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 38
 :|||||
 Db 553 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 590

RESULT 7
 ENV_HV1H3 STANDARD; PRT; 856 AA.
 ID ENV_HV1H3
 AC P04624;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11707;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=85228248; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HTLV-III env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
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 CC -----
 CC EMBL: M4100; AAA44679.1; -.
 DR PDB; 1JAN; 17-OCT-01.
 DR PDB; 1JAN; 17-OCT-01.
 DR HIV; M4100; ENVSHXB3.
 DR Interpro; IPR000328; Env GP41.
 DR Interpro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
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 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;
 Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQITWQIKOLARILAVRYLKDQ 38
 Db 553 NMLRAIEAQOHLQITWQIKOLARILAVRYLKDQ 590
 RESULT 8
 ID ENV_HV1LW STANDARD; PRT; 856 AA.
 AC 070626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (TM12.3 isolate) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner M.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HTLV type IIIB).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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 CC -----
 CC EMBL: U12055; AA76690.1; -.
 DR PDB; 1IF3; 02-MAY-01.
 DR GlycoStatedB; 070626; -.
 DR Interpro; IPR000328; Env GP41.
 DR Interpro; IPR000777; GP130.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
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 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
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 FT CARBOHYD 234 234
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 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
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 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;
 Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SNLIRAEAOQHLLQTLTWGKIQOLQARILAVERYLKQ 38
 Db 553 NNILIRAEAOQHLLQTLTWGKIQOLQARILAVERYLKQ 590
 RESULT 9
 ENV_HV1PV STANDARD; PRT; 856 AA.
 ID ENV_HV1PV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11700;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=5111157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laasy L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
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 CC
 CC EMBL: K02083; AAB59873.1;
 DR EMBL: X01762; CAA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCBIDC3C1209B3 CRC64;
 Query Match 94.6%; Score 175; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SNLIRAEAOQHLLQTLTWGKIQOLQARILAVERYLKQ 38
 Db 553 NNILIRAEAOQHLLQTLTWGKIQOLQARILAVERYLKQ 590
 RESULT 10
 ENV_HV1PV STANDARD; PRT; 861 AA.
 ID ENV_HV1PV
 AC P03377;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11686;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=5509333; PubMed=2981635;
 RA Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RL Cell 40:9-17(1985).
 CC
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 CC

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CC -----
DR EMBL; K02013; AAB59751.1; -.
DR EMBL; A04321; CA000352.1; -.
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV5BRU.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
  3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516
FT DISULFID 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 235 235
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
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FT CARBOHYD 306 306
FT CARBOHYD 337 337
FT CARBOHYD 344 344
FT CARBOHYD 361 361
FT CARBOHYD 391 391
FT CARBOHYD 397 397
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 453 453
FT CARBOHYD 468 468
FT CARBOHYD 616 616
FT CARBOHYD 621 621
FT CARBOHYD 630 630
FT CARBOHYD 642 642
FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4D63A CRC64;

Query Match 94.6%; Score 175; DB 1; Length 861;
Best Local Similarity 94.7%; Pred. No. 2.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SNLLRAIEAOOHLQLTVMQIKQARILAVERYLKQD 38
Db 558 NMLLRATEAQOHLLQTLVWGKIQARILAVERYLKQD 595

RESULT 11
ENV_HV1S1 STANDARD; PRT; 847 AA.
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; Pubmed=2384920;
RX Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.,
RA "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
  J. Virol. 64:4390-4398(1990).
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; M65024; AAA45072.1; -.
DR PDB; 1OBE; 15-MAY-97.
DR HIV; M38428; ENV5SF162.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
  3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT DISULFID 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT DISULFID 87 87
FT CARBOHYD 135 135
FT CARBOHYD 154 154
FT CARBOHYD 186 186
FT CARBOHYD 195 195
FT CARBOHYD 232 232
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 336 336
FT CARBOHYD 352 352
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 401 401
FT CARBOHYD 438 438
FT CARBOHYD 454 454
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7F2AB CRC64;

Query Match 94.1%; Score 174; DB 1; Length 847;
Best Local Similarity 92.1%; Pred. No. 3e-16;

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Matches	35;	Conservative	2;	Mismatches	1;	Indels	0;	Gaps	0;
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OY 1 SNLRPAIEAQOHLLQLTWTWIKOIQARLAVERYIKDQ 38
 : |||||
Db 544 NMLRAIEAQQHLLQLTWWGIGIKOLQARVLAVERYIKDQ 581

RESULT 12

ID	ENV_HVIOY	STANDARD;	PRT;	855 AA.
AC	P20888;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last annotation update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirae.			
OX	NCBI_TaxID=11699;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90148544; PubMed=2559749;			
RA	Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;			
RT	"A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";			
RL	AIDS 3:707-715(1989).			
CC	-1- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.			
CC	-----			
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CC	-----			
DR	EMBL; M26727; AAA83397.1; -. .			
DR	HIV; M26727; ENVSOXY.			
DR	InterPro; IPR000328; Env GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120_1.			
KM	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL.	1	29	
FT	CHAIN	30	509	
FT	CHAIN	510	855	
FT	DISULFID	53	73	
FT	DISULFID	118	210	
FT	DISULFID	125	201	
FT	DISULFID	130	162	
FT	DISULFID	223	252	
FT	DISULFID	233	244	
FT	DISULFID	301	335	
FT	DISULFID	381	442	
FT	DISULFID	388	415	
FT	CARBOHYD	87	87	
FT	CARBOHYD	134	134	
FT	CARBOHYD	142	142	
FT	CARBOHYD	145	145	
FT	CARBOHYD	161	161	
FT	CARBOHYD	165	165	
FT	CARBOHYD	192	192	
FT	CARBOHYD	202	202	
FT	CARBOHYD	229	239	
FT	CARBOHYD	246	246	
FT	CARBOHYD	267	267	
FT	CARBOHYD	281	281	
FT	CARBOHYD	294	294	
FT	CARBOHYD	300	300	
FT	CARBOHYD	306	306	

EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.

Query Match	Best Local	Similarity	Score 174;	DB 1;	Length 855;
Matches 35;	Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	NNLRRAIEAOQHLLQLTWVQIKQOLAVERYLKDQ 38			
Db	552	NNLRRAIEAOQHLLQLTWVQIKQOLAVERYLKDQ 589			
RESULT .13					
ID	ENV_HVLJR	STANDARD;	PRT;	848 AA.	
AC	P20877.1				
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [containing: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11688;				
RA	[1]				
RP	SEQUENCE FROM N.A. Koyanagi S., Chen I.S.Y.,				
RL	Submitted (DEC-1988) to the HIV data bank.				
CC	-----				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).				
CC	-----				
DR	EMBL; M38429; AAB03749.1; -.				
DR	PDB; 1CE4; 18-MAR-99.				
DR	HIV; M38429; ENVJRCSF.				
DR	InterPro; IPR000328; Env GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120.1.				
DR	Pfam; PF00517; GP41.1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;				
KW	3D-structure.				
FT	SIGNAL	1	32		
FT	CHAIN	33	503		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	504	848		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73		BY SIMILARITY.
FT	DISULFID	118	203		BY SIMILARITY.
FT	DISULFID	125	194		BY SIMILARITY.
FT	DISULFID	130	154		BY SIMILARITY.
FT	DISULFID	216	245		BY SIMILARITY.
FT	DISULFID	226	237		BY SIMILARITY.
FT	DISULFID	294	328		BY SIMILARITY.
FT	DISULFID	374	437		BY SIMILARITY.
FT	DISULFID	381	410		BY SIMILARITY.
FT	CARBOHYD	87	87		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	134	134		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	137	137		N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;

Query Match 93.0%; Score 172; DB 1; Length 848;
 Best Local Similarity 89.5%; Pred. No. 5.6e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAOQHLLQTLVWGIKOLQARVLAVERYLKQ 38
 Db 545 NNLRAIEAOQHMLQTLVWGIKOLQARVLAVERYLKQ 582

RESULT 14
 ENV_HV1MN STANDARD; PRT; 856 AA.
 AC POS877;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11696;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8219542; Pubmed=3369091;
 RA Gargo C., Guo H.-G., Franchini G., Aldrovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC - MISCILLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS PATIENT IN 1984.
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 CC
 CC EMBL; M17449; AAA44857.1; -
 DR PDB; 1ACJ; 31-JUL-94.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1N1Z; 25-FEB-03.
 DR PDB; 1NU0; 25-FEB-03.
 DR HIV; M17449; ENVSMN.

DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
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 FT DISULFID 130 162
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 FT DISULFID 388 418
 FT CARBOHYD 87 87
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 FT CARBOHYD 135 135
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 FT CARBOHYD 448 448
 FT CARBOHYD 465 465
 FT CARBOHYD 612 612
 FT CARBOHYD 617 617
 FT CARBOHYD 626 626
 FT CARBOHYD 638 638
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;
 Query Match 93.0%; Score 172; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 5.7e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAOQHLLQTLVWGIKOLQARVLAVERYLKQ 38
 Db 554 NNLRAIEAOQHMLQTLVWGIKOLQARVLAVERYLKQ 591

RESULT 15
 ENV_HV1Y2 STANDARD; PRT; 843 AA.
 AC P35561;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;


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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2B83 CRC64;

Query Match 92.4%; Score 171; DB 1; Length 846;
Best Local Similarity 89.5%; Pred. No. 7,7e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 543 NLLRAIEAQOHLQTLTWGIKOLQARILAVERYLKDQ 580

RESULT 17
ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BHS isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11684;
RN [1]
RP MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran B.R., Rafelson E.A.,
RA Baumstark K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).

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CC or send an email to license@isb-sib.ch).
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CC
CC EMBL: K02011; AAA44661.1; -.
DR PDB: 1DH; 13-JAN-99.
DR PDB: 1HHG; 31-OCT-93.
DR PDB: 1OC3; 02-JAN-00.
DR PDB: 1S2T; 24-DEC-97.
DR HIV; K02011; ENV5B8.
DR Glycerolated; P04582; -.
DR Interpro; IPR000328; Env GP41.
DR Interpro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 506 506 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 851 851 BY SIMILARITY.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.

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FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 440 BY SIMILARITY.
FT DISULFID 385 413 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 92.4%; Score 171; DB 1; Length 851;
Best Local Similarity 92.1%; Pred. No. 7,7e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 548 NLLRAIEAQOHLQTLTWGIKOLQARILAVERYLKDQ 585

RESULT 18
ENV_HV1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11690;
RN [1]
RP MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RA "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).

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DR EMBL: AY522275; AA017031.1; -
DR PDB: 1ME0; 11-DEC-02.
DR HIV: M38427; ENVSSP33.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; E7B7BF8D23C9910D CRC64;
Query Match 92.4%; Score 171; DB 1; Length 852;
Best Local Similarity 89.5%; Pred. No. 7,7e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQD 38
DB 549 NNLLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQD 586
RESULT 19
ENV_HV1A2 STANDARD; PRT; 855 AA.
ID ENV_HV1A2
AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retrovirus; Retroviridae; Lentiviruses.
OX NCBI:Taxid=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
(ARV-2)".
RT Science 227:484-492 (1985).
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DR EMBL: K02007; AAB59882.1; -
DR PIR: A03976; VCLJ32.
DR HIV: K02007; ENVSSP2.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 208 BY SIMILARITY.
FT DISULFID 125 199 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 221 250 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 299 333 BY SIMILARITY.
FT DISULFID 380 442 BY SIMILARITY.
FT DISULFID 387 415 BY SIMILARITY.
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FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
 Query Match 92.4%; Score 171; DB 1; Length 855;
 Best Local Similarity 89.5%; Pred. No. 7.8e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SNLRAIEAQOHLLQTLTWQIKOLARILAVERYLKDQ 38
 Db 553 NNLLRAIEAQOHLLQTLTWQIKOLARILAVERYLKDQ 589
 RESULT 20
 ENV_HV1SC STANDARD; PRT; 856 AA.
 ID ENV_HV1SC
 AC P05878;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=11702;
 RN [1]
 RP MEDLINE=88219542; Pubmed=3369091;
 RA Guirgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536 (1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
 1984 IN SOUTHERN CALIFORNIA.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M17450; -; NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL. 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;
 Query Match 92.4%; Score 171; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 7.8e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SNLRAIEAQOHLLQTLTWQIKOLARILAVERYLKDQ 38
 Db 553 NNLLRAIEAQOHLLQTLTWQIKOLARILAVERYLKDQ 590
 RESULT 21
 ENV_HV1M1 STANDARD; PRT; 856 AA.
 ID ENV_HV1M1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=31678;
 RN [1]
 RP MEDLINE=86218077; Pubmed=2423250;
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable
 regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 AIDS."
 RL Cell 45:637-646 (1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
 BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 WAS PERINATALLY INFECTED BY HER MOTHER.
 DR PIR; A24774; VCLJ3W.
 DR PDB; 1LB0; 04-DEC-02.
 DR PDB; 1LCK; 04-DEC-02.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL. 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.


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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB6BD1E49C4049D9 CRC64;

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Query Match 92.4%; Score 171; DB 1; Length 856;
Best Local Similarity 89.5%; Pred. No. 7.8e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 SNLLRAIEAQOHLTLTWQIKOLARILAVERYLKQ 38
Db 553 NNLLRAIEAQOHLTLTWQIKOLARILAVERYLKQ 590

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RESULT 22
ENV_HV1ZH STANDARD; PRT; 856 AA.
AC P0581;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11692;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69228766; Pubmed=2713163;
RA Srinivasan A., York D., Butler D. Jr., Jannou-Nasr R., Getchell J.,
McCormick J., Ou C.Y., Myers G., Smith T., Chen B.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of hybrid HIV-1."
RL AIDS Res. Hum. Retroviruses 5:121-129 (1989).
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CC -----
DR EMBL; M15896; AAB53948.1;
DR PIR; A44963; A44963.
DR HIV; M15896; ENV52321.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00516; GP120; 1.
KW signal.
FT SIGNAL 1 29
FT CHAIN 30 511
FT CHAIN 512 856
FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 153
FT DISULFID 219 248
FT DISULFID 229 240
FT DISULFID 297 331
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FT DISULFID 386 418
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FT CARBOHYD 138 138
FT CARBOHYD 152 152
FT CARBOHYD 156 156
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FT CARBOHYD 277 277
FT CARBOHYD 294 294
FT CARBOHYD 302 302
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 355 355
FT CARBOHYD 364 364
FT CARBOHYD 387 387
FT CARBOHYD 393 393
FT CARBOHYD 398 398
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 448 448
FT CARBOHYD 461 461
FT CARBOHYD 462 462
FT CARBOHYD 465 465
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 637 637
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;

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Query Match 92.4%; Score 171; DB 1; Length 856;
Best Local Similarity 92.4%; Pred. No. 7.8e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 SNLLRAIEAQOHLTLTWQIKOLARILAVERYLKQ 38
Db 553 NNLLRAIEAQOHLTLTWQIKOLARILAVERYLKQ 590

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RESULT 23
ENV_HV1KB STANDARD; PRT; 861 AA.
AC P1819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.

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FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 865 AA; 97809 MW; 28828BC314ADCAC CRC64;

Query Match 92.4%; Score 171; DB 1; Length 865;
Best Local Similarity 89.5%; Pred. No. 7.9e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SNLLRAIEAQOHLTLTWQIKOLARILAVERYLKDQ 38
Db 562 NNLLRAIEAQOHLTLTWQIKOLARILAVERYLKDQ 599

RESULT 25
ENV_HV1J3 STANDARD; PRT; 867 AA.
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GPI60 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RX NCBI_TaxID=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; Pubmed=2669897;
RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria.";
RL AIDS Res. Hum. Retroviruses 5:411-419(1989).

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DR EMBL; M21138; EMB03526.1; -
DR HIV; M21138; EMB03526.1; -
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
FT SIGNAL 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
FT DISUFID 53 73 BY SIMILARITY.

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FT DISUFID 118 217 BY SIMILARITY.
FT DISUFID 125 208 BY SIMILARITY.
FT DISUFID 130 160 BY SIMILARITY.
FT DISUFID 230 259 BY SIMILARITY.
FT DISUFID 240 251 BY SIMILARITY.
FT DISUFID 308 342 BY SIMILARITY.
FT DISUFID 388 457 BY SIMILARITY.
FT DISUFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA; 98399 MW; 5F2310146BBE8680 CRC64;

Query Match 92.4%; Score 171; DB 1; Length 867;
Best Local Similarity 92.1%; Pred. No. 7.9e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNLLRAIEAQOHLTLTWQIKOLARILAVERYLKDQ 38
Db 564 NNLLRAIEAQOHLTLTWQIKOLARILAVERYLKDQ 601

RESULT 26
ENV_HV1C4 STANDARD; PRT; 868 AA.
AC P05879;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GPI60 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; Pubmed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
RN [2]
RP SEQUENCE OF 34-43.

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Query Match	Best Local Similarity	Score 171;	DB 1;	Length 868;	
Matches 35;	Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;
RA	Katlyanarman V.S., Rodriguez V., Veronese F., Rahman R., Russo P., Medlinarman V.S., Rodriguez V., Veronese F., Rahman R., Russo P., Devico A.L., Copeland T., Oroszian S., Gallo R.C., Sarsaghdaran M.G., "Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1."/	92.14%	Pred. No. 7.9e-16;		
RT	AIDS Res. Hum. Retroviruses 6:371-380(1990).				
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CC	or send an email to license@isb-sib.ch .				
CC	-----				
DR	EMBL; M13137; AAA44311.1; -.				
DR	PIR; C25523; VCLMH4.				
DR	HIV; M13137; ENV5CDD45.				
DR	Interpro; IPR000328; Env GP41.				
DR	Interpro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120.1.				
DR	Pfam; PF00517; GP41.1.				
KM	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL	1	33		
FT	CHAIN	34	522		
FT	CHAIN	523	868		
FT	DISULFID	55	75		
FT	DISULFID	120	216		
FT	DISULFID	127	207		
FT	DISULFID	132	163		
FT	DISULFID	229	258		
FT	DISULFID	239	250		
FT	DISULFID	307	341		
FT	DISULFID	387	456		
FT	DISULFID	394	429		
FT	CARBOHYD	89	89		
FT	CARBOHYD	131	131		
FT	CARBOHYD	138	138		
FT	CARBOHYD	139	139		
FT	CARBOHYD	142	142		
FT	CARBOHYD	162	162		
FT	CARBOHYD	166	166		
FT	CARBOHYD	195	195		
FT	CARBOHYD	198	198		
FT	CARBOHYD	208	208		
FT	CARBOHYD	245	245		
FT	CARBOHYD	252	252		
FT	CARBOHYD	273	273		
FT	CARBOHYD	287	287		
FT	CARBOHYD	300	300		
FT	CARBOHYD	306	306		
FT	CARBOHYD	312	312		
FT	CARBOHYD	342	342		
FT	CARBOHYD	349	349		
FT	CARBOHYD	365	365		
FT	CARBOHYD	371	371		
FT	CARBOHYD	395	395		
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FT	CARBOHYD	409	409		
FT	CARBOHYD	459	459		
FT	CARBOHYD	473	473		
FT	CARBOHYD	623	623		
FT	CARBOHYD	628	628		
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FT	CARBOHYD	649	649		
FT	CARBOHYD	828	828		
SO	SEQUENCE	868 AA;	98698 MM;	A11527FC52A6F0C8 CRC64;	

Oy	1	SUHLRAIEAQOHHLLQTLTWGCIKQLQARILLAVEVYLKQQ	38
	:	:	
Dd	565	NNLIRAIKAQHLLQTLTWGCIKQLQARILLAVEVYLKQQ	602
 RESULT 27			
ID	_ENV_HV1MA	STANDARD;	PRT; 859 AA.
AC	P04583;		
Dt	13-AUG-1987	(Rel. 05, Created)	
Dt	13-AUG-1987	(Rel. 05, Last sequence update)	
Dt	15-JUN-1999	(Rel. 38, Last annotation update)	
De	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
Gn	ENV.		
Os	Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).		
Oc	Viruses; Retrovirdae; Lentiviridae; Retroviridae; Lentivirus.		
Cx	NCBI_Taxid=11697;		
Rn	[1]		
Rp	SEQUENCE FROM N.A.		
Rx	MEDLINE=66245056; PubMed=242612;		
Ra	Allison M., Wain-Hobson S., Montagnier L., Soulgou P.;		
Rt	"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";		
Rl	Cell 46:63-74(1986).		
Cc	-----		
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Cc	-----		
Dr	EMBL; X04415; CAA28016.1; -		
Dr	EMBL; A07116; CAA00623.1; -		
Dr	PIR; T01672; T01672.		
Dr	HIV; K03456; ENV\$MAL.		
Dr	InterPro; IPR000328; Env_GP41.		
Dr	InterPro; IPR000777; GP120.		
Dr	Pfam; PF00516; GP120; 1.		
Dr	Pfam; PF00517; GP41; 1.		
Kw	AIDS; Coat protein; Polypeptidein; Glycoprotein; Transmembrane; Signal.		
Kw	Signal.		
Ft	FT SIGNAL	1	30
Ft	FT CHAIN	31	513
Ft	FT CHAIN	514	859
Ft	FT DISULFID	53	73
Ft	FT DISULFID	118	210
Ft	FT DISULFID	125	201
Ft	FT DISULFID	130	162
Ft	FT DISULFID	223	252
Ft	FT DISULFID	233	244
Ft	FT DISULFID	301	334
Ft	FT DISULFID	380	445
Ft	FT DISULFID	387	418
Ft	FT CARBOHYD	87	87
Ft	FT CARBOHYD	129	129
Ft	FT CARBOHYD	134	134
Ft	FT CARBOHYD	139	139
Ft	FT CARBOHYD	146	139
Ft	FT CARBOHYD	161	161
Ft	FT CARBOHYD	193	193
Ft	FT CARBOHYD	202	202
Ft	FT CARBOHYD	239	239
Ft	FT CARBOHYD	246	246
Ft	FT CARBOHYD	267	267
Ft	FT CARBOHYD	281	281
Ft	FT CARBOHYD	294	294
Ft	FT CARBOHYD	300	300
Ft	FT CARBOHYD	306	306
Ft	FT CARBOHYD	337	337
Ft	FT CARBOHYD	357	357
Ft	FT SIGNAL	1	30
Ft	FT CHAIN	31	513
Ft	FT CHAIN	514	859
Ft	FT DISULFID	53	73
Ft	FT DISULFID	118	210
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Ft	FT DISULFID	130	162
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Ft	FT DISULFID	233	244
Ft	FT DISULFID	301	334
Ft	FT DISULFID	380	445
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Ft	FT CARBOHYD	202	202
Ft	FT CARBOHYD	239	239
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Ft	FT CARBOHYD	294	294
Ft	FT CARBOHYD	300	300
Ft	FT CARBOHYD	306	306
Ft	FT CARBOHYD	337	337
Ft	FT CARBOHYD	357	357
Ft	FT SIGNAL	1	30
Ft	FT CHAIN	31	513
Ft	FT CHAIN	514	859
Ft	FT DISULFID	53	73
Ft	FT DISULFID	118	210
Ft	FT DISULFID	125	201
Ft	FT DISULFID	130	162
Ft	FT DISULFID	223	252
Ft	FT DISULFID	233	244
Ft	FT DISULFID	301	334
Ft	FT DISULFID	380	445
Ft	FT DISULFID	387	418
Ft	FT CARBOHYD	87	87
Ft	FT CARBOHYD	129	129
Ft	FT CARBOHYD	134	134
Ft	FT CARBOHYD	139	139
Ft	FT CARBOHYD	146	139
Ft	FT CARBOHYD	16	

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 859 AA; 97109 MW; DBCF9AAS23ABP29 CRC64;
 Query Match 91.8%; Score 170; DB 1; Length 859;
 Best Local Similarity 89.5%; Pred. No. 1, 1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 555 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLQDQ 592
 RESULT 28
 ENV_HV1W2 STANDARD; PRT; 847 AA.
 ID ENV_HV1W2
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86235450; Pubmed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.,
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
 at risk for AIDS."
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 CC WAS PERINATALLY INFECTED BY HER MOTHER.
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 CC -----
 CC EMBL: M12507; AAB12990.1; -
 DR HIV; M12507; ENVSMWJ2
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW signal.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
 FT DISULFID 379 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73AASBAC6 CRC64;
 Query Match 90.8%; Score 168; DB 1; Length 847;
 Best Local Similarity 86.8%; Pred. No. 2e-15;
 Matches 33; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 544 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLQDQ 581
 RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.
 ID ENV_HV1Z8
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; Pubmed=3395517;
 RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.,
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1."
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
 CC ZAIREAN MALE.
 CC -----
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 CC -----

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CC -----
DR EMBL; J03653; AAA44684.1; -.
DR HIV; J03653; ENV5JY1.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL. 1 29
FT CHAIN 30 518
FT CHAIN 53 863
FT DISULFID 53 73
FT DISULFID 118 217
FT DISULFID 125 208
FT DISULFID 130 160
FT DISULFID 230 259
FT DISULFID 240 251
FT DISULFID 308 342
FT DISULFID 388 452
FT DISULFID 395 425
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FT CARBOHYD 129 129
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FT CARBOHYD 142 142
FT CARBOHYD 143 143
FT CARBOHYD 159 159
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FT CARBOHYD 455 455
FT CARBOHYD 468 468
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FT CARBOHYD 472 472
FT CARBOHYD 618 618
FT CARBOHYD 623 623
FT CARBOHYD 632 632
FT CARBOHYD 644 644
FT CARBOHYD 823 823
SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FD1641 CRC64;

Query Match 89.7%; Score 166; DB 1; Length 863;
Best Local Similarity 86.8%; Pred. No. 3.9e-15;
Matches 33; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNLLRAEQOHLLQTLVMOIKOLARILIAVERLYKXQ 38
Db 560 NNLRLRAEQOHMLQLTWGKIQOLARVAVESLYKXQ 597

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OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; Pubmed=2789516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RA Dandekar S.;
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia.";
RL Virology 168:79-89(1989).
CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M21098; AAA44221.1; -.
CC PIR; A31677; VCLJBR.
DR PDB; 1HW7; 23-OCT-02.
DR HIV; M21098; ENV5BRVA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL. 1 30
FT CHAIN 31 507
FT CHAIN 508 852
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 155
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 330
FT DISULFID 376 439
FT DISULFID 383 412
FT DISULFID 49 49
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FT CARBOHYD 154 154
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FT CARBOHYD 400 400
FT CARBOHYD 442 442
FT CARBOHYD 456 456
FT CARBOHYD 607 607
FT CARBOHYD 612 612
FT CARBOHYD 621 621
FT CARBOHYD 633 633
FT CARBOHYD 670 670

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FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match
Best Local Similarity 88.1%; Score 163; DB 1; Length 852;
Matches 32; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDO 38
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 549 NNLLMAIEAQOHLQLTWQIKQLQARILAVERYLKDO 586

Search completed: June 2, 2004, 11:42:59
Job time: 7.19565 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 31.9076 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-542
Perfect score: 185
Sequence: 1 SNLRAIEAQOHLQUTWQIKQIQARIIAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	96.8	852	15	Q8UJ55 human immun
2	178	96.2	131	15	Q7SM43 human immun
3	178	96.2	145	15	Q7ZC52 human immun
4	178	96.2	173	15	Q8UJW9 human immun
5	178	96.2	826	15	Q9DVL1 human immun
6	178	96.2	845	15	Q9ID89 human immun
7	178	96.2	859	15	Q9WUJ1 human immun
8	178	96.2	866	15	Q9WPZ4 human immun
9	178	96.2	870	15	Q8Q2X1 human immun
10	178	96.2	870	15	Q8Q2X0 human immun
11	177	95.7	113	15	Q7ZC55 human immun
12	177	95.7	133	15	Q8UQZ6 human immun
13	177	95.7	133	15	Q8UQZ7 human immun
14	177	95.7	133	15	Q8UQZ8 human immun
15	177	95.7	133	15	Q8UQZ4 human immun
16	177	95.7	133	15	Q8UQZ3 human immun

17	177	95.7	134	15	Q9IWK6 human immun
18	177	95.7	137	15	Q9DQW0 human immun
19	177	95.7	142	15	Q9IWK3 human immun
20	177	95.7	143	15	Q9IWK1 human immun
21	177	95.7	143	15	Q7ZC46 human immun
22	177	95.7	144	15	Q9IWK4 human immun
23	177	95.7	144	15	Q7ZC66 human immun
24	177	95.7	144	15	Q7ZC68 human immun
25	177	95.7	144	15	Q7ZC45 human immun
26	177	95.7	145	15	Q7ZC53 human immun
27	177	95.7	145	15	Q7ZC51 human immun
28	177	95.7	145	15	Q7ZC50 human immun
29	177	95.7	145	15	Q7ZC47 human immun
30	177	95.7	145	15	Q7ZC44 human immun
31	177	95.7	145	15	Q7ZC34 human immun
32	177	95.7	145	15	Q7ZC32 human immun
33	177	95.7	155	15	Q8UJ3R0 human immun
34	177	95.7	188	15	Q8UJAL1 human immun
35	177	95.7	199	15	Q8UJAL3 human immun
36	177	95.7	543	15	Q9YUY7 human immun
37	177	95.7	607	15	P88161 human immun
38	177	95.7	621	15	Q9OVE9 human immun
39	177	95.7	781	15	Q70159 human immun
40	177	95.7	783	15	Q9BXX4 human immun
41	177	95.7	788	15	Q9BXY6 human immun
42	177	95.7	790	15	Q9BXY4 human immun
43	177	95.7	791	15	Q9BXY1 human immun
44	177	95.7	795	15	Q9BXX6 human immun
45	177	95.7	798	15	Q9BXX3 human immun
46	177	95.7	800	15	Q9BXY1 human immun
47	177	95.7	801	15	Q9BXY7 human immun
48	177	95.7	801	15	Q9BXY7 human immun
49	177	95.7	804	15	Q9BXY7 human immun
50	177	95.7	829	15	Q76122 human immun
51	177	95.7	840	15	Q9QNX7 human immun
52	177	95.7	844	15	Q9QNX2 human immun
53	177	95.7	845	15	Q41797 human immun
54	177	95.7	846	15	Q89292 human immun
55	177	95.7	847	15	Q8Q854 human immun
56	177	95.7	848	15	Q76123 human immun
57	177	95.7	849	15	Q9PXX0 human immun
58	177	95.7	849	15	Q9YUY1 human immun
59	177	95.7	849	15	Q7ZUJ1 human immun
60	177	95.7	849	15	Q7SV13 human immun
61	177	95.7	850	15	Q70003 human immun
62	177	95.7	850	15	O11946 human immun
63	177	95.7	850	15	Q9WLG7 human immun
64	177	95.7	851	15	Q73361 human immun
65	177	95.7	851	15	O56562 human immun
66	177	95.7	851	15	Q73365 human immun
67	177	95.7	852	15	Q8UL54 human immun
68	177	95.7	852	15	Q76120 human immun
69	177	95.7	853	15	Q9YMY8 human immun
70	177	95.7	853	15	Q70018 human immun
71	177	95.7	853	15	Q9WBT5 human immun
72	177	95.7	853	15	Q9YUY6 human immun
73	177	95.7	854	15	Q70020 human immun
74	177	95.7	854	15	Q9DKG6 human immun
75	177	95.7	854	15	Q9IJ29 human immun
76	177	95.7	855	15	Q9YUY3 human immun
77	177	95.7	855	15	Q9YUY3 human immun
78	177	95.7	855	15	Q9E1R7 human immun
79	177	95.7	855	15	Q99C05 human immun
80	177	95.7	855	15	Q99C05 human immun
81	177	95.7	856	15	Q9YUY5 human immun
82	177	95.7	856	15	Q9YUY4 human immun
83	177	95.7	857	15	Q80192 human immun
84	177	95.7	857	15	Q9OVG5 human immun
85	177	95.7	857	15	Q9QML6 human immun
86	177	95.7	857	15	Q9OV58 human immun
87	177	95.7	857	15	Q97065 human immun
88	177	95.7	857	15	Q9YUY2 human immun
89	177	95.7	857	15	Q8QY00 human immun
90	177	95.7	857	15	Q8UJ12 human immun

90 177 95.7 857 15 Q7ZL08 Q7ZL08 human immun
ALIGNMENTS

RESULT 1

Q8UL55 PRELIMINARY; PRT; 852 AA.
AC Q8UL55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp160 protein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;
RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells
RT and Herpesvirus satmmit transformed T-cells is comparable.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418531; CAD10941.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR KEGG; K00001; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 852 AA; 96711 MW; 57D8CA06A42371F CRC64;

Query Match 96.8%; Score 179; DB 15; Length 852;
Best Local Similarity 94.7%; Pred. No. 3.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 548 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 585

RESULT 2

Q7SM43 PRELIMINARY; PRT; 131 AA.
AC Q7SM43;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529973; AB87704.1; -
KW Envelope protein.
FT NON TER 131 131
FT NON TER 131 131
SQ SEQUENCE 131 AA; 15539 MW; C1BA4FEFEB1A860F CRC64;

Query Match 96.2%; Score 178; DB 15; Length 131;
Best Local Similarity 97.4%; Pred. No. 6.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 11 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 48

RESULT 3

Q7ZC52 PRELIMINARY; PRT; 145 AA.
AC Q7ZC52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Derou S., Fischer A., Baurith T.;
RT "Roman F., Boule R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185468; AAC65743.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
DR KEGG; K00001; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 145 145
FT NON TER 145 145
SQ SEQUENCE 145 AA; 17020 MW; AC8C32E97B09D1A1 CRC64;

Query Match 96.2%; Score 178; DB 15; Length 145;
Best Local Similarity 97.4%; Pred. No. 7.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 22 SNLLRAIEAQHLLQLTWQIKOLQARILAVERYLKQ 59

RESULT 4

Q8JAJ9 PRELIMINARY; PRT; 173 AA.
AC Q8JAJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Galimzaev M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463445; AA90821.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON TER 1 1
 RT
 SO SEQUENCE 173 AA; 19858 MW; 300D69C94C03AD14 CRC64;

Query Match 96.2%; Score 178; DB 15; Length 173;
 Best Local Similarity 97.4%; Pred. No. 8.5e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQTLTWQIKOLQARIILAVERYLKQ 38
 |||
 Db 56 SNLRAIEAQHLLQTLTWGIGIKOLQARIILAVERYLKQ 93

RESULT 5
 Q9DVL1 PRELIMINARY; PRT; 826 AA.

AC Q9DVL1; 16; Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DE Envelope protein (Fragment).
 GN ENV OR GP160.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzambi N., Robertson D.,
 Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.,
 "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
 group M genetic diversity in the Democratic Republic of Congo suggests
 that the HIV-1 pandemic originated in Central Africa."
 J. Virol. 74:10498-10507(2000).
 EMBL: AJ401042; CAC15050.1; -

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON TER 1 1
 RT
 SO SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;

Query Match 96.2%; Score 178; DB 15; Length 826;
 Best Local Similarity 97.4%; Pred. No. 4.3e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQTLTWQIKOLQARIILAVERYLKQ 38
 |||
 Db 540 SNLRAIEAQHLLQTLTWGIGIKOLQARIILAVERYLKQ 577

RESULT 6
 Q9IDB9 PRELIMINARY; PRT; 845 AA.

AC Q9IDB9; 15; Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DE ENV protein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

Qy 1 SNLRAIEAQHLLQTLTWQIKOLQARIILAVERYLKQ 38
 |||
 Db 556 SNLRAIEAQHLLQTLTWGIGIKOLQARIILAVERYLKQ 593

RP SEQUENCE FROM N.A.
 RC STRAIN=95127;
 RA Montavon C., Delaporte E., Peeters M.,
 RT "Two new complete genomes of HIV-1 recombinant AGJ BP90-like
 circulating in Mali and Senegal."
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ288982; CAB98175.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 845 AA; 95239 MW; 39439B37713EBD2A CRC64;

Query Match 96.2%; Score 178; DB 15; Length 845;
 Best Local Similarity 97.4%; Pred. No. 4.4e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQTLTWQIKOLQARIILAVERYLKQ 38
 |||
 Db 542 SNLRAIEAQHLLQTLTWGIGIKOLQARIILAVERYLKQ 579

RESULT 7
 Q9WLU1 PRELIMINARY; PRT; 859 AA.

AC Q9WLU1; 12; Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzambi N., Robertson D.,
 Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.,
 "Unprecedented degree of human immunodeficiency virus type 1 (HIV-1)
 group M genetic diversity in the Democratic Republic of Congo suggests
 that the HIV-1 pandemic originated in Central Africa."
 J. Virol. 74:10498-10507(2000).
 EMBL: AJ401042; CAC15050.1; -

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 859 AA; 96504 MW; 41B85F110C38E0C CRC64;

Query Match 96.2%; Score 178; DB 15; Length 859;
 Best Local Similarity 97.4%; Pred. No. 4.4e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQTLTWQIKOLQARIILAVERYLKQ 38
 |||
 Db 556 SNLRAIEAQHLLQTLTWGIGIKOLQARIILAVERYLKQ 593

RESULT 8

Q9MPZ4 PRELIMINARY; PRT; 866 AA.

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Envelope protein.

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99236722; PubMed=10221533;

RA Quinman G.V., Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;

RT "Expression and characterization of HIV type 1 envelope protein associated with a broadly reactive neutralizing antibody response.";

RL AIDS Res. Hum. Retroviruses 15:561-570(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Quinman G.V., Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF128126; AAD40637.2; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SO SEQUENCE 866 AA; 98081 MW; 44D9329789833122 CRC64;

QY 1 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 38

DB 562 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 599

Query Match 96.2%; Score 178; DB 15; Length 866;

Best Local Similarity 97.4%; Pred. No. 4.5e-16;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

Q8Q2X1 PRELIMINARY; PRT; 870 AA.

AC Q8Q2X1;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Envelope glycoprotein.

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Gorry P.R., Taylor J., Holm G., Menle A., Morgan T., Cayabyab M., Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P., Molinsky S.M., Gabuzda D.;

RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a neurovirulent primary human immunodeficiency virus type 1 isolate.";

RL J. Virol. 0:0-0(2002).

RN EMBL; AF491741; AAM09794.1; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SO SEQUENCE 870 AA; 99067 MW; 067C44F6526160DF CRC64;

QY 1 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 38

DB 567 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 604

Query Match 96.2%; Score 178; DB 15; Length 870;

Best Local Similarity 97.4%; Pred. No. 4.5e-16;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10

Q8Q2X0 PRELIMINARY; PRT; 870 AA.

AC Q8Q2X0;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Envelope glycoprotein.

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Gorry P.R., Taylor J., Holm G., Menle A., Morgan T., Cayabyab M., Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P., Molinsky S.M., Gabuzda D.;

RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a neurovirulent primary human immunodeficiency virus type 1 isolate.";

RL J. Virol. 0:0-0(2002).

RN EMBL; AF491742; AAM09795.1; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SO SEQUENCE 870 AA; 98932 MW; 924EB3A64FD6A9B1 CRC64;

QY 1 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 38

DB 567 SNLLRAIEAQOHLLQTLTWGIKQLQARILAVERYLKQ 604

Query Match 96.2%; Score 178; DB 15; Length 870;

Best Local Similarity 97.4%; Pred. No. 4.5e-16;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11

Q7ZCES PRELIMINARY; PRT; 113 AA.

AC Q7ZCES;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX48-2;

RA Roman F., Gonzalez D., Lambert C., Derco S., Fischer A., Baurich T., Staub T., Boule R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;

RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naïve patients infected with subtype B

RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185375; AA065650.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12955 MW; 70A54C05D4C06225 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 113;
Best Local Similarity 94.7%; Pred. No. 7.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 24 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 61

RESULT 12
Q8UQZ6 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=002M148F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fidel U., Chen Y., Meleth S., Kasolo F.,
Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia.";
RL J. Virol. 76:397-405(2002).
RL EMBL: AF405152; AAL6672.1; -
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 16145 MW; 6DBD34C92AFDA77D CRC64;

Query Match 95.7%; Score 177; DB 15; Length 133;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38

RESULT 13
Q8UQZ7 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98ZM091F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fidel U., Chen Y., Meleth S., Kasolo F.,
Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia.";
RL J. Virol. 76:397-405(2002).
RL EMBL: AF405151; AAL6671.1; -
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 16143 MW; B2BD0FB5DDCA7A9 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 133;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38

RESULT 14
Q8UQZ8 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98ZM091M;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fidel U., Chen Y., Meleth S., Kasolo F.,
Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia.";
RL J. Virol. 76:397-405(2002).
RL EMBL: AF405150; AAL6670.1; -
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 16125 MW; 0A68876413C8D56 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 133;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38

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RESULT 15
Q8UQZ4 PRELIMINARY; PRT; 133 AA.
ID Q8UQZ4
AC Q8UQZ4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=98ZM043M;
MEDLINE=21602569; PubMed=11739704;
RA Traak S.A., Deteyn C.A., Fidele U., Chen Y., Meleth S., Kasolo F.,
  Nwonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
  transmission in a heterosexual cohort of discordant couples in
  Zambia."
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405154; AL66674.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1 1
FT TER 133 133
SQ SEQUENCE 133 AA; 16057 MW; 6650D8E2480703B0 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 133;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 16
Q8UQZ3 PRELIMINARY; PRT; 133 AA.
ID Q8UQZ3
AC Q8UQZ3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=97ZM043F;
MEDLINE=21602569; PubMed=11739704;
RA Traak S.A., Deteyn C.A., Fidele U., Chen Y., Meleth S., Kasolo F.,
  Nwonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
  transmission in a heterosexual cohort of discordant couples in
  Zambia."
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405155; AL66675.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1 1
FT TER 133 133
SQ SEQUENCE 133 AA; 15361 MW; EA6E5DPE360A0322 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 134;
Best Local Similarity 94.7%; Pred. No. 9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 8 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 45

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FT NON_TER 133 133
SQ SEQUENCE 133 AA; 16058 MW; 665E360246E9B3B0 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 133;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 17
Q9IWQ6 PRELIMINARY; PRT; 134 AA.
ID Q9IWQ6
AC Q9IWQ6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=85CD260;
MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
  Colebunders R.C., St Louis M., Quinn T.C., Polke T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
  from Kinshasa, Democratic Republic of Congo."
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260470; AAF71937.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1 1
FT TER 134 134
SQ SEQUENCE 134 AA; 15361 MW; EA6E5DPE360A0322 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 134;
Best Local Similarity 94.7%; Pred. No. 9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 8 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 45

RESULT 18
Q9DQW0 PRELIMINARY; PRT; 137 AA.
ID Q9DQW0
AC Q9DQW0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SP-M1270;
MEDLINE=20584646; PubMed=1153079;
RA Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorrugino A.,
  Vadiillo J., Salas A., Moreno A., Garcia-Saiz A.;
RT "Molecular characterization of Non-B HIV Type 1 Subtypes from Africa
  in Spain."

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RL AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
DR EMBL: AF255938; AAG36893.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 16458 MW; 94CED7A1B23984C1 CRC64;
Query Match 95.7%; Score 177; DB 15; Length 137;
Best Local Similarity 94.7%; Pred. No. 9.2e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 9 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 46
RESULT 19
Q91WQ3 PRELIMINARY; PRT; 142 AA.
AC Q91WQ3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD357;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Prevalence of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo."
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL: AF260473; AAF71940.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 17007 MW; 8E8CC29B047698E CRC64;
Query Match 95.7%; Score 177; DB 15; Length 142;
Best Local Similarity 94.7%; Pred. No. 9.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 9 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 46
RESULT 20
Q91WQ1 PRELIMINARY; PRT; 143 AA.
AC Q91WQ1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD350;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Prevalence of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo."
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL: AF260475; AAF71942.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 17160 MW; DB157A905740B24E CRC64;
Query Match 95.7%; Score 177; DB 15; Length 143;
Best Local Similarity 94.7%; Pred. No. 9.6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 9 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 46
RESULT 21
Q7ZC46 PRELIMINARY; PRT; 143 AA.
ID Q7ZC46;
AC Q7ZC46;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HR1DX24;
RA Roman F., Gonzalez D., Lambert C., Deroc S., Fischer A., Baurith T.,
RA Staud T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;
RT "Uncommon mutations at residue positions critical for envutritide (T-
RT 20) resistance in envutritide-naïve patients infected with B and non-B
RT subtype HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185474; AAO65749.1; -
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16723 MW; 5B64B9D8DB8B05D CRC64;
Query Match 95.7%; Score 177; DB 15; Length 143;
Best Local Similarity 94.7%; Pred. No. 9.6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 38
Db 22 SNLLRAIEAQOHLQLTWGIKQLQARVLAVERYLKQ 59
RESULT 22
Q91WQ4 PRELIMINARY; PRT; 144 AA.
ID Q91WQ4

AC 091W04;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD32;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Ntambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folke T.M., Lai R.B.,
RT "Prevalence of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo."
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260472; AF71939.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 17350 MW; 57EF59A42C6441D8 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 144;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 38
Db 10 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 47

RESULT 23
07ZCE6 PRELIMINARY; PRT; 144 AA.
AC 07ZCE6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLIX48-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185374; AA06569.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16841 MW; 716AC7C07B46CF90 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 144;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 38
Db 24 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 61

RESULT 24
07ZCD8 PRELIMINARY; PRT; 144 AA.
AC 07ZCD8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLIX52-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185382; AA065657.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16795 MW; 23E382827E63D165 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 144;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 38
Db 24 SNLRAIEAQOHLLQTLTWGIKQLQARVLAVERYLKQ 61

RESULT 25
07ZC45 PRELIMINARY; PRT; 144 AA.
AC 07ZC45;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLIX25;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
subtype HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185475; AA065750.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144

FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16887 MW; 7E4C6B67D343B8 CRC64;
Query Match
Best Local Similarity 95.7%; Score 177; DB 15; Length 144;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 22 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 59
RESULT 26
Q7ZC53 PRELIMINARY; PRT; 145 AA.
ID Q7ZC53
AC Q7ZC53;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX17;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with B and non-B
subtype HIV-1.";
RT subType HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185467; AAO65742.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
DR Envelope protein.
KM NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 17105 MW; 97E2D3C5036A8C9 CRC64;
Query Match
Best Local Similarity 95.7%; Score 177; DB 15; Length 145;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 22 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 59
RESULT 27
Q7ZC51 PRELIMINARY; PRT; 145 AA.
ID Q7ZC51
AC Q7ZC51;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX19;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with B and non-B
subtype HIV-1.";
RT subType HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY185469; AAO65744.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
DR Envelope protein.
KM NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16964 MW; F5290FBCAF33DEA2 CRC64;
Query Match
Best Local Similarity 95.7%; Score 177; DB 15; Length 145;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 22 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 59
RESULT 28
Q7ZC50 PRELIMINARY; PRT; 145 AA.
ID Q7ZC50
AC Q7ZC50;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX20;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmitz J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with B and non-B
subtype HIV-1.";
RT subType HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185470; AAO65745.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
DR Envelope protein.
KM NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16971 MW; FA8CED8CAF33DEA2 CRC64;
Query Match
Best Local Similarity 95.7%; Score 177; DB 15; Length 145;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 22 SNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 59
RESULT 29
Q7ZC47 PRELIMINARY; PRT; 145 AA.
ID Q7ZC47
AC Q7ZC47;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=HRLUX23;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurilh T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
RT subtype HIV-1."
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY185473; AA065748.1; -.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 17062 MW; 05BFA1F6ACD23F99 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 145;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 22 SNLLRAIEAQOHLQLTWGIGIKQLQARVLAVERYLKDQ 59

RESULT 30
ID 07ZC44 PRELIMINARY; PRT; 145 AA.
AC 07ZC44;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX26;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurilh T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with B and non-B
RT subtype HIV-1."
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY185476; AA065751.1; -.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 17076 MW; 339BEDCBACD2373 CRC64;

Query Match 95.7%; Score 177; DB 15; Length 145;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 22 SNLLRAIEAQOHLQLTWGIGIKQLQARVLAVERYLKDQ 59

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Search completed: June 2, 2004, 11:48:24
 Job time : 34.9076 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 14.0435 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-542
Perfect score: 185
Sequence: 1 SNLRAIEAQHLLQLTWQIKOLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/2/iaa/6A COMB .pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB .pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB .pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1 .pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	182	98.4	38	4	US-08-973-952-82	Sequence 82, App1
2	177	95.7	198	3	US-08-965-056-97	Sequence 97, App1
3	177	95.7	198	3	US-08-965-056-98	Sequence 97, App1
4	177	95.7	198	3	US-08-965-056-101	Sequence 101, App1
5	177	95.7	268	3	US-08-965-056-39	Sequence 39, App1
6	177	95.7	269	3	US-08-965-056-24	Sequence 24, App1
7	177	95.7	269	3	US-08-965-056-96	Sequence 96, App1
8	175	94.6	38	1	US-08-374-666-1	Sequence 1, App1
9	175	94.6	38	3	US-08-486-099-89	Sequence 89, App1
10	175	94.6	38	3	US-08-360-107A-99	Sequence 99, App1
11	175	94.6	38	3	US-08-360-107A-132	Sequence 132, App1
12	175	94.6	38	3	US-08-484-223B-89	Sequence 89, App1
13	175	94.6	38	3	US-08-919-597-89	Sequence 89, App1
14	175	94.6	38	3	US-08-475-668A-89	Sequence 89, App1
15	175	94.6	38	3	US-08-485-551A-89	Sequence 89, App1
16	175	94.6	38	3	US-08-471-913A-89	Sequence 89, App1
17	175	94.6	38	3	US-08-485-264A-89	Sequence 89, App1
18	175	94.6	38	3	US-08-082-279B-16	Sequence 16, App1
19	175	94.6	38	3	US-09-082-279B-507	Sequence 507, App1
20	175	94.6	38	3	US-09-082-279B-604	Sequence 604, App1
21	175	94.6	38	4	US-08-474-349A-89	Sequence 89, App1
22	175	94.6	38	4	US-08-474-349A-441	Sequence 441, App1
23	175	94.6	38	4	US-09-315-304B-16	Sequence 16, App1
24	175	94.6	38	4	US-09-315-304B-507	Sequence 507, App1
25	175	94.6	38	4	US-09-315-304B-604	Sequence 604, App1
26	175	94.6	38	4	US-08-255-208A-25	Sequence 25, App1
27	175	94.6	38	4	US-08-470-896-89	Sequence 89, App1

28	175	94.6	38	4	US-08-485-546A-89	Sequence 89, App1
29	175	94.6	38	4	US-09-796-202-11	Sequence 11, App1
30	175	94.6	38	4	US-09-834-784-16	Sequence 16, App1
31	175	94.6	38	4	US-09-834-784-507	Sequence 507, App1
32	175	94.6	38	4	US-09-834-784-604	Sequence 604, App1
33	175	94.6	38	4	US-08-464-003-1	Sequence 1, App1
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35	175	94.6	38	4	US-09-515-965A-16	Sequence 16, App1
36	175	94.6	38	4	US-09-515-965A-507	Sequence 507, App1
37	175	94.6	38	4	US-09-515-965A-604	Sequence 604, App1
38	175	94.6	38	4	US-09-350-641C-16	Sequence 16, App1
39	175	94.6	38	4	US-09-350-641C-507	Sequence 507, App1
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41	175	94.6	41	1	US-08-073-028-8	Sequence 3, App1
42	175	94.6	41	1	US-08-374-666-9	Sequence 9, App1
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44	175	94.6	41	3	US-08-486-099-8	Sequence 8, App1
45	175	94.6	41	3	US-08-360-107A-8	Sequence 8, App1
46	175	94.6	41	3	US-08-484-223B-8	Sequence 8, App1
47	175	94.6	41	3	US-08-484-223B-242	Sequence 242, App1
48	175	94.6	41	3	US-08-484-223B-243	Sequence 243, App1
49	175	94.6	41	3	US-08-919-597-8	Sequence 8, App1
50	175	94.6	41	3	US-08-475-668A-8	Sequence 8, App1
51	175	94.6	41	3	US-08-485-551A-8	Sequence 8, App1
52	175	94.6	41	3	US-08-471-913A-8	Sequence 8, App1
53	175	94.6	41	3	US-08-554-616-8	Sequence 8, App1
54	175	94.6	41	3	US-08-485-264A-8	Sequence 8, App1
55	175	94.6	41	3	US-09-082-279B-496	Sequence 496, App1
56	175	94.6	41	3	US-09-082-279B-601	Sequence 601, App1
57	175	94.6	41	3	US-09-082-279B-633	Sequence 633, App1
58	175	94.6	41	3	US-09-082-279B-1163	Sequence 1163, App1
59	175	94.6	41	4	US-08-474-349A-8	Sequence 8, App1
60	175	94.6	41	4	US-09-315-304B-496	Sequence 496, App1
61	175	94.6	41	4	US-09-315-304B-601	Sequence 601, App1
62	175	94.6	41	4	US-09-315-304B-633	Sequence 633, App1
63	175	94.6	41	4	US-09-315-304B-1163	Sequence 1163, App1
64	175	94.6	41	4	US-08-255-208A-8	Sequence 8, App1
65	175	94.6	41	4	US-08-973-952-8	Sequence 8, App1
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67	175	94.6	41	4	US-08-485-546A-8	Sequence 8, App1
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70	175	94.6	41	4	US-09-834-784-633	Sequence 633, App1
71	175	94.6	41	4	US-09-834-784-1163	Sequence 1163, App1
72	175	94.6	41	4	US-08-464-003-9	Sequence 9, App1
73	175	94.6	41	4	US-08-464-003-9	Sequence 9, App1
74	175	94.6	41	4	US-09-515-965A-496	Sequence 496, App1
75	175	94.6	41	4	US-09-515-965A-601	Sequence 601, App1
76	175	94.6	41	4	US-09-515-965A-633	Sequence 633, App1
77	175	94.6	41	4	US-09-515-965A-1163	Sequence 1163, App1
78	175	94.6	41	4	US-09-350-641C-496	Sequence 496, App1
79	175	94.6	41	4	US-09-350-641C-601	Sequence 601, App1
80	175	94.6	41	4	US-09-350-641C-633	Sequence 633, App1
81	175	94.6	41	4	US-09-350-641C-1163	Sequence 1163, App1
82	175	94.6	44	1	US-08-374-666-10	Sequence 10, App1
83	175	94.6	44	1	US-08-464-003-10	Sequence 10, App1
84	175	94.6	45	3	US-09-082-279B-1164	Sequence 1164, App1
85	175	94.6	45	4	US-09-315-304B-1164	Sequence 1164, App1
86	175	94.6	45	4	US-09-834-784-1164	Sequence 1164, App1
87	175	94.6	45	4	US-09-779-451-9	Sequence 9, App1
88	175	94.6	45	4	US-09-515-965A-1164	Sequence 1164, App1
89	175	94.6	45	4	US-09-350-641C-1164	Sequence 1164, App1
90	175	94.6	49	4	US-09-796-202-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-08-973-952-82
Sequence 82, Application US/08973952A
Patent No. 6475491
GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTION
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973.952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 98.4%; Score 182; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 9.6e-19;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38

RESULT 2

US-08-965-056-97
Sequence 97, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/952-9881
TELEFAX: 650/225-8674
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-97

Query Match 95.7%; Score 177; DB 3; Length 198;
Best Local Similarity 94.7%; Pred. No. 3.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 120

RESULT 3

US-08-965-056-98
Sequence 98, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/952-9881
TELEFAX: 650/225-8674
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-98

Query Match 95.7%; Score 177; DB 3; Length 198;
Best Local Similarity 94.7%; Pred. No. 3.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 83 SNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 120

RESULT 4

US-08-965-056-101
Sequence 101, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/952-9881
TELEFAX: 650/225-8674
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-101

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-965-056-101

Query Match 95.7%; Score 177; DB 3; Length 198;
Best Local Similarity 94.7%; Pred. No. 3.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 83 SNLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 120

RESULT 5
US-08-965-056-39
Sequence 39, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovaanik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-965-056-39

Query Match 95.7%; Score 177; DB 3; Length 268;
Best Local Similarity 94.7%; Pred. No. 4.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 83 SNLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 120

RESULT 6
US-08-965-056-24
Sequence 24, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovaanik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-965-056-24

Query Match 95.7%; Score 177; DB 3; Length 269;
Best Local Similarity 94.7%; Pred. No. 4.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 84 SNLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 121

RESULT 7

US-08-965-056-96
; Sequence 96, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPac (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-NO. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-96

Query Match 95.7%; Score 177; DB 3; Length 269;
Best Local Similarity 94.7%; Pred. No. 4.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 84 SNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 121

RESULT 8
US-08-374-666-1
; Sequence 1, Application US/08374666
; Patent No. 5656480
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Biolognesi, Dani P.
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,666
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-374-666-1

Query Match 94.6%; Score 175; DB 1; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 SNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 9
US-08-486-099-89
; Sequence 89, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Biolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38
DB 1 NNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38

RESULT 10
US-08-360-107A-99

Sequence 99, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-99

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38
DB 1 NNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38

RESULT 11
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-132

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38
DB 1 NNLRAIEAQOHLLQLTWQIKQLQARILLAVERTLKQ 38

RESULT 12
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38
1 NMLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 13
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 SNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38
1 NMLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 14
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 15
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 16
US-08-471-913A-89

Sequence 89, Application US/08471913A
Patent No. 6093794

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 17
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRLAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 18
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Wierucka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRLAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 19
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Wierucka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRLAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 20
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Wierucka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match 94.6%; Score 175; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRLAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 21
US-08-474-349A-89
Sequence 89, Application US/08474349A

Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38

RESULT 22
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38

RESULT 23
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PatsSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLTLTWQIKQLQARILAVERYLKQ 38

Db 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38

RESULT 24

US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Lamber, M.
APPLICANT: Lamber, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-507

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Gaps 0;

Qy 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38
Db 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38

RESULT 25

US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Lamber, M.
APPLICANT: Lamber, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Gaps 0;

Qy 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38
Db 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38

RESULT 26

US-08-255-208A-25
Sequence 25, Application US/08255208A
Patent No. 6440656
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lamber, Dennis M.
APPLICANT: Petteway, Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1994
APPLICATION NUMBER: US/08/255,208A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Gaps 0;

Qy 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38
Db 1>NNLRAIEAQOHLTLTWGIGIKOLQARILAVERYLKQ 38

RESULT 27

US-08-470-896-89
Sequence 89, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lamber, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 273

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036-2711
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,896
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7872-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 89:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;;
;; US-08-470-896-89
;;
Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
;
RESULT 28
US-08-485-546A-89
; Sequence 89, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995

;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7872-028
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 89:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;;
;; US-08-485-546A-89
;;
Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
;
RESULT 29
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olsom, William
; TITLE OF INVENTION: SUBSTITUTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
;;
US-09-796-202-11
;
Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 SNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARILLAVERYLKQ 38
;
RESULT 30
US-09-834-784-16
; Sequence 16, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784

; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 94.6%; Score 175; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.1e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRRAIEAQQHLLQLTWGKIQARILAVERYLKDQ 38
:|||||
Db 1 NNLRRAIEAQQHLLQLTWGKIQARILAVERYLKDQ 38

Search completed: June 2, 2004, 11:52:40
Job time : 13.0435 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 2, 2004, 11:48:34 ; Search time 35.0054 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-542
Perfect score: 185
Sequence: 1 SNLRAIEAQHLLQITWQIKQLQARILAVERYLKXQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PTCTUS_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	98.4	38	14	US-10-252-136-82
2	177	95.7	198	9	US-09-854-816-97
3	177	95.7	198	9	US-09-854-816-98
4	177	95.7	198	9	US-09-854-816-101
5	177	95.7	268	9	US-09-854-816-39
6	177	95.7	268	9	US-09-854-816-24
7	177	95.7	268	9	US-09-854-816-96
8	177	95.7	651	12	US-10-296-734-8
9	176	95.1	860	14	US-10-190-435-145
10	176	95.1	860	14	US-10-190-435-146
11	175	94.6	38	9	US-09-796-302-11
12	175	94.6	38	9	US-09-779-451-2
13	175	94.6	38	10	US-09-933-346-2
14	175	94.6	38	12	US-10-267-682-89
15	175	94.6	38	12	US-10-267-748-89

16	175	94.6	38	12	US-09-809-060-6	Sequence 6, App1
17	175	94.6	38	12	US-09-809-060-7	Sequence 7, App1
18	175	94.6	38	12	US-10-663-589-3	Sequence 3, App1
19	175	94.6	38	12	US-10-681-879-2	Sequence 2, App1
20	175	94.6	38	12	US-09-828-615-2	Sequence 2, App1
21	175	94.6	38	14	US-10-116-797-2	Sequence 2, App1
22	175	94.6	38	14	US-10-323-314-11	Sequence 11, App1
23	175	94.6	38	14	US-10-414-192-1	Sequence 1, App1
24	175	94.6	38	14	US-10-351-641-16	Sequence 16, App1
25	175	94.6	38	14	US-10-351-641-507	Sequence 507, App
26	175	94.6	38	14	US-10-351-641-604	Sequence 604, App
27	175	94.6	38	15	US-10-005-305-165	Sequence 165, App
28	175	94.6	38	15	US-10-005-305-202	Sequence 202, App
29	175	94.6	38	15	US-10-005-305-203	Sequence 203, App
30	175	94.6	38	15	US-10-420-194-1234	Sequence 1234, App
31	175	94.6	38	16	US-10-664-021-2	Sequence 2, App1
32	175	94.6	38	16	US-10-671-316-2	Sequence 2, App1
33	175	94.6	41	12	US-10-267-682-8	Sequence 8, App1
34	175	94.6	41	12	US-10-267-748-8	Sequence 8, App1
35	175	94.6	41	12	US-10-663-589-30	Sequence 30, App1
36	175	94.6	41	12	US-10-663-589-33	Sequence 33, App1
37	175	94.6	41	12	US-10-663-589-35	Sequence 35, App1
38	175	94.6	41	14	US-10-252-136-8	Sequence 8, App1
39	175	94.6	41	14	US-10-414-192-3	Sequence 9, App1
40	175	94.6	41	14	US-10-414-192-9	Sequence 9, App1
41	175	94.6	41	14	US-10-351-641-496	Sequence 496, App
42	175	94.6	41	14	US-10-351-641-601	Sequence 601, App
43	175	94.6	41	14	US-10-351-641-633	Sequence 633, App
44	175	94.6	41	14	US-10-351-641-1163	Sequence 1163, App
45	175	94.6	41	16	US-10-664-021-27	Sequence 27, App1
46	175	94.6	41	16	US-10-671-316-27	Sequence 27, App1
47	175	94.6	44	12	US-10-663-589-36	Sequence 36, App1
48	175	94.6	44	14	US-10-414-192-10	Sequence 10, App1
49	175	94.6	45	9	US-09-779-451-9	Sequence 9, App1
50	175	94.6	45	12	US-09-809-060-50	Sequence 50, App1
51	175	94.6	45	12	US-10-663-589-29	Sequence 29, App1
52	175	94.6	45	14	US-10-351-641-1164	Sequence 1164, App
53	175	94.6	45	16	US-10-664-021-26	Sequence 26, App1
54	175	94.6	45	16	US-10-671-316-26	Sequence 26, App1
55	175	94.6	49	9	US-09-796-202-3	Sequence 3, App1
56	175	94.6	49	14	US-10-323-314-3	Sequence 3, App1
57	175	94.6	51	12	US-10-663-589-27	Sequence 27, App1
58	175	94.6	51	14	US-10-351-641-745	Sequence 745, App
59	175	94.6	51	16	US-10-664-021-24	Sequence 24, App1
60	175	94.6	51	16	US-10-671-316-24	Sequence 24, App1
61	175	94.6	52	14	US-10-351-641-1119	Sequence 1119, App
62	175	94.6	53	14	US-10-351-641-955	Sequence 955, App
63	175	94.6	53	14	US-10-351-641-1062	Sequence 1062, App
64	175	94.6	53	9	US-09-779-451-1	Sequence 1, App1
65	175	94.6	55	12	US-09-809-060-14	Sequence 14, App1
66	175	94.6	57	15	US-10-438-691-1	Sequence 1, App1
67	175	94.6	59	16	US-10-664-021-1	Sequence 1, App1
68	175	94.6	59	16	US-10-671-316-1	Sequence 1, App1
69	175	94.6	60	12	US-10-663-589-1	Sequence 1, App1
70	175	94.6	63	12	US-10-267-682-201	Sequence 201, App
71	175	94.6	63	12	US-10-267-748-201	Sequence 201, App
72	175	94.6	63	14	US-10-252-136-54	Sequence 54, App1
73	175	94.6	103	14	US-10-263-103-29	Sequence 29, App1
74	175	94.6	103	15	US-10-438-691-3	Sequence 3, App1
75	175	94.6	113	15	US-10-438-691-4	Sequence 4, App1
76	175	94.6	117	14	US-10-040-349B-2	Sequence 2, App1
77	175	94.6	138	9	US-09-854-816-88	Sequence 88, App1
78	175	94.6	138	9	US-09-854-816-89	Sequence 89, App1
79	175	94.6	138	9	US-09-854-816-99	Sequence 99, App1
80	175	94.6	200	15	US-10-263-103-25	Sequence 25, App1
81	175	94.6	200	14	US-10-438-691-8	Sequence 8, App1
82	175	94.6	232	14	US-10-059-271-81	Sequence 81, App1
83	175	94.6	232	14	US-10-059-271-82	Sequence 82, App1
84	175	94.6	256	14	US-10-059-271-97	Sequence 97, App1
85	175	94.6	258	9	US-09-854-816-16	Sequence 16, App1
86	175	94.6	258	9	US-09-854-816-17	Sequence 17, App1
87	175	94.6	258	9	US-09-854-816-18	Sequence 18, App1
88	175	94.6	258	9	US-09-854-816-19	Sequence 19, App1

89 175 94.6 269 9 US-09-854-816-43
90 175 94.6 338 12 US-10-267-682-90

ALIGNMENTS

RESULT 1

US-10-252-136-82
Sequence 82, Application US/10252136
Publication No. US20030103998A1
GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/10/252,136
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/08/973,952
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 98.4%; Score 182; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 7,1e-18;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNLRRAEAGQHLLQLTWGIKQLQARILAVERYLKDQ 38
1 NNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 2

US-09-854-816-97
Sequence 97, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Pheasant
Melissa A. Starovashnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,780
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-854-816-97
SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Query Match 95.7%; Score 177; DB 9; Length 198;
Best Local Similarity 94.7%; Pred. No. 2,1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRRAEAGQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 83 NNLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 120

RESULT 3

US-09-854-816-98
Sequence 98, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Pheasant
Melissa A. Starovashnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,780
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-854-816-98

Query Match 95.7%; Score 177; DB 9; Length 198;
Best Local Similarity 94.7%; Pred. No. 2,1e-16;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 38
Db 83 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 120

RESULT 4
US-09-854-816-101
; Sequence 101, Application US/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-09-854-816-101

Query Match 95.7%; Score 177; DB 9; Length 198;

Best Local Similarity 94.7%; Pred. No. 2, 1e-16;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 38
Db 83 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 120

RESULT 5
US-09-854-816-39

; Sequence 39, Application US/09854816

; Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-854-816-39

Qy 1 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 38
Db 83 SNLLRAIEAQOHLQLTVMGIKQLQARVLAVERYLKQ 120

RESULT 6
US-09-854-816-24

; Sequence 24, Application US/09854816

; Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-854-816-24

Query Match 95.7%; Score 177; DB 9; Length 269;
Best Local Similarity 94.7%; Pred. No. 2.9e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 84 SNLLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 121

RESULT 7
US-09-854-816-96
Sequence 96, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovansk
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-854-816-96

Query Match 95.7%; Score 177; DB 9; Length 269;
Best Local Similarity 94.7%; Pred. No. 2.9e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 84 SNLLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 121

RESULT 8
US-10-296-734-8
Sequence 8, Application US/10296734
Publication No. US20040054137A1
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU P0761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 651
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: ENV consensus polypeptide
US-10-296-734-8

Query Match 95.7%; Score 177; DB 12; Length 651;
Best Local Similarity 94.7%; Pred. No. 7.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLLRAIEAQOHLLQLTWQIKOLQARILAVERYLKQ 38
Db 341 SNLLRAIEAQOHLLQLTWQIKOLQARVLAVERYLKQ 378

RESULT 9
US-10-190-435-145
Sequence 145, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P118133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 145
LENGTH: 860
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TW013CH17
US-10-190-435-145

Query Match 95.1%; Score 176; DB 14; Length 860;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 550 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 587

RESULT 10
US-10-190-435-146
; Sequence 146, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TW013CB20
US-10-190-435-146

Query Match 95.1%; Score 176; DB 14; Length 860;
Best Local Similarity 92.1%; Pred. No. 1.4e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 550 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 587

RESULT 11
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068613A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBLATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 94.6%; Score 175; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 12
US-09-779-451-2
; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

QY 1 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 13
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J
; APPLICANT: Olson, William C
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 94.6%; Score 175; DB 10; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 14
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.

Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match 94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRATEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRATEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 15
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRATEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRATEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 16
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRATEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRATEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

```
RESULT 17
US-09-809-060-7
; Sequence 7, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match          94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 18
US-10-663-589-3
; Sequence 3, Application US/10663589
; Publication No. US200400637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match          94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 19
US-10-681-879-2
; Sequence 2, Application US/10681879
; Publication No. US2004006767A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
US-10-681-879-2
```

```
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/10/681,879
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/493,346
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match          94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 20
US-09-828-615-2
; Sequence 2, Application US/09828615
; Publication No. US20020146415A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672
; CURRENT APPLICATION NUMBER: US/09/828,615
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-615-2

Query Match          94.6%; Score 175; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 21
US-10-116-797-2
; Sequence 2, Application US/10116797
; Publication No. US2003004411A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-797-2
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Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38

RESULT 22

US-10-323-314-11
; Sequence 11, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBRATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323.314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(38)
; OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38

RESULT 23
US-10-414-192-1
; Sequence 1, Application US/10414192
; Publication No. US20030181382A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Bolgneal, Dani P.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414.192
FILING DATE: 15-Apr-2003

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-107-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-414-192-1
Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38

RESULT 24

US-10-351-641-16
; Sequence 16, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 38

RESULT 25

US-10-351-641-507
; Sequence 507, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: 09/350,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-507

FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 26

US-10-351-641-604
Sequence 604, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 94.6%; Score 175; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 27
US-10-005-305-165
Sequence 165, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 165
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 94.6%; Score 175; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 28

US-10-005-305-202
Sequence 202, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match 94.6%; Score 175; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 29
US-10-005-305-203
Sequence 203, Application US/10005305
Publication No. US20030203841A1
APPLICANT: The Government of the United States of America, represented by the

APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORNYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005.305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 94.6%; Score 175; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 30
US-10-420-194-1234

Sequence 1234, Application US/10420194
Publication No. US2004006035A1

GENERAL INFORMATION:

APPLICANT: Sigma Therapeutics, Inc.

APPLICANT: MCSwissgen, Jim

APPLICANT: Blact, Larry

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide

TITLE OF INVENTION: Interactions

FILE REFERENCE: MBH02-305-A (400/011)

CURRENT APPLICATION NUMBER: US/10/420,194

CURRENT FILING DATE: 2003-04-22

PRIOR APPLICATION NUMBER: PCT/US 03/05190

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 60/398,036

PRIOR FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/374,722

PRIOR FILING DATE: 2002-04-22

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1234

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1234

LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match 94.6%; Score 175; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKDQ 38

Search completed: June 2, 2004, 12:29:26
Job time : 35.0054 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 47.6033 Seconds
(without alignments)
225,548 Million cell updates/sec

Title: US-09-657-336a-543
Perfect score: 188
Sequence: 1 NNILRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

A_Geneseq_29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	184	97.9	38 2 AAR98408	AAR98408 DP107 cor
2	184	97.9	38 4 AAB54785	AAB54785 HIV anti-HIV
3	184	97.9	38 4 AAB55005	AAB55005 Anti-HIV
4	184	97.9	38 4 AAB54970	AAB54970 Anti-HIV
5	184	97.9	38 4 AAB92244	AAB92244 Virus rel
6	184	97.9	38 4 AAU14011	AAU14011 DP107 pep
7	184	97.9	38 5 AAOL8771	AAOL8771 HIV SP41
8	179	95.2	37 3 AAB14705	AAB14705 HIV-1 iso
9	179	95.2	37 4 AAB54969	AAB54969 Anti-HIV
10	178	94.7	37 3 AAB14739	AAB14739 HIV-1 iso
11	178	94.7	37 4 AAB55004	AAB55004 Anti-HIV
12	177	94.1	38 2 AAR55635	AAR55635 DP-139 -
13	177	94.1	38 2 AAR55636	AAR55636 DP-140 -
14	177	94.1	38 2 AAR47216	AAR47216 DP-107 -
15	177	94.1	38 2 AAW27614	AAW27614 Human imm
16	177	94.1	38 3 AAY88666	AAY88666 Core poly
17	177	94.1	38 3 AAY88730	AAY88730 Core poly
18	177	94.1	38 3 AAY88731	AAY88731 Core poly
19	177	94.1	38 3 AAY89145	AAY89145 Core poly
20	177	94.1	38 3 AAY89146	AAY89146 Core poly
21	177	94.1	38 3 AAY89243	AAY89243 Core poly
22	177	94.1	38 3 AAB14530	AAB14530 HIV-1 iso
23	177	94.1	38 3 AAB52824	AAB52824 T21/DP107
24	177	94.1	38 3 AAB52786	AAB52786 T21/DP107
25	177	94.1	38 3 AAB52823	AAB52823 T21/DP107

26	177	94.1	38 4 AAG63858	AAG63858 Amino aci
27	177	94.1	38 4 AAB92349	AAB92349 Virus rel
28	177	94.1	38 4 AAB77021	AAB77021 Core poly
29	177	94.1	38 4 AAB77085	AAB77085 Core poly
30	177	94.1	38 4 AAB77086	AAB77086 Core poly
31	177	94.1	38 4 AAB77596	AAB77596 Core poly
32	177	94.1	38 4 AAB77500	AAB77500 Core poly
33	177	94.1	38 4 AAB77624	AAB77624 Core poly
34	177	94.1	38 4 AAU70185	AAU70185 HIV viral
35	177	94.1	38 4 AAU70184	AAU70184 HIV viral
36	177	94.1	38 4 AAB85690	AAB85690 DP107 pep
37	177	94.1	38 4 AAB01489	AAB01489 Viral cor
38	177	94.1	38 4 AAB00505	AAB00505 Viral cor
39	177	94.1	38 4 AAB00090	AAB00090 Viral cor
40	177	94.1	38 4 AAB02077	AAB02077 Viral cor
41	177	94.1	38 4 ABB00025	ABB00025 HIV-1 gp4
42	177	94.1	38 4 ABB00089	ABB00089 Viral DP1
43	177	94.1	38 4 ABB00504	ABB00504 Viral DP1
44	177	94.1	38 4 ABB00629	ABB00629 Viral DP1
45	177	94.1	38 4 ABB00601	ABB00601 RSV Fl pr
46	177	94.1	38 4 ABB01980	ABB01980 Viral cor
47	177	94.1	38 4 AAU12638	AAU12638 DP178-1ik
48	177	94.1	38 4 AAU13053	AAU13053 DP178-1ik
49	177	94.1	38 4 AAU13149	AAU13149 DP178-1ik
50	177	94.1	38 4 AAU13177	AAU13177 DP178-1ik
51	177	94.1	38 4 AAU12574	AAU12574 DP178-1ik
52	177	94.1	38 4 AAU12639	AAU12639 DP178-1ik
53	177	94.1	38 4 AAB82962	AAB82962 Anti-HIV
54	177	94.1	38 5 AAB22292	AAB22292 gp41 fusi
55	177	94.1	38 5 AAB02097	AAB02097 Hybrid po
56	177	94.1	38 5 ADE01509	ADE01509 Hybrid po
57	177	94.1	38 6 ABB75976	ABB75976 HIV-1 gp4
58	177	94.1	38 6 ABB09553	ABB09553 Peptide F
59	177	94.1	38 6 ABO10245	ABO10245 HIV1-I gp
60	177	94.1	38 7 ADC99756	ADC99756 DP-107 an
61	177	94.1	38 7 ADE73011	ADE73011 HIV gp41
62	177	94.1	41 2 AAR52840	AAR52840 DP-125 -
63	177	94.1	41 2 AAR98406	AAR98406 Peptide D
64	177	94.1	41 2 AAU17019	AAU17019 DP-178-1i
65	177	94.1	41 2 AAW27616	AAW27616 Human imm
66	177	94.1	41 2 AAW27622	AAW27622 Human imm
67	177	94.1	41 3 AAY89779	AAY89779 Core poly
68	177	94.1	41 3 AAY89240	AAY89240 Core poly
69	177	94.1	41 3 AAY89134	AAY89134 Core poly
70	177	94.1	41 4 AAB54791	AAB54791 HIV anti-H
71	177	94.1	41 4 AAB92250	AAB92250 Virus rel
72	177	94.1	41 4 AAB77593	AAB77593 Core poly
73	177	94.1	41 4 AAB78180	AAB78180 Core poly
74	177	94.1	41 4 AAB77489	AAB77489 Core poly
75	177	94.1	41 4 ABB02106	ABB02106 Viral cor
76	177	94.1	41 4 ABB01187	ABB01187 Viral DP1
77	177	94.1	41 4 ABB02636	ABB02636 Viral cor
78	177	94.1	41 4 ABB01969	ABB01969 Viral cor
79	177	94.1	41 4 AAG67047	AAG67047 Control p
80	177	94.1	41 4 ABB00493	ABB00493 Viral cor
81	177	94.1	41 4 ABB002074	ABB002074 Viral cor
82	177	94.1	41 4 ABB00598	ABB00598 Control DP1
83	177	94.1	41 4 AAU14018	AAU14018 Control p
84	177	94.1	41 4 AAU13733	AAU13733 DP178-1ik
85	177	94.1	41 4 AAU13146	AAU13146 DP178-1ik
86	177	94.1	41 4 AAU13042	AAU13042 DP178-1ik
87	177	94.1	41 5 AAOL8828	AAOL8828 HIV gp41
88	177	94.1	41 5 AAOL8776	AAOL8776 HIV gp41
89	177	94.1	41 5 AAOL8829	AAOL8829 HIV gp41
90	177	94.1	41 5 ADE01989	ADE01989 Hybrid po

ALIGNMENTS

RESULT 1
AAR98408 standard; peptide; 38 AA.

XX AAR98408;
AC 16-OCT-2003 (revised)
XX 17-FEB-1997 (first entry)
DT
XX DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.
DE
XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;
KM influenza virus; hepatitis B virus.
XX Human immunodeficiency virus 1.
OS
XX WO9619495-A1.
PN
XX 27-JUN-1996.
PD
XX 20-DEC-1995; 95WO-US016733.
PF
XX 20-DEC-1994; 94US-00360107.
PR 06-JUN-1995; 95US-00470896.
XX
XX (UYDU-) UNIV DUKE.
PA (TRIM-) TRIMERIS INC.
XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
PI Petteway SR, Langlois AJ;
XX WPI, 1996-309517/31.
DR
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence
PT search motif.
XX
XX Disclosure; Page 30; 471pp; English.
PS
XX The sequences given in AAR98398-408 represent peptides which exhibit
CC antifusogenic activity, antiviral capability and/or the ability to
CC structure intracellular processes involving coiled-coil peptide
CC structures. These peptides are recognised by the ALLMOTIS, 107x178x4 and
CC PLZIP search motifs. These peptides may be used to inhibit the
CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 97.9%; Score 184; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.2e-17;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLLQTLTWQIQKQARILAVERYLKQ 38
DB 1 NNLRAIDAQOHLLQTLTWQIQKQARILAVERYLKQ 38
RESULT 2
AAB54785
ID AAB54785 standard; peptide; 38 AA.
XX
AC AAB54785;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX HIV antiviral activity exhibiting peptide SEQ ID NO:2.
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX Human immunodeficiency virus 1.
OS

XX WO200069902-A1.
EN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US013651.
PE
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI WPI, 2001-007496/01.
DR
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Claim 6; Page 173; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This maintains the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 97.9%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.2e-17;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLLQTLTWQIQKQARILAVERYLKQ 38
DB 1 NNLRAIDAQOHLLQTLTWQIQKQARILAVERYLKQ 38
RESULT 3
AAB55005
ID AAB55005 standard; peptide; 38 AA.
XX
AC AAB55005;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 amino truncation peptide #35.
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX Human immunodeficiency virus 1.
OS

XX	PD	WO20069902-A1.
XX	PB	
XX	PF	23-NOV-2000.
XX	PP	17-MAY-2000; 2000WO-US013651.
XX	PR	17-MAY-1999; 99US-0134406P.
XX	PT	10-SEP-1999; 99US-0153406P.
XX	PA	(CONU-) CONUTCHEM INC.
XX	PI	Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX	PS	WPI: 2001-007496/01.
XX	PT	A modified peptide and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds useful for treatment of viral infections, e.g. human immunodeficiency virus.
XX	PS	Disclosure; Page 139; 21pp; English.
XX	CC	The present invention describes a modified anti-viral peptide (I) comprising a peptide that exhibits anti-viral activity and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds. (I) has anti-viral and anti-fusogenic activities. (I) inhibits viral infection of cells by inhibiting cell-cell fusion or free virus infection or to reduce the level of membrane fusion events between two or more entities, e.g., virus-cell or cell-cell, relative to the level of membrane fusion that occurs in the absence of the peptide. (I) is useful in the treatment of patients who are suffering from viral infection, e.g. HIV, RSV, HPIV, Mev, and SIV. (I) may be administered prophylactically to previously uninfected individuals. This is useful in cases where an individual has been subjected to a high risk of exposure to a virus. By bonding of long-lived components of the blood, such as immunoglobulin, serum albumin, red blood cells and platelets the activity is extended for days to weeks. CC This is due to improved stability in vivo and a reduced susceptibility to peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 to CC AAB55431 represent peptides used in the exemplification of the present invention. (updated on 11-SEP-2003 to standardise OS field)
XX	SQ	Sequence 38 AA;
XX	Query Match	97.9%; Score 184; DB 4; Length 38;
XX	Best Local Similarity	97.4%; Pred. NO. 1.2e-17;
XX	Matches	37; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
Oy		1>NNLRAIDAOQHLLQLTWGQIKQDARILAAVERYLKDD 38 Db 1>NNLRATIEAQHLLQLTWGQIKQDARILAAVERYLKDD 38
RESULT 4		
ID	AAB54970	standard; peptide; 38 AA.
AC	AAB54970;	
XX	DT	11-SEP-2003 (revised)
DT	05-MAR-2001	(first entry)
DE		Anti-HIV peptide DPI07 carboxy truncation peptide #35.
KW		Long lasting fusion peptide inhibitor; viral infection; antiviral; antifusogenic; mobile blood component; measles virus; Mev; SIV; sindan immunodeficiency virus; human parainfluenza virus; HPIV; RSV; human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX		Human immunodeficiency virus 1.
XX		WO20069902-A1.

PD	23-NOV-2000.
XX	
PF	17-MAY-2000; 2000MO-US013651.
XX	
PR	17-MAY-1999; 99US-0134406P.
XX	
PR	10-SEP-1999; 99US-0153406P.
XX	
PA	(CONU-) CONUTCHEM INC.
XX	
P1	Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX	
DR	WPI; 2001-007496/01.
XX	
PT	A modified peptide and a reactive group which is reactive with amino
PT	groups, hydroxyl groups, or thiol groups on blood components to form
PT	stable covalent bonds useful for treatment of viral infections, e.g.
PT	human immunodeficiency virus.
XX	
PS	Disclosure; Page 137; 21pp; English.
XX	
CC	The present invention describes a modified anti-viral peptide (I)
CC	comprising a peptide that exhibits anti-viral activity and a reactive
CC	group which is reactive with amino groups, hydroxyl groups, or thiol
CC	groups on blood components to form stable covalent bonds. (I) has anti-
CC	viral and anti-fusogenic activities. (I) inhibits viral infection of
CC	cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC	the level of membrane fusion events between two or more entities, e.g.,
CC	virus-cell or cell-cell, relative to the level of membrane fusion that
CC	occurs in the absence of the peptide. (II) is useful in the treatment of
CC	patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC	Mey, and SIV. (I) may be administered prophylactically to previously
CC	uninfected individuals. This is useful in cases where an individual has
CC	been subjected to a high risk of exposure to a virus. By bonding of long-
CC	lived components of the blood, such as immunoglobulin, serum albumin, red
CC	blood cells and platelets the activity is extended for days to weeks.
CC	This is due to improved stability in vivo and a reduced susceptibility to
CC	peptidase or protease degradation. This minimises the need for more
CC	frequent, or even continual, administration of the peptides. AAB54784 to
CC	AAB55431 represent peptides used in the exemplification of the present
CC	invention. (Updated on 11-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 38 AA;
	Query Match 97.9%; Score 184; DB 4; Length 38;
	Best Local Similarity 97.4%; Pred. No. 1.2e-17;
	Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 NNILRAIDAOQHLLQLTVMQIKQLOARILAVERYLKQ 38
DB	1 NNILRAIDAOQHLLQLTVMQIKQLOARILAVERYLKQ 38
RESULT 5	
AAB92244	standard; peptide; 38 AA.
XX	
AC	AAB92244;
XX	
DT	22-JUN-2001 (first entry)
XX	
DE	Virus related peptide SEQ ID NO:1420.
XX	
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW	blood component; modification; succinimidy; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200069900-A2.
XX	
PD	23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.
 PF
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI, 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 662; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 38 AA;
 XX
 Query Match 97.9%; Score 184; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 1.2e-17;
 Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLIRAIQAQHHLLQTLTWQIKQLQARILAVERYLKQ 38
 Db 1 NNLIRAIQAQHHLLQTLTWQIKQLQARILAVERYLKQ 38
 XX
 RESULT 6
 AAU14011
 ID AAU14011 standard; peptide; 38 AA.
 XX
 AC AAU14011;
 XX
 DT 11-SEP-2003 (revised)
 DT 21-NOV-2001 (first entry)
 XX
 DE DP107 peptide from HIV-1 transmembrane protein gp41.
 XX
 KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KW antitubercogenic; antiviral; HIV transmission.
 XX
 OS Human immunodeficiency virus 1; isolate LAI.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..35
 FT /note="Amino acids 1-35 can be optionally and serially
 FT deleted from the N-terminus"
 FT Misc-difference 4..38
 FT /note="Amino acids 4-38 can be optionally and serially
 FT deleted from the C-terminus"
 XX
 PN WO200151673-A2.
 XX

PD 19-JUL-2001.
 XX
 PF 05-JUL-2000; 2000WO-US035727.
 XX
 PR 09-JUL-1999; 99US-00350841.
 XX
 PA (TRIM-) TRIMERIS INC.
 PI Jeffe P, Lackey JM, Erickson JB, Lawless MK, Merutka G;
 DR WPI, 2001-442157/47.
 XX
 PT Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitubercogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Page 33; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antitubercogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 CC
 SQ Sequence 38 AA;
 XX
 Query Match 97.9%; Score 184; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 1.2e-17;
 Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLIRAIQAQHHLLQTLTWQIKQLQARILAVERYLKQ 38
 Db 1 NNLIRAIQAQHHLLQTLTWQIKQLQARILAVERYLKQ 38
 XX
 RESULT 7
 AAO18771
 ID AAO18771 standard; peptide; 38 AA.
 XX
 AC AAO18771;
 XX
 DT 29-OCT-2002 (first entry)
 DT
 XX
 DE HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
 XX
 KW Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
 KW gp41.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO200256902-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 17-DEC-2001; 2001WO-US048802.
 XX
 PR 19-DEC-2000; 2000US-0256657P.
 XX
 PA (SCHE) SCHERING CORP.
 XX

PI Baroudy BM;
XX
DR WPI; 2002-636513/68.
XX
PT Treatment of HIV infection in an individual involves administration of a
PT combination of chemokine co-receptor five antagonist and a specified HIV
PT envelope polypeptide.
XX
PS Disclosure; Page 34; 52pp; English.
XX
CC The present invention relates to a method of treating an HIV infection in
CC an individual, which involves administering in combination a chemokine co-
CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
CC derivative. Other viral infections can also be treated using the method.
CC The present sequence is a peptide derived from HIV and useful in the
CC method of the invention
XX
SQ Sequence 38 AA;
XX
Query Match 97.9%; Score 184; DB 5; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.2e-17;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
XX
RESULT 8
AAB14705
XX AAB14705 standard; peptide; 37 AA.
XX
AC AAB14705;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
DE
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy; group W; subtype B;
XX isolate LAI.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000MO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
XX 07-JAN-2000; 2000US-00480336.
XX
XX (WIILD/) WIILD C T.
XX (WEIS/) WEISS C D.
XX
XX Wild CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
XX comprises administering a polypeptide capable of forming a stable coiled-
XX coil solution structure.
XX
XX Disclosure; Page 36; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
XX domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
XX isolate LAI. The invention relates to raising a neutralising antibody
XX response to a broad spectrum of HIV (human immunodeficiency virus)

CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 37 AA;
XX
Query Match 95.2%; Score 179; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLLQLTWQIKQLQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
XX
RESULT 9
AAB54969
XX AAB54969 standard; peptide; 37 AA.
XX
XX AAB54969;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #34.
DE
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; Mev; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000MO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONU-) CONUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjelal N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.

XX XX Disclosure; Page 137; 211pp; English.
 XX PS
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 37 AA;
 Query Match 95.2%; Score 179; DB 4; Length 37;
 Best Local Similarity 97.3%; Pred. No. 5,4e-17;
 Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRAIDAQOHLLQLTWQIKQLQARILAVERYLKD 37
 Db 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKD 37
 RESULT 10
 AAB14739
 XX AAB14739 standard; peptide; 37 AA.
 AC AAB14739;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 PI Wild CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.

XX XX Disclosure; Page 38; 97pp; English.
 XX PS
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralising antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 37 AA;
 Query Match 94.7%; Score 178; DB 3; Length 37;
 Best Local Similarity 97.3%; Pred. No. 7,3e-17;
 Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NNLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 Db 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 37
 RESULT 11
 AAB55004
 XX AAB55004 standard; peptide; 37 AA.
 AC AAB55004;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #34.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX MPI; 2001-007496/01.
 DR A modified peptide and a reactive group which is reactive with amino
 XX groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX Sequence 37 AA;
 SQ
 Query Match 94.7%; Score 178; DB 4; Length 37;
 Best Local Similarity 97.3%; Pred. No. 7.3e-17;
 Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLLRAIDAQOHLQLTWGIKQLOARILAVERYLKDQ 38
 DB 1 NLLRAIEAQOHLQLTWGIKQLOARILAVERYLKDQ 37
 RESULT 12
 AAR55635
 ID AAR55635 standard; peptide; 38 AA.
 XX
 AC AAR55635;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX
 DE DP-139 - DP-107 analogue.
 XX
 KW Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KM antiviral; gp41.
 XX
 OS Synthetic.
 XX
 PN WO9402505-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006769.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Wild CT, Matthews TJ, Bolognesi DP;
 XX MPI; 1994-048790/06.
 DR

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Disclosure; Page 25; 38pp; English.
 XX
 CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 38 AA;
 Query Match 94.1%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NLLRAIDAQOHLQLTWGIKQLOARILAVERYLKDQ 38
 DB 1 NLLRAIEAQOHLQLTWGIKQLOARILAVERYLKDQ 38
 RESULT 13
 AAR55636
 ID AAR55636 standard; peptide; 38 AA.
 XX
 AC AAR55636;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX
 DE DP-140 - DP-107 analogue.
 XX
 KW Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KM antiviral; gp41.
 XX
 OS Synthetic.
 XX
 PN WO9402505-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006769.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Wild CT, Matthews TJ, Bolognesi DP;
 XX MPI; 1994-048790/06.
 DR
 PT New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Disclosure; Page 25; 38pp; English.
 XX
 CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWGIKQLQARILAVERYLKQ 38
 DB 1 NNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKQ 38

RESULT 14
 AAR47216
 ID AAR47216 standard; peptide; 38 AA.

AC AAR47216;

DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (558-595).

KW Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KW antiviral; gp41.

OS Synthetic.

FX Key Location/Qualifiers

FT MSC-difference 12 /note= "residue 12 of the sequence in Fig 1 is H; residue
 FT 12 of the sequence in Table 4 is G"

PN W09402505-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93MO-US006769.

PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.

PA (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

PT New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.

PS Claim 1; Page 27; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWGIKQLQARILAVERYLKQ 38
 DB 1 NNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKQ 38

RESULT 15
 AAM27614
 ID AAM27614 standard; peptide; 38 AA.

AC AAM27614;

DT 25-MAR-2003 (revised)
 DT 22-DEC-1997 (first entry)

DE Human immunodeficiency virus gp41 derived peptide DP-107.

KW Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
 KW inhibition; induction; cell fusion; transmembrane; type 1.

OS Human immunodeficiency virus.

PN US5656480-A.

PD 12-AUG-1997.

PF 27-JAN-1995; 95US-00374666.

PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.

PR 19-JUL-1993; 93MO-US006769.

PA (UYDU-) UNIV DUKE.

PI Bolognesi DP, Wild CT, Matthews TJ;

DR WPI; 1997-414595/38.

PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
 PT syncytia formation and transmembrane.

PS Claim 1; Col 13-14; 18pp; English.

CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein
 CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
 CC cell fusion in a culture and cell free HIV transmembrane in a culture to a
 CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
 CC MAR-2003 to correct PF field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWGIKQLQARILAVERYLKQ 38
 DB 1 NNLLRAIEAQOHLLQLTWGIKQLQARILAVERYLKQ 38

RESULT 16

AAV8666
 ID AAV8666 standard; peptide; 38 AA.

AC AAV8666;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 21.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.

XX	Unidentified.
XX	
PN	W09959615-A1.
PD	25-NOV-1999.
PF	20-MAY-1999; 99WO-US011219.
PR	20-MAY-1998; 98US-00082279.
PA	(TRIM-) TRIMERIS INC.
PI	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
DR	WPI; 2000-136792/12.
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
PS	comprises enhancer sequence.
XX	
XX	Disclosure; Page 21; 124pp; English.
CC	
CC	The invention relates to hybrid polypeptides comprising enhancer peptide
CC	sequence linked to core polypeptides. The enhancer polypeptides are
CC	derived from various retroviral envelope (gp41) protein sequences,
CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC	pharmacokinetic properties such as increasing the half-life of any core
CC	polypeptide that they are linked to. The core polypeptides are any
CC	polypeptide that may be introduced into a living system and that can
CC	function as a pharmacologically useful peptide for the treatment or
CC	prevention of a disease. The core polypeptides are bioactive peptides
CC	selected from a growth factor, cytokine, differentiation factor,
CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC	factor. The peptides of the invention can be used for inhibiting viral
CC	infection and can be used in anti-viral and anti-fusogenic treatments.
CC	Sequences AAY88651-99005 represent core polypeptide fragments that can
CC	be used in the invention. Some sequences among those indicated also
CC	comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX	
SQ	Sequence 38 AA;
Query Match	94.1%; Score 177; DB 3; Length 38;
Best Local Similarity	94.7%; Pred. No. 1e-16; Mismatches 0; Gaps 0;
Matches 36; Conservative 1; Indels 1;	
CY	1 NNLRAIDAOQHLLQLTWGKIQOLARILAAVERYLKDQ 38 : 1 NNLRATFAOQHLLQLTWGKIKOLOARILAAVERYLKDQ 38
DB	
RESULT 17	
ID	AAY88730 AAY88730 standard; peptide; 38 AA.
AC	AAY88730;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	Core polypeptide fragment T No. 85.
XX	
KM	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX	anti-fusogenic; differentiation factor; interleukin; interferon;
XX	colony stimulating factor; hormone; angiogenic factor.
OS	Unidentified.
PN	W09959615-A1.
PD	25-NOV-1999.
PF	20-MAY-1999; 99WO-US011219.
XX	

```

XX 20-MAY-1998; 98US-00082279.
XX (TRIM-) TRIMERIS INC.
XX Barney S, Guthrie KI, Nerutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX Disclosure; Page 22; 124p; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AA18651-Y9005 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
XX Sequence 38 AA:
XX
XX Query Match 94.1%; Score 177; DB 3; Length 38;
XX Best Local Similarity 94.7%; Pred. No. 1e-16;
XX Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 NNLIRATDAQOHLQLTFWQIKQIQAIRILAVERYLKQD 38
XX | | | | | | | | | | | | | | | | | | | |
XX 1 NNLIRATDAQOHLQLTFWQIKQIQAIRILAVERYLKQD 38
XX
XX RESULT 18
XX AA186731
XX ID AA186731 standard; peptide; 38 AA.
XX
XX AA186731;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 86.
XX
XX Retrovirins; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Nerutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX

```

PT comprises enhancer sequence.
 XX
 PS Disclosure; Page 22; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 XX
 SO Sequence 38 AA:
 Query Match 94.1%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRRAIDAOQHLLQLTWGIKQLOARILAVERYLKQ 38
 DB 1 NNLRRAIDAOQHLLQLTWGIKQLOARILAVERYLKQ 38
 RESULT 19
 AAY89145
 ID AAY89145 standard; peptide; 38 AA.
 XX
 AC AAY89145;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 OS Core polypeptide fragment T No. 583.
 XX
 DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 XX anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN WO959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US011219.
 XX
 PR 20-MAY-1998; 98US-00082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX
 DR WPI; 2000-136792/12.
 XX
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.
 XX
 PS Disclosure; Page 30; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC

CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 XX
 SO Sequence 38 AA:
 Query Match 94.1%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRRAIDAOQHLLQLTWGIKQLOARILAVERYLKQ 38
 DB 1 NNLRRAIDAOQHLLQLTWGIKQLOARILAVERYLKQ 38
 RESULT 20
 AAY89146
 ID AAY89146 standard; peptide; 38 AA.
 XX
 AC AAY89146;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 OS Core polypeptide fragment T No. 583.
 XX
 DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 XX anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN WO959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US011219.
 XX
 PR 20-MAY-1998; 98US-00082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX
 DR WPI; 2000-136792/12.
 XX
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.
 XX
 PS Disclosure; Page 30; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y90055 represent core polypeptide fragments that can

CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKQD 38
DB 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKQD 38

RESULT 21
AAY89243
ID AAY89243 standard; peptide; 38 AA.

AC AAY89243;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 681.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS

PN WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Mernutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties

PS comprises enhancer sequence.

XX Disclosure; Page 32; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are

CC derived from various retroviral envelope (gp41) protein sequences,

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

CC pharmacokinetic properties such as increasing the half-life of any core

CC polypeptide that they are linked to. The core polypeptides are any

CC polypeptide that may be introduced into a living system and that can

CC function as a pharmacologically useful peptide for the treatment or

CC prevention of a disease. The core polypeptides are bioactive peptides

CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKQD 38
DB 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKQD 38

RESULT 22
AB14530
ID AB14530 standard; peptide; 38 AA.

AC AB14530;

DT 12-SEP-2003 (revised)

DT 24-NOV-2000 (first entry)

DE HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).

XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KW humoral response; broad spectrum vaccine; anti-HIV;

XX envelope glycoprotein; prophylaxis; therapy.

OS Human immunodeficiency virus 1.

PN WO200040616-A1.

XX 13-JUL-2000.

PF 10-JAN-2000; 2000WO-US000456.

PR 08-JAN-1999; 99US-0115404P.

PR 07-JAN-2000; 2000US-00480336.

XX (WILD/) WILD C.T.

PA (WEIS/) WEISS C.D.

XX WILD CT, Weiss CD;

XX WPI; 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,

PT comprises administering a polypeptide capable of forming a stable coiled-

PT coil solution structure.

PS Claim 5; Page 56; 97pp; English.

XX Sequences AB14529-B14531 and AB14537-B14568 represent specifically

CC claimed peptides derived from the N-helical domain of the gp41 envelope

CC glycoprotein from a variety of HIV-1 isolates. The invention relates to

CC raising a neutralizing antibody response to a broad spectrum of HIV

CC (human immunodeficiency virus) strains and isolates, comprising the

CC administration of a peptide which corresponds to or mimics highly

CC conserved portions of gp41 which are important in mediating the process

CC of viral entry into host cells. Such peptides can correspond to or mimic

CC the coiled coil solution structure of the N-helical domain (the heptad

CC repeat region), or can correspond or mimic the C-helical domain (the

CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41

CC core 6-helix bundle, which is formed by the interaction of the N- and C-

CC helical domains of three gp41 proteins. The peptides can be administered

CC either singly or as a combination (particularly a combination of N-

CC helical and C-helical peptides), and can be multimerised. For example, N-

CC and C-helical domain peptides can be alternately linked together to form

CC a peptide which mimics the core 6-helix bundle. Administration of the

CC peptide(s) generates a humoral response, with the production of

CC antibodies against gp41 structures involved in viral entry. As these

CC portions of gp41 are well conserved, such antibodies may be effective

CC against a broad range of HIV strains and isolates. The peptide

CC compositions may be administered as a prophylactic or therapeutic vaccine

CC to generate antibodies which reduce or inhibit the ability of HIV to

CC infect uninfected cells. A composition comprising polyclonal or

CC monoclonal antibodies can be administered to reduce HIV infection of

CC uninfected cells. Antibodies raised against entry-relevant gp41

CC structures may also be used therapeutically and as tools to further

CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to

CC standardise OS field)
XX
SQ Sequence 38 AA;

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 23
AAB52824
ID AAB52824 standard; peptide; 38 AA.
XX
AC AAB52824;

XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)

DE T21/DP107 peptide fragment #101.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.

OS Human immunodeficiency virus 1.

PN WQ200066622-A1.

PD 09-NOV-2000.

PF 05-MAY-2000; 2000MO-US012371.

PR 05-MAY-1999; 99US-0132686P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

XX WPI; 2000-656493/63.

PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
is used to modulate inflammation.

XX Disclosure; Page 28; 148pp; English.

XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 24
AAB52786

ID AAB52786 standard; peptide; 38 AA.

XX AAB52786;

AC 12-SEP-2003 (revised)

DT 23-FEB-2001 (first entry)

DE T21/DP107 peptide fragment #68.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.

OS Human immunodeficiency virus 1.

PN WQ200066622-A1.

PD 09-NOV-2000.

PF 05-MAY-2000; 2000MO-US012371.

PR 05-MAY-1999; 99US-0132686P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

XX WPI; 2000-656493/63.

PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
is used to modulate inflammation.

XX Claim 12; Page 29; 148pp; English.

XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 25

AAB52823
ID AAB52823 standard; peptide; 38 AA.

XX AAB52823;

AC 12-SEP-2003 (revised)

DT 23-FEB-2001 (first entry)

DE T21/DP107 peptide fragment #100.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.

OS Human immunodeficiency virus 1.

PN W0200066622-A1.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000MO-US012371.
XX
PR 05-MAY-1999; 99US-0132686P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang JM, Oppenheim JT, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
DR Administration of peptide agents with a sequence corresponding to a
XX partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
PS Claim 15; Page 42; 148pp; English.
XX
CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
XX helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
XX critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
XX
Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIDAQOHLQLTWQIKQLQARIILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGICIKQLQARIILAVERYLKQ 38
RESULT 26
AAG63858
ID AAG63858 standard; peptide; 38 AA.
XX
AC AAG63858;
XX
AC 11-SEP-2003 (revised)
XX
DT 29-OCT-2001 (first entry)
XX
DE Amino acid sequence of a HIV-1 gp41 peptide fragment.
XX
XX HIV-1; isolate LAI; gp41; viral entry; envelope protein; glycoprotein;
XX viral infection; antiviral.
XX
OS Human immunodeficiency virus 1.
XX
PN W0200159457-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001MO-US004030.
XX
PR 10-FEB-2000; 2000US-0181543P.
XX
PR 28-SEP-2000; 2000US-0235901P.
XX
PA (PANA-) PANACOS PHARM INC.
XX
PI Wild CT, Allaway GP;
XX WPI; 2001-522493/57.
XX
DR Screening for inhibitors of viral entry structure formation by
PT

PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.
XX
PS Disclosure; Page 23; 68pp; English.
XX
CC The present sequence represents a fragment of a Human immunodeficiency
CC virus type 1 (HIV-1) isolate LAI gp41 protein. The peptide is used to
CC raise antibodies for use in the method of the invention. The
CC specification describes a method of screening for inhibitors of viral
CC entry structure formation. The method comprises contacting a viral
CC envelope protein or glycoprotein (e.g. gp41) with a triggering agent and
CC a candidate compound to form a mixture, and measuring the effect that the
CC candidate compound has on the formation of conformational intermediates.
CC The effect of the candidate compound can be measured by antibody binding
CC to these conformational intermediates. The compounds identified by the
CC method are useful as inhibitors for inhibiting or preventing viral
CC infection and to treat humans infected with HIV-1 or other viruses. This
CC antiviral compounds can also be used to inactivate viruses in body
CC fluids, e.g. blood or blood compounds used for therapeutic purposes. The
CC assay is also useful for detecting antibodies in virus-infected
CC individuals or virus-infected body fluids or tissues that inhibit entry-
CC relevant conformational changes in one or more viral envelope proteins or
CC glycoproteins. The presence of the antibodies in infected individuals or
CC samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 38 AA;
XX
Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIDAQOHLQLTWQIKQLQARIILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWGICIKQLQARIILAVERYLKQ 38
RESULT 27
AAB92349
ID AAB92349 standard; peptide; 38 AA.
XX
AC AAB92349;
XX
DT 22-JUN-2001 (first entry)
XX
DE Virus related peptide SEQ ID NO:1525.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidy1; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN W0200063900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
XX
PR 10-SEP-1999; 99US-0153406P.
XX
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONU-) CONUTCHEM INC.
XX
PI Bridon DF, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
DR Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
PT

XX Disclosure; Page 704; 733bp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimideyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 38 AA:
Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
RESULT 28
AAB77021
ID AAB77021 standard; peptide; 38 AA.
XX
AC AAB77021;
XX
DT 19-APR-2001 (first entry)
XX
DE Core polypeptide T21.
XX
XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
OS Unidentified.
XX
XX WO200103723-A1.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000MO-US018772.
XX
XX 09-JUL-1999; 99US-00350641.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI, 2001-147136/15.
XX
XX
XX New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
XX Disclosure; Page 30; 151pp; English.
XX
XX The present sequence is a core polypeptide which may be linked to an
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX system. It is used to increase the in vitro or ex vivo half-life of the

CC core polypeptide. The hybrid and core polypeptides can be used for
CC modulating fusogenic events and intracellular processes involving coiled-
CC coil peptide interactions. Other uses include preventing, treating and/or
CC diagnosing disorders involving fusion events (e.g. modulation of
CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
CC involving coiled-coil peptides (e.g. bacterial infections) and viral
CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
CC infections caused by human immunodeficiency virus, respiratory syncytial
CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
CC polio virus). The enhancer peptide sequence increases the half-life and
CC reduces the clearance rate of therapeutic peptides, which increases their
CC efficacy and minimises the incidence and severity of adverse side
CC effects. In addition, this increases the sensitivity of the diagnostic
CC procedure in which they are used
XX
SQ Sequence 38 AA:
Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
RESULT 29
AAB77085
ID AAB77085 standard; peptide; 38 AA.
XX
AC AAB77085;
XX
XX 19-APR-2001 (first entry)
XX
XX Core polypeptide T85.
XX
XX
XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
OS Unidentified.
XX
XX WO200103723-A1.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000MO-US018772.
XX
XX 09-JUL-1999; 99US-00350641.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI, 2001-147136/15.
XX
XX
XX New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
XX Disclosure; Page 31; 151pp; English.
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XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX core polypeptide. The hybrid and core polypeptides can be used for
XX modulating fusogenic events and intracellular processes involving coiled-
XX coil peptide interactions. Other uses include preventing, treating and/or
XX diagnosing disorders involving fusion events (e.g. modulation of
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
XX involving coiled-coil peptides (e.g. bacterial infections) and viral

infections that involve cell-cell and/or virus-cell fusion (e.g. viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects. In addition, this increases the sensitivity of the diagnostic procedure in which they are used

Sequence 38 AA:

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLLQLTWGIKOLQARILAVERYLKDQ 38

RESULT 30

AAB77086 standard; peptide; 38 AA.

AAB77086;

19-APR-2001 (first entry)

Core polypeptide T86.

Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.

Unidentified.

WO200103723-A1.

18-JAN-2001.

10-JUL-2000; 2000MO-US018772.

09-JUL-1999; 99US-00350641.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI; 2001-147136/15.

New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.

Disclosure; Page 31; 151pp; English.

The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating fusogenic events and intracellular processes involving coiled-coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus-cell fusion (e.g. viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side

CC effects. In addition, this increases the sensitivity of the diagnostic procedure in which they are used

Sequence 38 AA:

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLLQLTWGIKOLQARILAVERYLKDQ 38

Search completed: June 2, 2004, 11:41:46
Job time : 48.6033 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.3261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336a-543
Perfect score: 188
Sequence: 1 NNILRAIDAOQHLLQLTWQIKQLQARILAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	95.7	729	1	env polypeptide pr
2	180	95.7	861	1	env polypeptide pr
3	177	94.1	357	2	env polypeptide pr
4	177	94.1	851	2	env polypeptide pr
5	177	94.1	853	2	env polypeptide pr
6	177	94.1	854	2	env polypeptide pr
7	177	94.1	855	1	env polypeptide pr
8	177	94.1	856	1	env polypeptide pr
9	177	94.1	856	1	env polypeptide pr
10	177	94.1	861	1	env polypeptide pr
11	176	93.6	357	2	env polypeptide pr
12	176	93.6	357	2	env polypeptide pr
13	176	93.6	357	2	env polypeptide pr
14	176	93.6	358	2	env polypeptide pr
15	176	93.6	358	2	env polypeptide pr
16	176	93.6	358	2	env polypeptide pr
17	174	92.6	357	2	env polypeptide pr
18	174	92.6	859	1	env polypeptide pr
19	174	92.6	868	1	env polypeptide pr
20	174	92.6	443	2	env polypeptide pr
21	173	92.0	445	2	env polypeptide pr
22	173	92.0	454	2	env polypeptide pr
23	173	92.0	843	1	env polypeptide pr
24	173	92.0	846	1	env polypeptide pr
25	173	92.0	852	2	env polypeptide pr
26	173	92.0	855	1	env polypeptide pr
27	173	92.0	856	1	env polypeptide pr
28	173	92.0	856	1	env polypeptide pr
29	173	92.0	861	1	env polypeptide pr

30	172	91.5	859	2	T01672	env polypeptide pr
31	169	89.9	357	2	S21998	env polypeptide pr
32	168	89.4	358	2	S21992	env polypeptide pr
33	165	87.8	852	1	VCLJBR	env polypeptide pr
34	162	86.2	854	1	VCLJST	env polypeptide pr
35	159	84.6	847	2	T09448	env polypeptide pr
36	159	84.6	847	2	S13289	env polypeptide pr
37	155	66.5	104	2	S52930	env polypeptide pr
38	152	64.9	864	1	VCLJG4	env polypeptide pr
39	152	64.9	877	2	S49197	env polypeptide pr
40	152	64.9	877	2	C46356	env polypeptide pr
41	152	64.9	877	2	S46352	env polypeptide pr
42	152	64.9	877	2	S46352	env polypeptide pr
43	152	64.9	877	2	S46352	env polypeptide pr
44	152	64.9	877	2	S46352	env polypeptide pr
45	152	64.9	877	2	S46352	env polypeptide pr
46	152	64.9	877	2	S46352	env polypeptide pr
47	152	64.9	877	2	S46352	env polypeptide pr
48	152	64.9	877	2	S46352	env polypeptide pr
49	152	64.9	877	2	S46352	env polypeptide pr
50	152	64.9	877	2	S46352	env polypeptide pr
51	152	64.9	877	2	S46352	env polypeptide pr
52	152	64.9	877	2	S46352	env polypeptide pr
53	152	64.9	877	2	S46352	env polypeptide pr
54	152	64.9	877	2	S46352	env polypeptide pr
55	152	64.9	877	2	S46352	env polypeptide pr
56	152	64.9	877	2	S46352	env polypeptide pr
57	152	64.9	877	2	S46352	env polypeptide pr
58	152	64.9	877	2	S46352	env polypeptide pr
59	152	64.9	877	2	S46352	env polypeptide pr
60	152	64.9	877	2	S46352	env polypeptide pr
61	152	64.9	877	2	S46352	env polypeptide pr
62	152	64.9	877	2	S46352	env polypeptide pr
63	152	64.9	877	2	S46352	env polypeptide pr
64	152	64.9	877	2	S46352	env polypeptide pr
65	152	64.9	877	2	S46352	env polypeptide pr
66	152	64.9	877	2	S46352	env polypeptide pr
67	152	64.9	877	2	S46352	env polypeptide pr
68	152	64.9	877	2	S46352	env polypeptide pr
69	152	64.9	877	2	S46352	env polypeptide pr
70	152	64.9	877	2	S46352	env polypeptide pr
71	152	64.9	877	2	S46352	env polypeptide pr
72	152	64.9	877	2	S46352	env polypeptide pr
73	152	64.9	877	2	S46352	env polypeptide pr
74	152	64.9	877	2	S46352	env polypeptide pr
75	152	64.9	877	2	S46352	env polypeptide pr
76	152	64.9	877	2	S46352	env polypeptide pr
77	152	64.9	877	2	S46352	env polypeptide pr
78	152	64.9	877	2	S46352	env polypeptide pr
79	152	64.9	877	2	S46352	env polypeptide pr
80	152	64.9	877	2	S46352	env polypeptide pr
81	152	64.9	877	2	S46352	env polypeptide pr
82	152	64.9	877	2	S46352	env polypeptide pr
83	152	64.9	877	2	S46352	env polypeptide pr
84	152	64.9	877	2	S46352	env polypeptide pr
85	152	64.9	877	2	S46352	env polypeptide pr
86	152	64.9	877	2	S46352	env polypeptide pr
87	152	64.9	877	2	S46352	env polypeptide pr
88	152	64.9	877	2	S46352	env polypeptide pr
89	152	64.9	877	2	S46352	env polypeptide pr
90	152	64.9	877	2	S46352	env polypeptide pr

ALIGNMENTS

RESULT 1
VCLJXK
env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N;Alternate names: coat protein gp120; coat protein gp32
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C/Accession: B42995
R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A/Reference number: A42995; MUID:92351552; PMID:11322587
A/Accession: B42995
A/Molecule type: mRNA
A/Residues: 1-729 <SHI>
A/Cross-references: GB:S41266; GB:D01206
C/Genetics:
A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F/1-689/Domain: extracellular #status predicted <EXT>
F/1-33/Domain: signal sequence #status predicted <SIG>
F/17-33/Region: hydrophobic #status predicted
F/34-517/Product: coat protein gp120 #status predicted <CP1>
F/514-517/Region: cleavage processing #status predicted
F/518-729/Product: coat protein gp12 #status predicted <CP2>
F/518-534/Region: hydrophobic #status predicted
F/690-711/Domain: transmembrane #status predicted <TM1>
F/712-729/Domain: intracellular #status predicted <INT>
F/93,141,145,146,163,191,192,237,241,248,269,283,308,338,345,361,367,397,403,408,414

Query Match 95.7%; Score 180; DB 1; Length 729;
Best Local Similarity 94.7%; Pred. No. 2,1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 559 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 596

RESULT 2

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
N/Alternate names: coat polyprotein
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
C/Accession: A42995
R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A/Reference number: A42995; MUID:92351552; PMID:11322587
A/Accession: A42995
A/Molecule type: mRNA
A/Residues: 1-861 <SHI>
A/Cross-references: GB:S41266; GB:D01206
C/Genetics:
A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F/1-689/Domain: extracellular #status predicted <EXT>
F/1-33/Domain: signal sequence #status predicted <SIG>
F/17-33/Region: hydrophobic #status predicted
F/34-517/Product: coat protein gp120 #status predicted <CP1>
F/514-517/Region: cleavage processing #status predicted
F/518-661/Product: coat protein gp41 #status predicted <CP2>
F/518-534/Region: hydrophobic #status predicted
F/690-711/Domain: transmembrane #status predicted <TM1>
F/712-861/Domain: intracellular #status predicted <INT>
F/756-772/Region: hydrophobic #status predicted
F/93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 95.7%; Score 180; DB 1; Length 861;
Best Local Similarity 94.7%; Pred. No. 2,1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38

DB 559 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 596

RESULT 3

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C/Accession: S70422; S21996
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A/Reference number: S70417; MUID:92144209; PMID:1136940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A/Experimental source: patient 27L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 177; DB 2; Length 357;
Best Local Similarity 94.7%; Pred. No. 2,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 54 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 91

RESULT 4

env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C/Accession: S33985
R/Carlini, F.
submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33985
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-851 <CAR>
A/Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C/Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 177; DB 2; Length 851;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 548 NNLRRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 585

RESULT 5

env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <THE>
A/Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 95.7%; Score 180; DB 1; Length 851;
Best Local Similarity 94.7%; Pred. No. 2,1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 94.1%; Score 177; DB 2; Length 853;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 550 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 587

RESULT 6

S13288
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C/Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 65-73, 1990
A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; MUID:91043044; PMID:2172833
A/Accession: S13288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OBR>
C/Superfamily: type E retrovirus env polypotein

Query Match 94.1%; Score 177; DB 2; Length 854;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 551 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 588

RESULT 7

VCLJLR
env polypotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polypotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Stinvaasen, A.; Anand, R.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Ch
Gene 52, 71-82, 1987
A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <SRI>
A/Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:9329403
C/Genetics:

A/Gene: env
C/Superfamily: type E retrovirus env polypotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypote
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-855/Product: env polypotein #status predicted <MNT>
F;20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F;501-855/Product: transmembrane glycoprotein #status predicted <TMM>
F;87,129,140,145,154,158,166,169,199,236,243,264,278,291,297,333,340,355,386,392,398,404
F;87,129,140,145,154,158,166,169,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 94.1%; Score 177; DB 1; Length 855;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 552 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 589

RESULT 8

VCLJH3
env polypotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N/Alternate names: coat polypotein
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03973
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorai
Nberger, J.A.; Papae, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93153; MUID:85111123; PMID:2578615
A/Accession: A03973
A/Molecule type: DNA
A/Residues: 1-856 <RAT>
A/Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA4420

C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypote
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicti

Query Match 94.1%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 553 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 590

RESULT 9

VCLJVL
env polypotein precursor - human immunodeficiency virus type 1 (isolate LV)
N/Alternate names: coat polypotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03974
R/Mesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A/Title: Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovir
A/Reference number: A93155; MUID:85111157; PMID:2982104
A/Accession: A03974
A/Molecule type: DNA
A/Residues: 1-856 <MTE>
A/Cross-references: GB:K02083; NID:9555008; PIDN:AAB5873.1; PID:9328559
C/Genetics:

A/Gene: env
C/Superfamily: type E retrovirus env polypotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypote
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicti

Query Match 94.1%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 6,4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 553 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 590

RESULT 10

VCLJLV
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N/Alternate names: coat polypotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C/Accession: A03975
R/Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A/Title: Nucleotide sequence of the AIDS virus, LAV.
A/Reference number: A90866; MUID:85099333; PMID:2981635
A/Accession: A03975
A/Molecule type: DNA
A/Residues: 1-861 <MWI>
A/Cross-references: GB:X02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C/Genetics:
A/Gene: env
C/Superfamily: type B retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 94.1%; Score 177; DB 1; Length 861;
Best Local Similarity 94.1%; Pred. No. 6.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 558 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 595

RESULT 11

S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C/Accession: S70420; S22006
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70420
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <STE2>
A/Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA3620.1; PID:G60191
A/Experimental source: Patient L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type B retrovirus env polyprotein

Query Match 93.6%; Score 176; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 91

RESULT 12

S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 278
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21994; S70421
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A/Reference number: S21990
A/Accession: S21994
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA3622.1; PID:G60180
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70421
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-140,'X',142-312,'X',314-357 <STE2>
A/Cross-references: EMBL:X61355; NID:G60179
C/Superfamily: type B retrovirus env polyprotein

Query Match 93.6%; Score 176; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 91

RESULT 13

S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 4B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:G60188; PIDN:CAA3618.1; PID:G60189
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292,'X',294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:G60188
C/Superfamily: type B retrovirus env polyprotein

Query Match 93.6%; Score 176; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 91

RESULT 14

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA3616.1; PID:G60187
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333,'X',335-358 <STE2>
A:Cross-references: EMBL:X61352; NID:g60186
C:Superfamily: type E retrovirus env polypeptide

Query Match 93.6%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 55 NNILRAIEAQOHLQLTWGIRKQLQARVLAVERYLKDQ 92

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

Submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21990

A:Accession: S22000

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.6%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 55 NNILRAIEAQOHLQLTWGIRKQLQARVLAVERYLKDQ 92

RESULT 16

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment

S70417

C/Species: human immunodeficiency virus type 1, HIV-1

A:Variety: patient 3B

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

C/Accession: S70417

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A:Reference number: S70417; MUID:92144209; PMID:1176940

A:Accession: S70417

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA3614.1; PID:g60185

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.6%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 3.3e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 55 NNILRAIEAQOHLQLTWGIRKQLQARVLAVERYLKDQ 92

RESULT 17

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 20

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C/Accession: S21990; S70423

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

Submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21990

A:Accession: S21990

A:Molecule type: DNA

A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A:Reference number: S70417; MUID:92144209; PMID:1176940

A:Accession: S70423

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332,'X',334-357 <STE2>

A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.6%; Score 174; DB 2; Length 357;
Best Local Similarity 89.5%; Pred. No. 6.2e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAQOHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 54 NNILRAIEAQOHLQLTWGIRKQLQARVLAVERYLKDQ 91

RESULT 18

env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)

N:Alternate names: coat polypeptide

C/Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C/Accession: A28922

R:Guirgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal

Virology 164, 531-536, 1988

A:Title: Envelope sequences of two new United States HIV-1 isolates.

A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: A28922

A:Molecule type: DNA

A:Residues: 1-859 <GUR>

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protei

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-859/Product: env polypeptide #status predicted <EP>

F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401,

RESULT 19

env polypeptide - human immunodeficiency virus type 1 (isolate CDC-451)

N:Alternate names: coat polypeptide

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: C25523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A/Reference number: A94136; NCID:87041461; PMID:3490666
A/Accession: C25523
A/Molecule type: DNA
A/Residues: 1-868 <DES>
A/Cross-references: GB:M13137; NID:9326460; PIDN:AAA44311.1; PID:9326467
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F:1-521/Product: coat protein gp120 #status predicted <GP1>
F:522-868/Product: coat protein gp41 #status predicted <GP2>
F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459
Query Match 92.6%; Score 174; DB 1; Length 868;
Best Local Similarity 94.7%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 20
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: C41621
R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; NCID:92107924; PMID:1763038
A/Accession: C41621
A/Molecule type: DNA
A/Residues: 1-443 <BUR>
A/Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015
A/Note: this virus was isolated from the mother's sexual partner
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca
Query Match 92.0%; Score 173; DB 2; Length 443;
Best Local Similarity 89.5%; Pred. No. 1,1e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 38
Db 293 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 330

RESULT 21
A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C/Accession: A41621
R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; NCID:92107924; PMID:1763038
A/Accession: A41621
A/Molecule type: DNA

A/Residues: 1-445 <BUR>
A/Cross-references: GB:M77228; NID:9328627; PIDN:AAB03790.1; PID:9555013
A/Note: this virus was isolated from the mother
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:426-445/Domain: transmembrane #status predicted <TMN>
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:
Query Match 92.0%; Score 173; DB 2; Length 445;
Best Local Similarity 89.5%; Pred. No. 1,1e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 38
Db 295 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 332

RESULT 22
B41621
env polyprotein D - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C/Accession: B41621
R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; NCID:92107924; PMID:1763038
A/Accession: B41621
A/Molecule type: DNA
A/Residues: 1-454 <BUR>
A/Cross-references: GB:M77279
A/Note: this virus was isolated from the daughter
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:435-454/Domain: transmembrane #status predicted <TMN>
F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo
Query Match 92.0%; Score 173; DB 2; Length 454;
Best Local Similarity 89.5%; Pred. No. 1,1e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 38
Db 304 NNLRRAIDAOQHLLQTLTWQIKOLQARILAVERYLKQ 341

RESULT 23
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N/Alternate names: coat polyprotein
N/Contains: coat protein gp120; coat protein gp41
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C/Accession: H44001
R/Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A/Title: Complete nucleotide sequence, genome organization, and biological properties of
A/Reference number: A44001; NCID:93021387; PMID:1404605
A/Accession: H44001
A/Molecule type: DNA
A/Residues: 1-843 <LTY>

A/Cross-references: GB:M3258
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypeptide
 C/Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:19-35/Region: hydrophobic
 F:30-489/Product: coat protein gp120 #status predicted <GP1>
 F:490-843/Product: coat protein gp41 #status predicted <GP2>
 F:499-515/Region: hydrophobic
 F:673-689/Region: hydrophobic
 F:738-755/Domain: transmembrane #status predicted <TM>
 F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 92.0%; Score 173; DB 1; Length 843;
 Best Local Similarity 89.5%; Pred. No. 2,2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 38
 DB 540 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 577

RESULT 24
 VCLJND
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate NDK)
 N/Alternate names: coat polypeptide
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
 C/Accession: J000066
 R/Sprite: B.; Size: J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
 Gene 81, 275-284, 1989
 A/Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus
 A/Reference number: J000065; MUID:90034200; PMID:2806917
 A/Accession: J000066
 A/Molecule type: DNA
 A/Residues: 1-846 <SP1>
 A/Cross-references: GB:M27323; NID:g328154; PIDN:AAA4873.1; PID:g328162
 A/Note: the authors translated the codon GCG for residue 523 as Arg
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypeptide
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-501/Product: coat protein gp120 #status predicted <GP1>
 F:502-846/Product: coat protein gp41 #status predicted <GP2>
 F:502-520/Domain: transmembrane #status predicted <TM1>
 F:674-692/Domain: transmembrane #status predicted <TM2>
 F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 92.0%; Score 173; DB 1; Length 846;
 Best Local Similarity 89.5%; Pred. No. 2,2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 38
 DB 543 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 580

RESULT 25
 T12016
 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: T12016
 R/McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Shepard, W.H.
 AIDS Res Hum Retroviruses 14, 329-337, 1998
 A/Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
 A/Reference number: Z17379; MUID:9818716; PMID:9519894
 A/Accession: T12016
 A/status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-852 <MCC>
 A/Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypeptide

Query Match 92.0%; Score 173; DB 2; Length 852;
 Best Local Similarity 89.5%; Pred. No. 2,2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 38
 DB 549 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 586

RESULT 26
 VCLJ7A2
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)
 N/Alternate names: coat polypeptide
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C/Accession: A03976
 R/Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi
 Science 227, 484-492, 1985
 A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
 A/Reference number: A04003; MUID:85090453; PMID:2578227
 A/Accession: A03976
 A/Molecule type: DNA
 A/Residues: 1-855 <SAN>
 A/Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypeptide
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
 F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458/
 F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.0%; Score 173; DB 1; Length 855;
 Best Local Similarity 89.5%; Pred. No. 2,2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 38
 DB 552 NNILRAIDAOQHLLQITWQIKQLQARILAVERYLKDQ 589

RESULT 27
 VCLJ3W
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMU1)
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
 C/Accession: A24774
 R/Scarich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.;
 Cell 45, 637-648, 1986
 A/Title: Identification and characterization of conserved and variable regions in the en
 A/Reference number: A24774; MUID:86218077; PMID:2423250
 A/Accession: A24774
 A/Molecule type: DNA
 A/Residues: 1-856 <STA>
 A/Cross-references: GB:K03455; GB:M38432; NID:g1906382
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polypeptide
 C/Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-501/Product: coat protein gp120 #status predicted <GP1>
 F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,455

Query Match 92.0%; Score 173; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 2.2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWGIKOLQARILAVERYLKDQ 38
 DB 553 NNILRAIEAQOHLLQLTWGIKOLQARVLAVERYLKDQ 590

RESULT 28

A44963
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
 N:Alternate names: coat polyprotein
 N:Contains: coat protein gp120; coat protein gp41
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
 C:Accession: A44963
 R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989
 A>Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
 A:Reference number: A44963; MUID:89228766; PMID:2713163
 A:Accession: A44963
 A:Molecule type: DNA
 A:Residues: 1-856 <SRI>
 A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-520/Product: coat protein gp120 #status predicted <CP1>
 F:521-856/Product: coat protein gp41 #status predicted <CP2>
 F:684-705/Domain: transmembrane #status predicted <TMN>
 F:87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611

Query Match 92.0%; Score 173; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 2.2e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWGIKOLQARILAVERYLKDQ 38
 DB 553 NNILRAIEAQOHLLQLTWGIKOLQARVLAVERYLKDQ 590

RESULT 29

VCLJSC
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
 N:Alternate names: coat polyprotein
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C:Accession: B28922
 R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
 Virology 164, 531-536, 1988
 A>Title: Envelope sequences of two new United States HIV-1 isolates.
 A:Reference number: A28922; MUID:88219542; PMID:3369091
 A:Accession: B28922
 A:Molecule type: DNA
 A:Residues: 1-861 <GUR>
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-661/Product: env polyprotein #status predicted <BP>
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 92.0%; Score 173; DB 1; Length 861;
 Best Local Similarity 89.5%; Pred. No. 2.3e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWGIKOLQARILAVERYLKDQ 38
 DB 558 NNILRAIEAQOHLLQLTWGIKOLQARVLAVERYLKDQ 595

RESULT 30

T01672
 envelope polyprotein precursor - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01672
 R:Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986
 A>Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
 A:Reference number: Z14389; MUID:86245056; PMID:2424612
 A:Accession: T01672
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-859 <MLI>
 A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
 C:Superfamily: type E retrovirus env polyprotein

Query Match 91.5%; Score 172; DB 2; Length 859;
 Best Local Similarity 89.5%; Pred. No. 3.1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLLQLTWGIKOLQARILAVERYLKDQ 38
 DB 555 NNILRAIEAQOHLLQLTWGIKOLQARVLAVERYLKDQ 592

Search completed: June 2, 2004, 11:50:11
 Job time: 10.3261 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 6.19565 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-543
Perfect score: 188
Sequence: 1 NNILRAIDAQOHILQLTWQIKQLQARILAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	95.7	861	1	ENV_HV1KB
2	177	94.1	847	1	ENV_HV1W2
3	177	94.1	853	1	ENV_HV1MF
4	177	94.1	853	1	ENV_HV1MF
5	177	94.1	853	1	ENV_HV1Z2
6	177	94.1	855	1	ENV_HV1Z6
7	177	94.1	856	1	ENV_HV1B1
8	177	94.1	856	1	ENV_HV1H2
9	177	94.1	856	1	ENV_HV1H3
10	177	94.1	856	1	ENV_HV1LM
11	177	94.1	856	1	ENV_HV1PV
12	177	94.1	861	1	ENV_HV1BR
13	176	93.6	847	1	ENV_HV1S1
14	176	93.6	855	1	ENV_HV1OY
15	174	92.6	848	1	ENV_HV1JR
16	174	92.6	856	1	ENV_HV1MN
17	174	92.6	868	1	ENV_HV1C4
18	173	92.0	843	1	ENV_HV1Y2
19	173	92.0	846	1	ENV_HV1ND
20	173	92.0	851	1	ENV_HV1B8
21	173	92.0	852	1	ENV_HV1S3
22	173	92.0	855	1	ENV_HV1A2
23	173	92.0	856	1	ENV_HV1S2
24	173	92.0	856	1	ENV_HV1M1
25	173	92.0	856	1	ENV_HV1Z1
26	173	92.0	855	1	ENV_HV1Z1
27	173	92.0	867	1	ENV_HV1J3
28	172	91.5	859	1	ENV_HV1A1
29	168	89.4	863	1	ENV_HV1Z8
30	165	87.8	852	1	ENV_HV1Z8
31	162	86.2	854	1	ENV_SIVCZ
32	122	64.9	865	1	ENV_SIVAT
33	122	64.9	877	1	ENV_SIVAG

34	119	63.3	854	1	ENV_SIVAT	Q02837 simian immu
35	117	62.2	768	1	ENV_SIVAT	P27757 simian immu
36	111	59.0	712	1	ENV_HV2S2	P32536 human immu
37	111	59.0	851	1	ENV_HV2D1	P17755 human immu
38	111	59.0	851	1	ENV_HV2G1	P18040 human immu
39	111	59.0	856	1	ENV_HV2NZ	P05883 human immu
40	111	59.0	859	1	ENV_HV2ST	P20872 human immu
41	110	58.5	859	1	ENV_HV2CA	P24105 human immu
42	109	58.0	380	1	ENV_SIVM2	P08810 simian immu
43	109	58.0	858	1	ENV_HV2RO	P04577 human immu
44	109	58.0	885	1	ENV_SIVS4	P12492 simian immu
45	109	58.0	889	1	ENV_SIVSP	P19503 simian immu
46	108	57.4	882	1	ENV_SIVM1	P05885 simian immu
47	107	56.9	859	1	ENV_HV2D2	P15831 human immu
48	106	56.4	880	1	ENV_SIVM1	P11267 simian immu
49	105	55.9	846	1	ENV_HV2SB	P12449 human immu
50	105	55.9	881	1	ENV_SIVMK	P05884 human immu
51	104	55.3	821	1	ENV_SIVGB	P22380 simian immu
52	104	55.3	857	1	ENV_HV2KR	Q74126 human immu
53	104	55.3	860	1	ENV_HV2BE	P18094 human immu
54	52	27.7	8797	1	SNEI_HUMAN	Q8N591 homo sapien
55	51.5	27.4	303	1	ALB3_MAIZE	P10593 zea mays (m
56	51.5	27.4	924	1	HXX3_RAT	P27926 rattus norv
57	51	27.1	2564	1	SPOC_HUMAN	Q9N254 homo sapien
58	50.5	26.9	536	1	CAR3_RAT	Q9EPY0 rattus norv
59	50	26.6	1379	1	M3K5_MOUSE	O35099 mus musculu
60	49.5	26.3	445	1	EXYL_STRAAN	O99C40 staphylococ
61	49.5	26.3	676	1	HS7C_TRYBB	P20030 trypanosoma
62	49	26.1	204	1	R115_DROME	O17445 drosophila
63	49	26.1	361	1	CG2B_HYDAT	P51988 hydra atten
64	48.5	25.8	300	1	R1P3_MAIZE	P25891 zea mays (m
65	48.5	25.8	301	1	R1P3_MAIZE	P28522 zea mays (m
66	48.5	25.8	304	1	R1P3_MAIZE	P25892 zea mays (m
67	48	25.5	140	1	PLGN_SALTY	P37406 salmonella
68	48	25.5	236	1	CT6_SCHEMA	P46435 schistosoma
69	48	25.5	392	1	CG2B_CHLVR	P51987 chlorohydra
70	48	25.5	702	1	AT11_VARV	P34011 variola vir
71	48	25.5	906	1	CTN1_HUMAN	P35221 homo sapien
72	48	25.5	906	1	CTN1_MOUSE	P26231 mus musculu
73	48	25.5	1374	1	M3K5_HUMAN	O99663 homo sapien
74	48	25.5	1756	1	PEPL_HUMAN	O60437 homo sapien
75	48	25.5	1849	1	T172_HUMAN	O14961 homo sapien
76	48	25.5	1938	1	MYH4_RABIT	Q28641 furocylagus
77	48	25.5	4349	1	DYHC_FUSO	P78716 mus musculu
78	47.5	25.3	132	1	RS8_CLOAB	O97632 clostridium
79	47.5	25.3	139	1	SOS1_MOUSE	O62245 mus musculu
80	47.5	25.3	1333	1	SOS1_HUMAN	O07889 homo sapien
81	47.5	25.3	1411	1	EEA1_HUMAN	O15075 homo sapien
82	47.5	25.3	1938	1	MYH4_HUMAN	O9UKX3 homo sapien
83	47	25.0	305	1	OTC_SYNP7	O935Y4 synchococc
84	47	25.0	376	1	O43A_DROME	P81917 drosophila
85	47	25.0	418	1	DADI_RHITO	O08508 rhizobium 1
86	47	25.0	551	1	YD25_YEAST	O07657 saccharomyc
87	47	25.0	688	1	DP3X_HAEIN	P43746 haemophilus
88	47	25.0	938	1	NMZ1_MOUSE	O05886 homo sapien
89	47	25.0	938	1	NMZ1_MOUSE	P35438 mus musculu
90	47	25.0	938	1	NMZ1_RAT	P35439 rattus norv

ALIGNMENTS

RESULT 1
ID ENV_HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).

CC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 CC NCBI_TaxID=36375;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=92351552; PubMed=1322587;
 CC RA Shintzu H., Haebe F., Tauchie H., Morikawa S., Ushijima H.,
 CC Kitanura T.;
 CC "Analysis of a human immunodeficiency virus type 1 isolate carrying a
 CC truncated transmembrane glycoprotein.";
 CC Virology 189:534-546(1992).
 CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
 CC THE CODONS FOR 723-ALA AND 730-ARG.
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 CC -----
 CC EMBL: D12582; BAA02124.1; ALT_SEQ.
 CC PIR: A42995; VCLJKB.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam: PF00516; GP120; 1.
 CC DR Pfam: PF00517; GP41; 1.
 CC KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 CC Signal.
 CC FT SIGNAL. 1 35
 CC FT CHAIN 36 517
 CC FT TRANSMEM 518 861
 CC FT TRANSMEMEM 690 711
 CC FT DISULFID 59 79
 CC FT DISULFID 124 212
 CC FT DISULFID 131 203
 CC FT DISULFID 136 160
 CC FT DISULFID 225 254
 CC FT DISULFID 235 246
 CC FT DISULFID 303 337
 CC FT DISULFID 383 446
 CC FT DISULFID 390 419
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 141 141
 CC FT CARBOHYD 145 145
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 CC FT CARBOHYD 622 622
 CC FT CARBOHYD 631 631
 CC FT CARBOHYD 643 643
 CC FT CARBOHYD 821 821

CC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 CC NCBI_TaxID=36375;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=92351552; PubMed=1322587;
 CC RA Shintzu H., Haebe F., Tauchie H., Morikawa S., Ushijima H.,
 CC Kitanura T.;
 CC "Analysis of a human immunodeficiency virus type 1 isolate carrying a
 CC truncated transmembrane glycoprotein.";
 CC Virology 189:534-546(1992).
 CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
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 CC -----
 CC EMBL: D12582; BAA02124.1; ALT_SEQ.
 CC PIR: A42995; VCLJKB.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam: PF00516; GP120; 1.
 CC DR Pfam: PF00517; GP41; 1.
 CC KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 CC Signal.
 CC FT SIGNAL. 1 35
 CC FT CHAIN 36 517
 CC FT TRANSMEM 518 861
 CC FT TRANSMEMEM 690 711
 CC FT DISULFID 59 79
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 CC FT CARBOHYD 631 631
 CC FT CARBOHYD 643 643
 CC FT CARBOHYD 821 821

FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CD1B33D73AA5BCAE CRC64;
 Query Match 94.1%; Score 177; DB 1; Length 847;
 Best Local Similarity 92.1%; Pred. No. 5e-17; 1; Indels 0; Gaps 0;
 Matches 35; Conservative 2; Mismatches 1;
 QY 1 NNILRAIDAQOHLQLTWGIKOLQARILAVERYLKQ 38
 Db 544 NNILRAIDAQOHLQLTWGIKOLQARILAVERYLKQ 581
 RESULT 3
 ENV_HVIMF STANDARD; PRT; 853 AA.
 ID ENV_HVIMF
 AC P04581;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP MEDLINE=86245056; PubMed=2424612;
 RA Alizen M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
 RL Cell 46:63-74(1986).
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 CC -----
 CC EMBL: K03454; AAA44329.1; -;
 DR EMBL: A07108; CAA00616.1; -;
 DR HIV: K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL. 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 853 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAAD07A5 CRC64;
 Query Match 94.1%; Score 177; DB 1; Length 853;
 Best Local Similarity 94.7%; Pred. No. 5.1e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNILRAIDAQOHLQLTWGIKOLQARILAVERYLKQ 38
 Db 550 NNILRAIDAQOHLQLTWGIKOLQARILAVERYLKQ 587

RESULT 4
 ENV_HVIMF STANDARD; PRT; 853 AA.
 ID ENV_HVIMF
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C., Wasiak A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";
 RL J. Virol. 64:3792-3803(1990).
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CC -----
 DR EMBL; M33943; AAA44850.1; -.
 DR PDB; 1AK; 16-JUN-97.
 DR HIV; M33943; ENVSMFA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 509
 FT CHAIN 510 853
 FT DISULFID 54 74
 FT DISULFID 119 203
 FT DISULFID 126 194
 FT DISULFID 131 157
 FT DISULFID 216 245
 FT DISULFID 226 237
 FT DISULFID 329 329
 FT DISULFID 376 443
 FT DISULFID 383 416
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 195 195
 FT CARBOHYD 232 232
 FT CARBOHYD 239 239
 FT CARBOHYD 260 260
 FT CARBOHYD 274 274
 FT CARBOHYD 287 287
 FT CARBOHYD 293 293
 FT CARBOHYD 299 299
 FT CARBOHYD 330 330
 FT CARBOHYD 354 354
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 395 395
 FT CARBOHYD 404 404
 FT CARBOHYD 446 446
 FT CARBOHYD 461 461
 FT CARBOHYD 609 609
 FT CARBOHYD 614 614
 FT CARBOHYD 623 623
 FT CARBOHYD 635 635
 FT CARBOHYD 672 672
 FT CARBOHYD 748 748
 FT CARBOHYD 814 814
 FT CARBOHYD 853 AA; 96912 MW; 3377B93BF22ABA CRC64;
 SQ SEQUENCE

Query Match 94.1%; Score 177; DB 1; Length 853;
 Best Local Similarity 94.7%; Pred. No. 5, 1e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (2Z/DC-234 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11683;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA Theodore T. Buckley-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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CC -----
 DR EMBL; M22639; AAA45370.1; -.
 DR PIR; S54384; S54384.
 DR HIV; M22639; ENV5R226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR00777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 508
 FT CHAIN 509 853
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 154
 FT DISULFID 130 154
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 330
 FT DISULFID 376 442
 FT DISULFID 383 415
 FT CARBOHYD 87 87
 FT CARBOHYD 137 137
 FT CARBOHYD 144 144
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 188 188
 FT CARBOHYD 198 198
 FT CARBOHYD 235 235
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
 FT CARBOHYD 296 296
 FT CARBOHYD 331 331
 FT CARBOHYD 338 338
 FT CARBOHYD 353 353
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 402 402
 FT CARBOHYD 441 441
 FT CARBOHYD 445 445
 FT CARBOHYD 458 458
 FT CARBOHYD 459 459
 FT CARBOHYD 462 462
 FT CARBOHYD 608 608
 FT CARBOHYD 613 613
 FT CARBOHYD 622 622
 FT CARBOHYD 634 634
 FT CARBOHYD 671 671
 FT CARBOHYD 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;
 SQ SEQUENCE

ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)

Query Match 94.1%; Score 177; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 5.1e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 NNLRAIDAOQHLLQTLTWGIKOLARILAVERYLKQ 38
 553 NNLRAIDAOQHLLQTLTWGIKOLARILAVERYLKQ 590

RESULT 9
 ENV_HV1H3 STANDARD; PRT; 856 AA.

AC P04624;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11707;
 RN [1]
 RP MEDLINE=8528248; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HTLV-III env gene products synthesized in E. coli are recognized by anti-bodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).

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CC -----
 CC EMBL: M14100; AAA4679.1; -.
 DR PDB; 1JAU; 17-OCT-01.
 DR HIV; M14100; ENVSHX3.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

Query Match 94.1%; Score 177; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 5.1e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 NNLRAIDAOQHLLQTLTWGIKOLARILAVERYLKQ 38
 553 NNLRAIDAOQHLLQTLTWGIKOLARILAVERYLKQ 590

RESULT 10
 ENV_HV1H3 STANDARD; PRT; 856 AA.

AC P070626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN [1]
 RP MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIb)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC -----
 DR EMBL; U12055; AA76690.1; -
 DR PDB; 1IF3; 02-MAY-01.
 DR GlycoSutEDB; 070626; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KM 3d-structure; 1

FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SOURCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

Query Match 94.1%; Score 177; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 5.1e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQTLVWQIKQLQARILAVERYLKQ 38
 DB 553 NNLRAIDAQOHLQTLVWQIKQLQARILAVERYLKQ 590

RESULT 11
 ENV_HVLPV STANDARD; PRT; 856 AA.
 ID ENV_HVLPV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 CX NCBI_TaxID=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511157; PubMed=2982104;
 RA Mesling M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
 RA Capon D.J.;
 RT "Nucleic acid structure and expression of the human
 RT Aids/Lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
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DR EMBL; K02083; AAB59873.1; -; ALT_SEQ.
 DR EMBL; X01762; CA425903.1; ALT_SEQ.
 DR PIR; A03974; VCLJVL.
 DR HIV; K02083; ENVSPV22.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 625 625
 FT CARBOHYD 637 637

FT	CARBOHYD	674	674	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
SO	SEQUENCE	856 AA;	97339 MW;	5FCDBD1DC3C120983	CRC64;				
Query Match									
Best Local Similarity		94.1%;		Score 177; DB 1;					
Matches		36; Conservative		1; Mismatches					
		1;		Indels					
		0;		Gaps					
		0;							
QY	1 NNLIRAIIDAQOHLIQLTWGIKQLQARILAVERYIKDQ 38								
Db	553>NNLIRAIIEAQOHLIQLTWGIKQLQARILAVERYIKDQ 590								
RESULT 12									
ENV_HV1BR	STANDARD;	PRT;	861 AA.						
ID	ENV_HV1BR								
AC	P03377;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	10-OCT-2003 (Rel. 42, Last annotation update)								
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].								
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)].								
GN	ENV.								
OS	Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).								
OC	Vitruase; Retroid vitruase; Retroviridae; Lenticivirus.								
OX	NCBI_TaxID=11686;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=8509333; PubMed=2981635;								
RA	Wain-Hobson S., Sonigo P., Danos O., Cole S., Allison M.;								
RT	"Nucleotide sequence of the AIDS virus, LAV.";								
RL	Cell 40:9-17(1985).								
CC	-----								
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CC	modified and this statement is not removed. Usage by and for commercial								
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; K02013; AA859751.1; -								
DR	EMBL; A04321; CA000352.1; -								
DR	PIR; A03975; VCLJLV.								
DR	PDB; 1ERF; 20-FEB-02.								
DR	HIV; K02013; ENVGBRU.								
DR	InterPro; IPR000328; Env GP41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120; 1.								
DR	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;								
KW	3D-structure.								
FT	SIGNAL	1	30						
FT	CHAIN	31	516	EXTERIOR MEMBRANE GLYCOPROTEIN.					
FT	CHAIN	517	861	TRANSMEMBRANE GLYCOPROTEIN.					
FT	DISULFID	54	74	BY SIMILARITY.					
FT	DISULFID	119	210	BY SIMILARITY.					
FT	DISULFID	126	201	BY SIMILARITY.					
FT	DISULFID	131	162	BY SIMILARITY.					
FT	DISULFID	223	252	BY SIMILARITY.					
FT	DISULFID	233	244	BY SIMILARITY.					
FT	DISULFID	301	336	BY SIMILARITY.					
FT	DISULFID	383	450	BY SIMILARITY.					

Query Match	Similarity	Score	DB	Length
Best Local	94.1%	177	DB 1	861
Matches	36	Conservative	1	Mismatches 1; Indels 0; Gaps 0;
DB	558	NTLIRALPAEQHLLQLTWVGIKQLQARILAVERYLKQ	595	
ENV_HV1S1	STANDARD	PRT	847 AA	
AC	P19550			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.			
OX	NCBI_TaxID=11691;			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90347835; PubMed=2384920;			
RX	Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.			
RA	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";			
RT	J. Virol. 64:4390-4398(1990).			
RL	J. Virol. 64:4390-4398(1990).			
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CC	or send an email to license@ebc.sib.ch .			
CC	EMBL; M65024; AAA45072.1; --			
DR	PDB; 1OBE; 15-MAY-97.			
DR	HIV; M38428; ENVSSP162.			
DR	InterPro; IPR000328; Env GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KM	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.			

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FT SIGNAL 1 29
FT CHAIN 30 502
FT CHAIN 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 136 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87 408
FT CARBOHYD 135 135
FT CARBOHYD 154 154
FT CARBOHYD 186 186
FT CARBOHYD 195 195
FT CARBOHYD 232 232
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 336 336
FT CARBOHYD 352 352
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 401 401
FT CARBOHYD 438 438
FT CARBOHYD 454 454
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

Query Match 93.6%; Score 176; DB 1; Length 847;
Best Local Similarity 92.1%; Pred. No. 7e-17;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQD 38
Db 544 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 581

RESULT 14
ENV_HV10Y STANDARD; PRT; 855 AA.
ID ENV_HV10Y
AC P20888;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M26727; AAA83397.1; -.
DR HIV; M26727; ENVSOIT.
DR Interpro; IPR000328; Env GP41.
DR Interpro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 442
FT DISULFID 388 415
FT DISULFID 87 87
FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 192 192
FT CARBOHYD 202 202
FT CARBOHYD 239 239
FT CARBOHYD 245 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 336 336
FT CARBOHYD 359 359
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 399 399
FT CARBOHYD 405 405
FT CARBOHYD 458 458
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 93.6%; Score 176; DB 1; Length 855;
Best Local Similarity 92.1%; Pred. No. 7e-17;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQD 38
Db 552 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 589

RESULT 15
ENV_HV10Y STANDARD; PRT; 848 AA.
ID ENV_HV10Y
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
```

GN ENV.
 OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11688;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koyanagi S.; Chen I.S.Y.;
 RL Submitted (DEC-1988) to the HIV data bank.
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 CC -----
 DR EMBL; M38429; AAB03749.1; --
 DR PDB; 1CE4; 18-MAR-99.
 DR HIV; M38429; ENV5JRCSP.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 503
 FT CHAIN 504 848
 FT DISULFID 53 73
 FT DISULFID 118 203
 FT DISULFID 125 194
 FT DISULFID 130 154
 FT DISULFID 216 245
 FT DISULFID 226 237
 FT DISULFID 294 328
 FT DISULFID 374 437
 FT DISULFID 381 410
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 137 137
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 195 195
 FT CARBOHYD 228 228
 FT CARBOHYD 239 239
 FT CARBOHYD 260 260
 FT CARBOHYD 274 274
 FT CARBOHYD 287 287
 FT CARBOHYD 293 293
 FT CARBOHYD 299 299
 FT CARBOHYD 329 329
 FT CARBOHYD 336 336
 FT CARBOHYD 352 352
 FT CARBOHYD 382 382
 FT CARBOHYD 388 388
 FT CARBOHYD 392 392
 FT CARBOHYD 403 403
 FT CARBOHYD 440 440
 FT CARBOHYD 453 453
 FT CARBOHYD 603 603
 FT CARBOHYD 608 608
 FT CARBOHYD 617 617
 FT CARBOHYD 629 629
 FT CARBOHYD 808 808
 SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;
 QY 1 NNLRAIDAQOHLQTLTWGQIKQLQARILAVERYLKDO 38

DB 545 NNLRAIDAQOHLQTLTWGQIKQLQARILAVERYLKDO 582
 RESULT 16
 ID ENV_HV1MN STANDARD; PRT; 856 AA.
 AC P05877;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP120 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11696;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88219542; PubMed=3369091;
 RA Gargo C.; Guo H.-G.; Franchini G.; Aldovini A.; Collalti E.;
 RA Farrell K.; Wong-Staal F.; Gallo R.C.; Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
 CC PATIENT IN 1984.
 CC -----
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 CC -----
 DR EMBL; M17449; AAA44857.1; --
 DR PDB; 1AC7; 31-JUL-94.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1N12; 25-FEB-03.
 DR PDB; 1N10; 25-FEB-03.
 DR HIV; M17449; ENV5JMN.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 445
 FT DISULFID 388 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 141 141
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT CARBOHYD 202 202
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 QY 1 NNLRAIDAQOHLQTLTWGQIKQLQARILAVERYLKDO 38

FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97140 MW; D197D809340BE732 CRC64;

Query Match 92.6%; Score 174; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 1.3e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
 DB 554 NNLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 591

RESULT 17
 ENV_HV1C4 STANDARD; PRT; 868 AA.

AC P05879; 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11687;
 RN [1]
 RX MEDLINE=3490666; PubMed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A., Andersen P.R., Devare S.G.;
 RT "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RL [2]
 RN SEQUENCE OF 34-43.

RP MEDLINE=90253924; PubMed=2187500;
 RA Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Russo P., Devito A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
 RT "Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1."
 RT AIDS Res. Hum. Retroviruses 6:371-380(1990).

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CC EMBL; M3137; AAA44311.1; -
 DR PIR; C25523; VCLJH4.
 DR HIV; M3137; ENVSCD45.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 FT SIGNAL 1 33
 FT CHAIN 34 522
 FT CHAIN 523 868
 FT CHAIN 55 75
 FT DISULFID 120 216
 FT DISULFID 127 207
 FT DISULFID 132 163
 FT DISULFID 229 258
 FT DISULFID 239 250
 FT DISULFID 307 341
 FT DISULFID 387 456
 FT DISULFID 394 429
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 FT CARBOHYD 162 162
 FT CARBOHYD 166 166
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 FT CARBOHYD 198 198
 FT CARBOHYD 208 208
 FT CARBOHYD 245 245
 FT CARBOHYD 252 252
 FT CARBOHYD 273 273
 FT CARBOHYD 287 287
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 FT CARBOHYD 459 459
 FT CARBOHYD 473 473
 FT CARBOHYD 623 623
 FT CARBOHYD 628 628
 FT CARBOHYD 637 637
 FT CARBOHYD 649 649
 FT CARBOHYD 828 828
 SQ SEQUENCE 868 AA; 98698 MW; A11527FC52A6F0C8 CRC64;

Query Match 92.6%; Score 174; DB 1; Length 868;
 Best Local Similarity 94.7%; Pred. No. 1.4e-16;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NNLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
 DB 565 NNLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 602

RESULT 18
 ENV_HV1Y2 STANDARD; PRT; 843 AA.

AC P35961; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93021387; PubMed=1404605;

[illegible]

D6		540	NNLRRAIEAOQHLLQTLTWGKIKOLQARVLAVERYLDRD	577
RESULT_19				
ENV_HVIND ID	ENV_HVIND STANDARD;	PRT;	846 AA.	
AC P18799;				
DT DT 01-NOV-1990 (Rel. 16, Created)				
DT DT 01-NOV-1990 (Rel. 16, Last sequence update)				
DT DT 15-JUL-1999 (Rel. 38, Last annotation update)				
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN ENV.				
OS Human immunodeficiency virus type 1 (NIX isolate) (HIV-1).				
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX NCBI TaxID=11695;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=90034200; Pubmed=2806917;				
RA Spire B., Site J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.,				
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus.";				
RL Gene 81:275-284(1989).				
CC -I. MISCELLANEOUS: NDK. ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.				
CC -----				
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CC DR EMBL; M27323; AAA44873.1; -.				
DR PIR; J00066; VCLJND.				
DR HIY; M27323; ENV\$NDK.				
DR InterPro; IPR000328; Env_GP41.				
DR InterPro; IPR000777; GP120.				
DR Pfam; PF00516; GP120; 1.				
KW Pfam; PF00517; GP41; 1.				
DR AIDS; Coat protein; Polypotein; Glycopoltein; Transmembrane; Signal.				
KM SIGNAL.	1	29		
FT FT CHAIN	30	501	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT FT CHAIN	502	846	TRANSMEMBRANE GLYCOPROTEIN.	
FT FT DISULFID	53	73	BY SIMILARTY.	
FT FT DISULFID	118	200	BY SIMILARTY.	
FT FT DISULFID	125	191	BY SIMILARTY.	
FT FT DISULFID	130	152	BY SIMILARTY.	
FT FT DISULFID	213	242	BY SIMILARTY.	
FT FT DISULFID	223	234	BY SIMILARTY.	
FT FT DISULFID	291	328	BY SIMILARTY.	
FT FT DISULFID	374	435	BY SIMILARTY.	
FT FT DISULFID	381	408	BY SIMILARTY.	
FT FT CARBOHYD	87		N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	129	129	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	151	151	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	179	179	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	182	182	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	229	229	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	236	236	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	257	257	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	271	271	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	284	284	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	290	290	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	351	351	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	382	382	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	388	388	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	392	392	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	395	395	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT FT CARBOHYD	401	401	N-LINKED (GLCNAC . .) (POTENTIAL).	

FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2883 CRC64;
 Query Match 92.0%; Score 173; DB 1; Length 846;
 Best Local Similarity 89.5%; Pred. No. 1, 9e-16;
 Matches 35; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 38
 Db 543 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 580
 RESULT 20
 ENV_HV1B8 STANDARD; PRT; 851 AA.
 ID ENV_HV1B8
 AC P04582;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11694;
 RN [1]
 RP MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peltway S.R., Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RT Nature 313:277-284(1985).
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 CC EMBL; KO2011; AAA44661.1; -
 DR PDB; 1DDH; 13-JAN-99.
 DR PDB; 1HHG; 31-OCT-93.
 DR PDB; 1QO3; 02-JAN-00.
 DR PDB; 1S2T; 24-DEC-97.
 DR HIV; KO2011; ENV5B8.
 DR GLYCOSULEDB; P04582; -
 DR InterPro: IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM SIGNAL 1 30
 FT CHAIN 31 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.

FT DISULFID 378 440 BY SIMILARITY.
 FT DISULFID 385 413 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
 Query Match 92.0%; Score 173; DB 1; Length 851;
 Best Local Similarity 92.1%; Pred. No. 1, 9e-16;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 38
 Db 548 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 585
 RESULT 21
 ENV_HV1S3 STANDARD; PRT; 852 AA.
 ID ENV_HV1S3
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SP3 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11690;
 RN [1]
 RP MEDLINE=90317906; PubMed=2370688;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RA "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";
 RT J. Virol. 64:4016-4020(1990).
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 CC EMBL; AY352275; AA017031.1; -

FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 444 BY SIMILARITY.
 FT DISULFID 383 417 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DB9 CRC64;

Query Match 92.0%; Score 173; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 1,9e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLTLTWQIKOLQARILAVERYLKQ 38
 Db 553 NNLRAIDAQOHLTLTWQIKOLQARILAVERYLKQ 590

RESULT 25
 ENV_HV12H STANDARD; PRT; 856 AA.
 ID ENV_HV12H
 AC P05881;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11692;
 RN [1]
 RX MEDLINE=9228766; Pubmed=2713163;
 RA Strinvaan A., York D., Butler D. Jr., Jannou-Nasr R., Getchell J., McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
 RT "Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence comparison to recent isolates and generation of hybrid HIV."
 RL AIDS Res. Hum. Retroviruses 5:121-129 (1989).

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CC -----
 CC EMBL; M15896; AAB53948.1; -
 CC DR PIR; A44963; A44963.

DR HIV; M15896; ENV\$Z321.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT CHAIN 1 29
 FT CHAIN 30 511
 FT CHAIN 512 856
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 153
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 331
 FT DISULFID 379 445
 FT DISULFID 386 418
 FT DISULFID 87 87
 FT CARBOHYD 132 132
 FT CARBOHYD 138 138
 FT CARBOHYD 152 152
 FT CARBOHYD 156 156
 FT CARBOHYD 183 183
 FT CARBOHYD 198 198
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 294 294
 FT CARBOHYD 302 302
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 355 355
 FT CARBOHYD 364 364
 FT CARBOHYD 387 387
 FT CARBOHYD 393 393
 FT CARBOHYD 398 398
 FT CARBOHYD 402 402
 FT CARBOHYD 411 411
 FT CARBOHYD 448 448
 FT CARBOHYD 461 461
 FT CARBOHYD 462 462
 FT CARBOHYD 465 465
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 637 637
 SQ SEQUENCE 856 AA; 96909 MW; 8396B3F8BBD174E CRC64;

Query Match 92.0%; Score 173; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 1,9e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLTLTWQIKOLQARILAVERYLKQ 38
 Db 553 NNLRAIDAQOHLTLTWQIKOLQARILAVERYLKQ 590

RESULT 26
 ENV_HV12H STANDARD; PRT; 865 AA.
 ID ENV_HV12H
 AC P04579;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11701;
 RN [1]
 RX SEQUENCE FROM N.A.

RX MEDLINE=66218077; PubMed=2423250.
 RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.,
 RT "Identification and characterization of conserved and variable
 RT regions in the envelope gene of HTLV-II/LAV, the retrovirus of
 RT AIDS";
 RL Cell 45:637-648(1986).
 CC -----
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 CC -----
 DR EMBL: M17451; AAA45057.1; -.
 DR HIV; M17451; ENVSRP.
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 519
 FT DISULFID 520 865
 FT DISULFID 53 73
 FT DISULFID 118 218
 FT DISULFID 125 209
 FT DISULFID 130 157
 FT DISULFID 231 260
 FT DISULFID 241 252
 FT DISULFID 309 343
 FT DISULFID 389 452
 FT DISULFID 396 425
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 136 136
 FT CARBOHYD 139 139
 FT CARBOHYD 156 156
 FT CARBOHYD 193 193
 FT CARBOHYD 194 194
 FT CARBOHYD 197 197
 FT CARBOHYD 198 198
 FT CARBOHYD 203 203
 FT CARBOHYD 210 210
 FT CARBOHYD 247 247
 FT CARBOHYD 254 254
 FT CARBOHYD 275 275
 FT CARBOHYD 289 289
 FT CARBOHYD 302 302
 FT CARBOHYD 308 308
 FT CARBOHYD 314 314
 FT CARBOHYD 344 344
 FT CARBOHYD 351 351
 FT CARBOHYD 367 367
 FT CARBOHYD 397 397
 FT CARBOHYD 403 403
 FT CARBOHYD 407 407
 FT CARBOHYD 413 413
 FT CARBOHYD 418 418
 FT CARBOHYD 455 455
 FT CARBOHYD 471 471
 FT CARBOHYD 620 620
 FT CARBOHYD 625 625
 FT CARBOHYD 634 634
 FT CARBOHYD 646 646
 FT CARBOHYD 825 825
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC314ADCAC CRC64;

Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NMLRAIDAQOHLQLTWQIKQLQARIVARYLKDQ 38
 Db 562 NMLRAIEAQOHLQLTWGIKQLQARIVARYLQDQ 599
 RESULT 27
 ID ENV_HV1J3 STANDARD; PRT; 867 AA.
 AC P12489;
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11694;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=89352108; PubMed=2669897;
 RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.,
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
 RT HIV-1 and their expression in bacteria";
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
 CC -----
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 CC -----
 DR EMBL: M21138; AAB03526.1; -.
 DR HIV; M21138; ENVSRP.
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 516
 FT DISULFID 517 867
 FT DISULFID 53 73
 FT DISULFID 118 217
 FT DISULFID 125 208
 FT DISULFID 130 160
 FT DISULFID 230 259
 FT DISULFID 240 251
 FT DISULFID 308 342
 FT DISULFID 388 457
 FT DISULFID 395 430
 FT CARBOHYD 87 87
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 143 143
 FT CARBOHYD 159 159
 FT CARBOHYD 163 163
 FT CARBOHYD 188 188
 FT CARBOHYD 189 189
 FT CARBOHYD 199 199
 FT CARBOHYD 209 209
 FT CARBOHYD 246 246
 FT CARBOHYD 253 253
 FT CARBOHYD 274 274
 FT CARBOHYD 288 288
 FT CARBOHYD 307 307
 FT CARBOHYD 350 350
 FT CARBOHYD 366 366

Query Match
Best Local Similarity 92.0%; Score 173; DB 1; Length 867;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 564 NNILRAIDAQOHLLQTLTWQIKQLQARILAVERYLKDQ 601

QY 1 NNILRAIDAQOHLLQTLTWQIKQLQARILAVERYLKDQ 38

ENV_HV128 STANDARD; PRT; 859 AA.

AC P0582; 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV. Human immunodeficiency virus type 1 (MNL isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11697;
[1] NCBI_TaxID=11697;
RN MEDLINE=86245056; PubMed=2424612;
RA Allison M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
RL Cell 46:63-74(1986).

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CC EMBL; X04415; CA28016.1; -
CC EMBL; A07116; CA00623.1; -
CC PIR; T01672; T01672.
DR HIV; K03456; ENVSMAL.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 513
FT CHAIN 514 859
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 334

Query Match
Best Local Similarity 91.5%; Score 172; DB 1; Length 859;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 555 NNILRAIDAQOHLLQTLTWQIKQLQARILAVERYLKDQ 592

QY 1 NNILRAIDAQOHLLQTLTWQIKQLQARILAVERYLKDQ 38

ENV_HV128 STANDARD; PRT; 863 AA.

AC P0582; 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV. Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11691;
[1] NCBI_TaxID=11691;
RN MEDLINE=88281278; PubMed=3395517;
RA Youniss J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).

CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC
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CC or send an email to license@isb-sib.ch).

CC	EMBL: J03653; AAA44684.1; -	
DR	HIV; J03653; ENV5121.	
DR	InterPro; IPR000328; Env GP41.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00516; GP120; 1.	
DR	Pfam; PF00517; GP41; 1.	
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.	
FT	CHAIN	1 29
FT	CHAIN	30 518
FT	DISULFID	519 863
FT	DISULFID	53 73
FT	DISULFID	118 217
FT	DISULFID	125 208
FT	DISULFID	130 160
FT	DISULFID	230 259
FT	DISULFID	240 251
FT	DISULFID	308 342
FT	DISULFID	388 452
FT	DISULFID	395 425
FT	CARBOHYD	87 87
FT	CARBOHYD	129 129
FT	CARBOHYD	136 136
FT	CARBOHYD	142 142
FT	CARBOHYD	143 143
FT	CARBOHYD	159 159
FT	CARBOHYD	163 163
FT	CARBOHYD	194 194
FT	CARBOHYD	199 199
FT	CARBOHYD	209 209
FT	CARBOHYD	246 246
FT	CARBOHYD	274 274
FT	CARBOHYD	288 288
FT	CARBOHYD	301 301
FT	CARBOHYD	307 307
FT	CARBOHYD	343 343
FT	CARBOHYD	350 350
FT	CARBOHYD	365 365
FT	CARBOHYD	402 402
FT	CARBOHYD	406 406
FT	CARBOHYD	412 412
FT	CARBOHYD	455 455
FT	CARBOHYD	468 468
FT	CARBOHYD	469 469
FT	CARBOHYD	472 472
FT	CARBOHYD	618 618
FT	CARBOHYD	623 623
FT	CARBOHYD	632 632
FT	CARBOHYD	644 644
FT	CARBOHYD	823 823
SO	SEQUENCE	863 AA; 97743 MW; B729C5A56AD1641 CRC64;
Qy	1 NNLLRAIDAOQHLLQLTWYQIKQGLARILAVESYKDKQ 38	
Db	560 NNLLRAIDAOQHMLQLTWGKIQGLARILAVESYKDKQ 597	
RESULT 30		
ENV_HV11EN	STANDARD; PRT; 852 AA.	
AC	P12488;	
DT	01-OCT-1989 (Rel. 12, Created)	
DT	01-OCT-1989 (Rel. 12, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	
EN	ENV.	

[illegible]

FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB86345DEC915F CRC64;

Query Match 87.8%; Score 165; DB 1; Length 852;
Best Local Similarity 84.2%; Pred. No. 2.5e-15;
Matches 32; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNILRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
DB 549 NNILMAIEAQOHLQLTWGIRKQLQARVLAVERYLKDQ 586

Search completed: June 2, 2004, 11:42:59
Job time : 6.19565 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 31.9076 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-543
Perfect score: 188
Sequence: 1 NNILRAIDAQQHLLDTTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	95.7	848	15	Q72B21 human immun
2	180	95.7	849	15	Q8Q851 human immun
3	180	95.7	851	15	Q8Q852 human immun
4	180	95.7	867	15	Q72B23 human immun
5	180	95.7	867	15	Q72B22 human immun
6	178	94.7	861	15	O56109 human immun
7	178	94.7	873	15	O91U23 human immun
8	178	94.7	876	15	O91U22 human immun
9	177	94.1	132	15	O90Q52 human immun
10	177	94.1	143	15	Q75L22 human immun
11	177	94.1	143	15	Q75M06 human immun
12	177	94.1	144	15	O7ZCD7 human immun
13	177	94.1	144	15	O7ZCD6 human immun
14	177	94.1	153	15	Q75M03 human immun
15	177	94.1	246	15	O8JF92 human immun
16	177	94.1	357	15	Q78119 human immun

17	177	94.1	588	15	Q933A8 human immun
18	177	94.1	588	15	Q933A7 human immun
19	177	94.1	589	15	Q933B1 human immun
20	177	94.1	590	15	Q933A9 human immun
21	177	94.1	616	15	Q933B0 human immun
22	177	94.1	618	15	Q933B2 human immun
23	177	94.1	727	15	Q9Q723 human immun
24	177	94.1	747	15	Q70607 human immun
25	177	94.1	748	15	Q70606 human immun
26	177	94.1	752	15	Q70604 human immun
27	177	94.1	752	15	Q70605 human immun
28	177	94.1	752	15	Q70608 human immun
29	177	94.1	757	15	Q9Q722 human immun
30	177	94.1	811	15	Q9DVL6 human immun
31	177	94.1	842	15	Q73341 human immun
32	177	94.1	842	15	Q70895 human immun
33	177	94.1	842	15	Q73340 human immun
34	177	94.1	847	15	O65996 human immun
35	177	94.1	851	15	Q78243 human immun
36	177	94.1	851	15	O56566 human immun
37	177	94.1	854	15	O85582 human immun
38	177	94.1	854	15	O72502 human immun
39	177	94.1	854	15	O90178 human immun
40	177	94.1	854	15	Q78705 human immun
41	177	94.1	855	15	Q8AQV7 human immun
42	177	94.1	855	15	Q8ADT7 human immun
43	177	94.1	856	15	Q74090 human immun
44	177	94.1	856	15	O92877 human immun
45	177	94.1	856	15	O74599 human immun
46	177	94.1	856	15	O41772 human immun
47	177	94.1	857	15	O92822 human immun
48	177	94.1	857	15	Q71013 human immun
49	177	94.1	857	15	O89654 human immun
50	177	94.1	864	15	O9YP39 human immun
51	177	94.1	864	15	O7ZJCF human immun
52	176	93.6	125	15	O91WP9 human immun
53	176	93.6	132	15	O91WQ5 human immun
54	176	93.6	133	15	O90Q20 human immun
55	176	93.6	137	15	O9QDM4 human immun
56	176	93.6	142	15	O91WQ7 human immun
57	176	93.6	144	15	O70207 human immun
58	176	93.6	144	15	O7ZCC6 human immun
59	176	93.6	144	15	O7ZCC5 human immun
60	176	93.6	144	15	O7ZCC2 human immun
61	176	93.6	144	15	O7ZCB1 human immun
62	176	93.6	144	15	O7ZCB0 human immun
63	176	93.6	144	15	O7ZC96 human immun
64	176	93.6	144	15	O7ZC95 human immun
65	176	93.6	144	15	O7ZC89 human immun
66	176	93.6	144	15	O7ZC88 human immun
67	176	93.6	144	15	O7ZC71 human immun
68	176	93.6	144	15	O7ZC70 human immun
69	176	93.6	145	15	O7ZC57 human immun
70	176	93.6	145	15	O7ZC40 human immun
71	176	93.6	145	15	O7ZC31 human immun
72	176	93.6	145	15	O7ZC31 human immun
73	176	93.6	146	15	O7ZSM37 human immun
74	176	93.6	155	15	O8J3P2 human immun
75	176	93.6	155	15	O8I3Q3 human immun
76	176	93.6	155	15	O8J3Q1 human immun
77	176	93.6	156	15	O8JAL7 human immun
78	176	93.6	174	15	O8JEO8 human immun
79	176	93.6	192	15	O8JAL2 human immun
80	176	93.6	219	15	O8JAL4 human immun
81	176	93.6	225	15	O991C1 human immun
82	176	93.6	225	15	O991B9 human immun
83	176	93.6	225	15	O991C5 human immun
84	176	93.6	225	15	O991C0 human immun
85	176	93.6	357	15	O78118 human immun
86	176	93.6	357	15	O78116 human immun
87	176	93.6	357	15	O78155 human immun
88	176	93.6	358	15	O78140 human immun
89	176	93.6	358	15	O78141 human immun

90 176 93.6 380 15 Q8GDY2 Q8GDY2 human immun

ALIGNMENTS

RESULT 1

Q7ZB21 PRELIMINARY; PRT; 848 AA.

AC Q7ZB21; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Envelope glycoprotein.

GN GP160.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Daniels R.S., Wilson P., Patel D., Longhurst H., Patterson S.,

RT "Analysis of full length HIV-1 env-genes indicates differences between

RT the virus infecting T-cells and dendritic cells in peripheral blood of

RT infected patients.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; A535618; CAD5965.1; -.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro: IPR000328; Env GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00517; GP41; 1.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

SQ SEQUENCE 848 AA; 96814 MW; 26907AA311E75917 CRC64;

Query Match 95.7%; Score 180; DB 15; Length 848;

Best Local Similarity 94.7%; Pred. No. 8.6e-17;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 38

DB 545 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 582

RESULT 2

Q8Q851 PRELIMINARY; PRT; 849 AA.

AC Q8Q851; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE GP160.

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.,

RT "Evidence for the spread of immune-escape HIV-1 subtype B in the

RT Korean population.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; A417427; CAD10139.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0006096; P:glycolysis; IEA.

DR InterPro: IPR000328; Env GP41.

DR InterPro: IPR000173; GAP_dhhydrogenase.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR PROSITE; PS00071; GAPDH; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SQ SEQUENCE 849 AA; 96428 MW; FDE60E39D1895C27 CRC64;

Query Match 95.7%; Score 180; DB 15; Length 849;

Best Local Similarity 94.7%; Pred. No. 8.6e-17;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 38

DB 546 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 583

RESULT 3

Q8Q852 PRELIMINARY; PRT; 851 AA.

AC Q8Q852; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE GP160.

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.,

RT "Evidence for the spread of immune-escape HIV-1 subtype B in the

RT Korean population.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; A417426; CAD10138.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0006096; P:glycolysis; IEA.

DR InterPro: IPR000328; Env GP41.

DR InterPro: IPR000173; GAP_dhhydrogenase.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR PROSITE; PS00071; GAPDH; 1.

KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

SQ SEQUENCE 851 AA; 96667 MW; ZCA447A865B9CFAD CRC64;

Query Match 95.7%; Score 180; DB 15; Length 851;

Best Local Similarity 94.7%; Pred. No. 8.6e-17;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 38

DB 548 NNLLRAIDAOQHLLQTLTWQIKQLQARILAVERYLKQ 585

RESULT 4

Q7ZB23 PRELIMINARY; PRT; 867 AA.

AC Q7ZB23; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Envelope glycoprotein.

GN GP160.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RA Daniels R.S., Wilson P., Patel D., Longhurst H., Patterson S.;
 RT "Analysis of full length HIV-1 env-genes indicates differences between
 RT the virus infecting T-cells and dendritic cells in peripheral blood of
 RT infected patients."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ53616; CAD59663.1; -
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Envelope protein.
 KW Envelope protein.
 SQ SEQUENCE 867 AA; 98600 MW; 451B1FA594BA167D CRC64;
 Query Match 95.7%; Score 180; DB 15; Length 867;
 Best Local Similarity 94.7%; Pred. No. 8, 8e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 564 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 601
 RESULT 5
 ID 072B22 PRELIMINARY; PRT; 867 AA.
 AC 072B22;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DR Envelope glycoprotein.
 GN GP160.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Daniels R.S., Wilson P., Patel D., Longhurst H., Patterson S.;
 RT "Analysis of full length HIV-1 env-genes indicates differences between
 RT the virus infecting T-cells and dendritic cells in peripheral blood of
 RT infected patients."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ53617; CAD59664.1; -
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Envelope protein.
 KW Envelope protein.
 SQ SEQUENCE 867 AA; 98912 MW; 0257E0A287C94842 CRC64;
 Query Match 95.7%; Score 180; DB 15; Length 867;
 Best Local Similarity 94.7%; Pred. No. 8, 8e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 564 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 601
 RESULT 6
 ID 056109 PRELIMINARY; PRT; 861 AA.
 AC 056109;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SPMHS4.1;
 RX MEDLINE=98178716; PubMed=9519894;
 RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
 RA Sheppard W.H.;
 RT "Diversity of the human immunodeficiency virus type 1 envelope
 RT glycoprotein in San Francisco Men's Health Study participants."
 RL AIDS Res. Hum. Retroviruses 14:329-337(1998).
 DR EMBL; AF025752; AAC40590.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 861 AA; 97898 MW; CBCDCBC2C88D7668 CRC64;
 Query Match 94.7%; Score 178; DB 15; Length 861;
 Best Local Similarity 92.1%; Pred. No. 1, 7e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 558 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 595
 RESULT 7
 ID 091UZ3 PRELIMINARY; PRT; 873 AA.
 AC 091UZ3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DR GP160.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PE124;
 RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
 RA Ives K.O., Baisterbrook P., Weber J.N.;
 RT "An association between amino acid substitutions in the 'Silent Face'
 RT of Human immunodeficiency virus type 1 gp120 and resistance to
 RT antibody mediated neutralization."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ286337; CAB86148.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 873 AA; 98829 MW; 7534EDCC394FC72 CRC64;
 Query Match 94.7%; Score 178; DB 15; Length 873;
 Best Local Similarity 92.1%; Pred. No. 1, 7e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 570 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKDQ 607

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RESULT 8
Q9IU22 PRELIMINARY; PRT; 876 AA.
AC Q9IU22;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BE124;
RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
  Ives K.J., Easterbrook P., Weber J.N.,
  "An association between amino acid substitutions in the 'Silent Face'
  of Human immunodeficiency virus type 1 gp120 and resistance to
  antibody mediated neutralization."
  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ286338; CAB6149.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp120; 1.
DR Pfam: PF00517; Gp41; 1.
DR AIDs: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 876 AA; 98515 MW; D0394F69B6485813 CRC64;

Query Match 94.7%; Score 178; DB 15; Length 876;
Best Local Similarity 92.1%; Pred. No. 1.7e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 573 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 610

RESULT 9
Q9O052 PRELIMINARY; PRT; 132 AA.
AC Q9O052;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MOI496;
RA MEDLINE=2132034; Pubmed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
  Garcia-Saiz A.;
  "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."
  AIDS Res. Hum. Retroviruses 17:851-855(2001).
RL EMBL: AF331089; AAK92300.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15708 MW; 519DDBA8D574FAE CRC64;

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Query Match 94.1%; Score 177; DB 15; Length 132;
Best Local Similarity 94.7%; Pred. No. 3.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 10 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 47

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RESULT 10
Q7SLZ2 PRELIMINARY; PRT; 132 AA.
AC Q7SLZ2;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT970;
RA Gonzalez Perez M.P., Garcia Saiz A.;
  "Epidemiological and molecular characteristics of HIV and HTLV
  infection in Equatorial Guinea, 1996-1998."
  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF530024; AAP87755.1; -.
DR Envelope protein.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;

Query Match 94.1%; Score 177; DB 15; Length 132;
Best Local Similarity 94.7%; Pred. No. 3.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 38
Db 11 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 48

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RESULT 11
Q7SM06 PRELIMINARY; PRT; 143 AA.
AC Q7SM06;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.;
  "Epidemiological and molecular characteristics of HIV and HTLV
  infection in Equatorial Guinea, 1996-1998."
  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF530010; AAP87741.1; -.
DR Envelope protein.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BEO CRC64;

Query Match 94.1%; Score 177; DB 15; Length 143;
Best Local Similarity 94.7%; Pred. No. 3.4e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLLQLTWQIKQLQARILAVERYLKQ 38

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DB 11 NNILRAIEAQHLLQITWGIKQLQARILAVERYLKDQ 48

RESULT 12

Q7ZCD7 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD7; 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11676;

SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-1;

RA Roman F., Gonzalez D., Lambert C., Deroc S., Fischer A., Baurith T.,
 Stab T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
 "uncommon mutations at residue positions critical for enfuvirtide (T-
 RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
 and non-B HIV-1.";
 RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY185383; AA065658.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1 144

FT NON_TER 1 144

SEQUENCE 144 AA; 16887 MW; A139D1C53D18EBE CRC64;

QY 1 NNILRAIDAOHLLQITWGIKQLQARILAVERYLKDQ 38

DB 24 NNILRAIEAQHLLQITWGIKQLQARILAVERYLKDQ 61

RESULT 13

Q7ZCD6 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD6; 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11676;

SEQUENCE FROM N.A.

RC STRAIN=HRLUX53-2;

RA Roman F., Gonzalez D., Lambert C., Deroc S., Fischer A., Baurith T.,
 Stab T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
 "uncommon mutations at residue positions critical for enfuvirtide (T-
 RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
 and non-B HIV-1.";
 RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY185384; AA065659.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1 144

FT NON_TER 1 144

SEQUENCE 144 AA; 16907 MW; A427C02C24218EBE CRC64;

Query Match 94.1%; Score 177; DB 15; Length 144;
 Best Local Similarity 94.7%; Pred. No. 3.4e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOHLLQITWGIKQLQARILAVERYLKDQ 38

DB 24 NNILRAIEAQHLLQITWGIKQLQARILAVERYLKDQ 61

RESULT 14

Q7SM03 PRELIMINARY; PRT; 153 AA.

AC Q7SM03; 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11676;

SEQUENCE FROM N.A.

RC STRAIN=GT598;

RA Gonzalez Perez M.P., Garcia Saiz A.;
 "Epidemiological and molecular characteristics of HIV and HTLV
 RT infection in Equatorial Guinea, 1996-1998.";
 RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF530013; AAP87744.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein; Transmembrane.

FT NON_TER 1 153

FT NON_TER 1 153

SEQUENCE 153 AA; 18136 MW; 014FA9E1FBEFC035 CRC64;

QY 1 NNILRAIDAOHLLQITWGIKQLQARILAVERYLKDQ 38

DB 11 NNILRAIEAQHLLQITWGIKQLQARILAVERYLKDQ 48

RESULT 15

Q8JF92 PRELIMINARY; PRT; 246 AA.

AC Q8JF92; 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 24, Last annotation update)
 DE Truncated envelope protein (Fragment).
 GN Human immunodeficiency virus 1.
 OS Viruses; Retrovird viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11676;

SEQUENCE FROM N.A.

RC STRAIN=RF;

RA Jones D.R., Suzuki K., Pillier S.C.;
 "A 100-Amino Acid Truncation in the Cytoplasmic Tail of Glycoprotein
 RT 41 in the Reference HIV Type 1 Strain RF.";
 RT AIDS Res. Hum. Retroviruses 18:513-517(2002).

DR EMBL; AF403705; AA021476.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein; Transmembrane.

FT NON_TER 1 246

FT NON_TER 1 246

SEQUENCE 246 AA; 27734 MW; 4F0058F96DE1C48B CRC64;

Query Match 94.1%; Score 177; DB 15; Length 246;
Best Local Similarity 92.1%; Pred. No. 6.1e-17;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 38
DB 43 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 80

RESULT 16

Q78119 PRELIMINARY; PRT; 357 AA.

AC Q78119; PRELIMINARY; PRT; 357 AA.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RT "distinct populations of Human immunodeficiency virus type 1 in blood
and cerebrospinal fluid";
RL AIDS Res. Hum. Retroviruses 8:55-59(1992).
DR EMBL; X61356; CAA43624.1; -.
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER
SQ SEQUENCE 357 AA; 4118 MW; FE4CA7E122AB86 CRC64;

Query Match 94.1%; Score 177; DB 15; Length 357;
Best Local Similarity 94.7%; Pred. No. 9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 38
DB 54 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 91

RESULT 17

Q993A8 PRELIMINARY; PRT; 588 AA.

AC Q993A8; PRELIMINARY; PRT; 588 AA.
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240B8 CRC64;

Query Match 94.1%; Score 177; DB 15; Length 588;
Best Local Similarity 94.7%; Pred. No. 1.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 38
DB 496 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 533

RESULT 18

Q993A7 PRELIMINARY; PRT; 588 AA.

AC Q993A7; PRELIMINARY; PRT; 588 AA.
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt1;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321148; AAK20296.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match 94.1%; Score 177; DB 15; Length 588;
Best Local Similarity 94.7%; Pred. No. 1.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 38
DB 496 NNLLRAIDAQOHLQLTWQIKOLQARILAVERYLKDD 533

RESULT 19

Q993B1 PRELIMINARY; PRT; 589 AA.

AC Q993B1; PRELIMINARY; PRT; 589 AA.
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=1F8;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL;AF321144;AAK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 589 589
SQ SEQUENCE 589 AA; 65753 MW; 00621646924FD66 CRC64;

Query Match 94.1%; Score 177; DB 15; Length 589;
Best Local Similarity 94.7%; Pred. No. 1.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 496 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 533

RESULT 20
Q993A9 PRELIMINARY; PRT; 590 AA.
AC Q993A9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL;AF321144;AAK20294.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 590 590
SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;

Query Match 94.1%; Score 177; DB 15; Length 590;
Best Local Similarity 94.7%; Pred. No. 1.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 497 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 534

RESULT 21
Q993B0

ID Q993B0 PRELIMINARY; PRT; 616 AA.
AC Q993B0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL;AF321143;AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 616 616
SQ SEQUENCE 616 AA; 69189 MW; 57A8E20F9A580A4F CRC64;

Query Match 94.1%; Score 177; DB 15; Length 616;
Best Local Similarity 94.7%; Pred. No. 1.5e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 38
Db 497 NNTLRATDQOHLQLTWGIKQLQARILAVERYLKDQ 534

RESULT 22
Q993B2 PRELIMINARY; PRT; 618 AA.
AC Q993B2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL;AF321143;AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 618 618
SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AB CRC64;


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DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match
Best Local Similarity 94.1%; Score 177; DB 15; Length 748;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 549 NNILRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 586

RESULT 26
Q70604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Shaw G., Kong L., Weis S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB894013B45A CRC64;

Query Match
Best Local Similarity 94.1%; Score 177; DB 15; Length 752;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 553 NNILRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 590

RESULT 27
Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

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OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Shaw G., Kong L., Weis S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB894013B45A CRC64;

Query Match
Best Local Similarity 94.1%; Score 177; DB 15; Length 752;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIDAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 553 NNILRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 590

RESULT 28
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RX MEDLINE=95127297; PubMed=7826699;
RA Shaw G., Kong L., Weis S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AAA7670.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.

```

DR Pfam: PF00516; GP120, 1.
DR Pfam: PF00517; GP41, 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C08F8 CRC64;
FT NON_TER 752

Query Match 94.1%; Score 177; DB 15; Length 752;
Best Local Similarity 94.7%; Pred. No. 2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIDAQOHLLQLTWQIKOLQARIILAVERYLKDQ 38
Db 553 NNLLRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 590

RESULT 29

ID Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope polyprotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chalken I., Hoxie J.A., Doms R.W.,
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein."
RT Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.,
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity."
RT J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BD2E CRC64;

Query Match 94.1%; Score 177; DB 15; Length 752;
Best Local Similarity 94.7%; Pred. No. 2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIDAQOHLLQLTWQIKOLQARIILAVERYLKDQ 38
Db 548 NNLLRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 585

RESULT 30

ID Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC_KCD4;
RX MEDLINE=20499072; PubMed=11044094;
RA Vidal N., Peeters M., Mlangua-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.,
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa."
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401037; CAC15045.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;

Query Match 94.1%; Score 177; DB 15; Length 811;
Best Local Similarity 94.7%; Pred. No. 2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIDAQOHLLQLTWQIKOLQARIILAVERYLKDQ 38
Db 557 NNLLRAIEAQHLLQLTWGIKQLQARIILAVERYLKDQ 594

Search completed: June 2, 2004, 11:48:24
Job time : 31.9076 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 / Search time 14.0435 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-543
Perfect score: 188
Sequence: 1 NMLRAIDAOHLLQTLWQIKOLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents_Aa:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	97.9	38	4	US-08-973-952-82
2	180	95.7	138	4	US-09-570-921-13
3	177	94.1	38	1	US-08-374-666-1
4	177	94.1	38	3	US-08-486-099-89
5	177	94.1	38	3	US-08-360-107A-99
6	177	94.1	38	3	US-08-360-107A-132
7	177	94.1	38	3	US-08-484-223B-89
8	177	94.1	38	3	US-08-919-597-89
9	177	94.1	38	3	US-08-475-668A-89
10	177	94.1	38	3	US-08-485-551A-89
11	177	94.1	38	3	US-08-471-913A-89
12	177	94.1	38	3	US-08-485-264A-89
13	177	94.1	38	3	US-08-082-279B-16
14	177	94.1	38	3	US-09-082-279B-507
15	177	94.1	38	3	US-09-082-279B-604
16	177	94.1	38	4	US-08-474-349A-89
17	177	94.1	38	4	US-08-474-349A-441
18	177	94.1	38	4	US-09-315-304B-16
19	177	94.1	38	4	US-09-315-304B-507
20	177	94.1	38	4	US-09-315-304B-604
21	177	94.1	38	4	US-08-255-208A-25
22	177	94.1	38	4	US-08-470-896-89
23	177	94.1	38	4	US-08-485-546A-89
24	177	94.1	38	4	US-09-796-202-11
25	177	94.1	38	4	US-09-834-784-16
26	177	94.1	38	4	US-09-834-784-507
27	177	94.1	38	4	US-09-834-784-604

28	177	94.1	38	4	US-08-464-003-1	Sequence 1, App1
29	177	94.1	38	4	US-09-779-451-2	Sequence 2, App1
30	177	94.1	38	4	US-09-515-965A-16	Sequence 16, App1
31	177	94.1	38	4	US-09-515-965A-507	Sequence 507, App
32	177	94.1	38	4	US-09-515-965A-604	Sequence 604, App
33	177	94.1	38	4	US-09-350-641C-16	Sequence 16, App1
34	177	94.1	38	4	US-09-350-641C-507	Sequence 507, App
35	177	94.1	38	4	US-09-350-641C-604	Sequence 604, App
36	177	94.1	41	1	US-08-073-028-8	Sequence 3, App1
37	177	94.1	41	1	US-08-374-666-3	Sequence 9, App1
38	177	94.1	41	1	US-08-374-666-9	Sequence 8, App1
39	177	94.1	41	3	US-08-486-099-8	Sequence 8, App1
40	177	94.1	41	3	US-08-360-107A-8	Sequence 8, App1
41	177	94.1	41	3	US-08-484-223B-8	Sequence 8, App1
42	177	94.1	41	3	US-08-484-223B-242	Sequence 242, App
43	177	94.1	41	3	US-08-484-223B-243	Sequence 243, App
44	177	94.1	41	3	US-08-919-597-8	Sequence 8, App1
45	177	94.1	41	3	US-08-475-668A-8	Sequence 8, App1
46	177	94.1	41	3	US-08-485-551A-8	Sequence 8, App1
47	177	94.1	41	3	US-08-471-913A-8	Sequence 8, App1
48	177	94.1	41	3	US-08-554-616-8	Sequence 8, App1
49	177	94.1	41	3	US-08-485-264A-8	Sequence 8, App1
50	177	94.1	41	3	US-09-082-279B-496	Sequence 496, App
51	177	94.1	41	3	US-09-082-279B-601	Sequence 601, App
52	177	94.1	41	3	US-09-082-279B-633	Sequence 633, App
53	177	94.1	41	3	US-09-082-279B-1163	Sequence 1163, App
54	177	94.1	41	4	US-08-474-349A-8	Sequence 8, App1
55	177	94.1	41	4	US-09-315-304B-496	Sequence 496, App
56	177	94.1	41	4	US-09-315-304B-601	Sequence 601, App
57	177	94.1	41	4	US-09-315-304B-633	Sequence 633, App
58	177	94.1	41	4	US-09-315-304B-1163	Sequence 1163, App
59	177	94.1	41	4	US-08-255-208A-8	Sequence 8, App1
60	177	94.1	41	4	US-08-973-952-8	Sequence 8, App1
61	177	94.1	41	4	US-08-470-896-8	Sequence 8, App1
62	177	94.1	41	4	US-08-485-546A-8	Sequence 8, App1
63	177	94.1	41	4	US-09-834-784-496	Sequence 496, App
64	177	94.1	41	4	US-09-834-784-601	Sequence 601, App
65	177	94.1	41	4	US-09-834-784-633	Sequence 633, App
66	177	94.1	41	4	US-09-834-784-1163	Sequence 1163, App
67	177	94.1	41	4	US-08-464-003-3	Sequence 3, App1
68	177	94.1	41	4	US-08-464-003-9	Sequence 9, App1
69	177	94.1	41	4	US-09-515-965A-496	Sequence 496, App
70	177	94.1	41	4	US-09-515-965A-601	Sequence 601, App
71	177	94.1	41	4	US-09-515-965A-633	Sequence 633, App
72	177	94.1	41	4	US-09-515-965A-1163	Sequence 1163, App
73	177	94.1	41	4	US-09-350-641C-496	Sequence 496, App
74	177	94.1	41	4	US-09-350-641C-601	Sequence 601, App
75	177	94.1	41	4	US-09-350-641C-633	Sequence 633, App
76	177	94.1	41	4	US-09-350-641C-1163	Sequence 1163, App
77	177	94.1	44	1	US-08-374-666-10	Sequence 10, App1
78	177	94.1	44	4	US-08-464-003-10	Sequence 10, App1
79	177	94.1	45	3	US-09-082-279B-1164	Sequence 1164, App
80	177	94.1	45	4	US-09-315-304B-1164	Sequence 1164, App
81	177	94.1	45	4	US-09-834-784-1164	Sequence 1164, App
82	177	94.1	45	4	US-09-779-451-9	Sequence 9, App1
83	177	94.1	45	4	US-09-515-965A-1164	Sequence 1164, App
84	177	94.1	45	4	US-09-350-641C-1164	Sequence 1164, App
85	177	94.1	49	4	US-09-796-202-3	Sequence 3, App1
86	177	94.1	51	3	US-09-082-279B-745	Sequence 745, App
87	177	94.1	51	4	US-09-315-304B-745	Sequence 745, App
88	177	94.1	51	4	US-09-834-784-745	Sequence 745, App
89	177	94.1	51	4	US-09-515-965A-745	Sequence 745, App
90	177	94.1	51	4	US-09-350-641C-745	Sequence 745, App

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORIAL THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,955A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 97.9%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 9e-20;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 2
US-09-570-921-13
Sequence 13, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-13

Query Match 95.7%; Score 180; DB 4; Length 138;
Best Local Similarity 94.7%; Pred. No. 1.6e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 14 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 51

RESULT 3
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1

Query Match 94.1%; Score 177; DB 1; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIDAOQHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 4
US-08-486-099-89
Sequence 89, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 5
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 6
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 7
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIDAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
RESULT 8
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIDAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 9
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 606065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKDQ 38

RESULT 10
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38

DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKDQ 38

RESULT 11
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKDQ 38

RESULT 12
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS: Fennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 13
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 94.1%; Score 177; DB 3; Length 38;

Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 14
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWTWGIKQLQARILAVERYLKQ 38

RESULT 15
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match 94.1%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWTWQIKQLQARILAVERYLKQ 38

Db 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 16
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 6333395

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-474-349A-89

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 17
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-474-349A-441

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIDAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38

RESULT 18
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-16

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKOLQARILAVERYLKQD 38
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQD 38

RESULT 19
US-09-315-304B-507

Sequence 507, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Metucka, G.

APPLICANT: Amer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 507

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-507

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKOLQARILAVERYLKQD 38
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQD 38

RESULT 20
US-09-315-304B-604

Sequence 604, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Metucka, G.

APPLICANT: Amer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 604

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-604

Query Match 94.1%; Score 177; DB 4; Length 38;

Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKOLQARILAVERYLKQD 38
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQD 38

RESULT 21
US-08-255-208A-25

Sequence 25, Application US/08255208A

Patent No. 6440656

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Jr., Stephen R.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

FILE REFERENCE: 111

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-255-208A-25

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKOLQARILAVERYLKQD 38
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKQD 38

RESULT 22
US-08-470-896-89

Sequence 89, Application US/08470896

Patent No. 6479055

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIGIKOLQARIILAVERYLKDQ 38

RESULT 23
US-08-485-546A-89
Sequence 89, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIGIKOLQARIILAVERYLKDQ 38

RESULT 24
US-09-796-202-11
Sequence 11, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CGRS PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKOLQARIILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIGIKOLQARIILAVERYLKDQ 38

RESULT 25
US-09-834-784-16
Sequence 16, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guttrie, Kelly
APPLICANT: Merutka, Gene

APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38

RESULT 26
US-09-834-784-507
Sequence 507, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guttrie, Kelly
APPLICANT: Metutka, Gene
APPLICANT: Amer, Mohamed
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-507

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERTLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38

RESULT 27
US-09-834-784-604
Sequence 604, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guttrie, Kelly
APPLICANT: Metutka, Gene
APPLICANT: Amer, Mohamed

APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-604

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERTLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38

RESULT 28
US-08-464-003-1
Sequence 1, Application US/08464003
Patent No. 6573078
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Paul P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,003
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-464-003-1

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLLRAIDAQQHLLQLTWQIKQLQARIILAVERYLKQ 38
DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARIILAVERYLKQ 38

DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARIILAVERYLKQ 38
Search completed: June 2, 2004, 11:52:40
Job time : 14.0435 secs

RESULT 29
US-09-779-451-2

; Sequence 2, Application US/09779451
; Patent No. 6605427
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.030003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLLRAIDAQQHLLQLTWQIKQLQARIILAVERYLKQ 38
DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARIILAVERYLKQ 38

RESULT 30
US-09-515-965A-16

; Sequence 16, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-16

Query Match 94.1%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.2e-19;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLLRAIDAQQHLLQLTWQIKQLQARIILAVERYLKQ 38
DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARIILAVERYLKQ 38

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 35.0054 Seconds
(Without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-543
Perfect score: 188
Sequence: 1 NNILRAIDAQOHLLQTVWIKOLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 28138677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	97.9	38	14	US-10-552-136-82
2	177	94.1	38	9	US-09-796-202-11
3	177	94.1	38	9	US-09-779-451-2
4	177	94.1	38	10	US-09-493-346-2
5	177	94.1	38	12	US-10-267-682-89
6	177	94.1	38	12	US-10-267-748-89
7	177	94.1	38	12	US-09-809-060-6
8	177	94.1	38	12	US-09-809-060-7
9	177	94.1	38	12	US-10-663-589-3
10	177	94.1	38	12	US-10-681-879-2
11	177	94.1	38	12	US-09-828-615-2
12	177	94.1	38	14	US-10-116-797-7
13	177	94.1	38	14	US-10-323-314-11
14	177	94.1	38	14	US-10-414-192-1
15	177	94.1	38	14	US-10-351-641-16

16	177	94.1	38	14	US-10-351-641-507	Sequence 507, App
17	177	94.1	38	14	US-10-351-641-604	Sequence 604, App
18	177	94.1	38	15	US-10-005-305-165	Sequence 165, App
19	177	94.1	38	15	US-10-005-305-202	Sequence 202, App
20	177	94.1	38	15	US-10-005-305-203	Sequence 203, App
21	177	94.1	38	15	US-10-420-194-1234	Sequence 1234, App
22	177	94.1	38	16	US-10-664-021-2	Sequence 2, Appli
23	177	94.1	38	16	US-10-671-316-2	Sequence 2, Appli
24	177	94.1	41	12	US-10-267-682-8	Sequence 8, Appli
25	177	94.1	41	12	US-10-267-748-8	Sequence 8, Appli
26	177	94.1	41	12	US-10-663-589-30	Sequence 30, Appli
27	177	94.1	41	12	US-10-663-589-35	Sequence 35, Appli
28	177	94.1	41	12	US-10-663-589-35	Sequence 35, Appli
29	177	94.1	41	14	US-10-351-641-633	Sequence 633, App
30	177	94.1	41	14	US-10-351-641-1163	Sequence 1163, App
31	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
32	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
33	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
34	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
35	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
36	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
37	177	94.1	41	16	US-10-664-021-27	Sequence 27, Appli
38	177	94.1	44	12	US-10-663-589-36	Sequence 36, Appli
39	177	94.1	44	14	US-10-414-192-10	Sequence 10, Appli
40	177	94.1	45	9	US-09-779-451-9	Sequence 9, Appli
41	177	94.1	45	12	US-09-809-060-50	Sequence 50, Appli
42	177	94.1	45	12	US-10-663-589-29	Sequence 29, Appli
43	177	94.1	45	14	US-10-351-641-1164	Sequence 1164, App
44	177	94.1	45	16	US-10-664-021-26	Sequence 26, Appli
45	177	94.1	45	16	US-10-671-316-26	Sequence 26, Appli
46	177	94.1	49	9	US-09-796-202-3	Sequence 3, Appli
47	177	94.1	49	14	US-10-323-314-3	Sequence 3, Appli
48	177	94.1	51	12	US-10-663-589-27	Sequence 27, Appli
49	177	94.1	51	12	US-10-663-589-27	Sequence 27, Appli
50	177	94.1	51	16	US-10-664-021-24	Sequence 24, Appli
51	177	94.1	51	16	US-10-671-316-24	Sequence 24, Appli
52	177	94.1	52	14	US-10-351-641-1119	Sequence 1119, App
53	177	94.1	53	14	US-10-351-641-955	Sequence 955, App
54	177	94.1	54	14	US-10-351-641-1062	Sequence 1062, App
55	177	94.1	55	9	US-09-779-451-1	Sequence 1, Appli
56	177	94.1	55	12	US-09-809-060-14	Sequence 14, Appli
57	177	94.1	57	15	US-10-438-691-1	Sequence 1, Appli
58	177	94.1	59	16	US-10-664-021-1	Sequence 1, Appli
59	177	94.1	59	16	US-10-671-316-1	Sequence 1, Appli
60	177	94.1	60	12	US-10-663-589-1	Sequence 1, Appli
61	177	94.1	63	12	US-10-267-682-201	Sequence 201, App
62	177	94.1	63	12	US-10-267-748-201	Sequence 201, App
63	177	94.1	63	14	US-10-252-136-54	Sequence 29, Appli
64	177	94.1	103	14	US-10-263-103-29	Sequence 29, Appli
65	177	94.1	103	15	US-10-438-691-3	Sequence 3, Appli
66	177	94.1	113	15	US-10-438-691-4	Sequence 4, Appli
67	177	94.1	177	14	US-10-040-349B-2	Sequence 2, Appli
68	177	94.1	198	9	US-09-854-816-88	Sequence 88, Appli
69	177	94.1	198	9	US-09-854-816-89	Sequence 89, Appli
70	177	94.1	200	14	US-10-263-103-25	Sequence 25, Appli
71	177	94.1	200	15	US-10-438-691-8	Sequence 8, Appli
72	177	94.1	232	14	US-10-059-271-81	Sequence 81, Appli
73	177	94.1	254	14	US-10-059-271-82	Sequence 82, Appli
74	177	94.1	256	14	US-10-059-271-97	Sequence 97, Appli
75	177	94.1	268	9	US-09-854-816-16	Sequence 16, Appli
76	177	94.1	268	9	US-09-854-816-17	Sequence 17, Appli
77	177	94.1	268	9	US-09-854-816-18	Sequence 18, Appli
78	177	94.1	268	9	US-09-854-816-19	Sequence 19, Appli
79	177	94.1	269	9	US-09-854-816-34	Sequence 34, Appli
80	177	94.1	269	9	US-09-854-816-43	Sequence 43, Appli
81	177	94.1	338	12	US-10-267-682-90	Sequence 90, Appli
82	177	94.1	338	12	US-10-267-748-90	Sequence 90, Appli
83	177	94.1	344	14	US-10-040-349B-1	Sequence 1, Appli
84	177	94.1	345	9	US-09-779-451-8	Sequence 8, Appli
85	177	94.1	345	14	US-10-026-741-49	Sequence 49, Appli
86	177	94.1	359	14	US-10-214-670-58	Sequence 58, Appli
87	177	94.1	351	14	US-10-059-271-93	Sequence 93, Appli
88	177	94.1	488	8	US-08-911-824-95	Sequence 95, Appli

89 177 94.1 491 8 US-08-911-824-56 Sequence 56, Appl
90 177 94.1 519 9 US-09-756-551A-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 97.9%; Score 184; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 2, 3e-18;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 2
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBSTITUTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1) - (38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 94.1%; Score 177; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 2, 3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 3
US-09-779-451-2

; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 94.1%; Score 177; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 2, 3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 4
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J
; APPLICANT: Olson, William C
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 94.1%; Score 177; DB 10; Length 38;
Best Local Similarity 94.7%; Pred. No. 2, 3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 5
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.

Query Match 94.1%; Score 177; DB 10; Length 38;
Best Local Similarity 94.7%; Pred. No. 2, 3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89
Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
RESULT 6
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petleway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89
Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
RESULT 7
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6
Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIDAQOHLQLTWGIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
RESULT 8
US-09-809-060-7

Sequence 7, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Allway, Graham P.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/169,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 9
US-10-663-589-3
Sequence 3, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TBM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 10
US-10-681-879-2
Sequence 2, Application US/10681879
Publication No. US20040062767A1
GENERAL INFORMATION:
APPLICANT: Olsson, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/10/681,879

CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/493,346
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 11
US-09-828-615-2
Sequence 2, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsson, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 94.1%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIDAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 12
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Olsson, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKQ 38

RESULT 13
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKQ 38

RESULT 14
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolgonesi, Daniel P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKQ 38

RESULT 15
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKQ 38

RESULT 16
US-10-351-641-507
Sequence 507, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641

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; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match          94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKDQ 38

RESULT 17
US-10-351-641-604
; Sequence 604, Application US/10351641
; Publication No. US20030166874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthe, K.
; APPLICANT: Mernicka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match          94.1%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKDQ 38

RESULT 18
US-10-005-305-165
; Sequence 165, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
```

```

; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match          94.1%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKDQ 38

RESULT 19
US-10-005-305-202
; Sequence 202, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match          94.1%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAQOHLQLTWQIKOLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKDQ 38

RESULT 20
US-10-005-305-203
; Sequence 203, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
```

FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 94.1%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 2,3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 21
US-10-420-194-1234

Sequence 1234, Application US/10420194
Publication No. US2004006035A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: MCSwiggan, Jim
APPLICANT: Blatt, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
FILE REFERENCE: MBHB02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/366,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1) (38)
US-10-420-194-1234

Query Match 94.1%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 2,3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 22
US-10-664-021-2

Sequence 2, Application US/10664021
Publication No. US20040076637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and Their Use in Therapy to Inhibit Transmission of Human
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 94.1%; Score 177; DB 16; Length 38;
Best Local Similarity 94.7%; Pred. No. 2,3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 23
US-10-671-316-2

Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match 94.1%; Score 177; DB 16; Length 38;
Best Local Similarity 94.7%; Pred. No. 2,3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIDAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

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RESULT 24
US-10-267-682-8
; Sequence 8, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;           Mathews, Thomas J.
;           Wild, Carl T.
;           Barney, Shawn O.
;           Lambert, Dennis M.
;           Petteway, Stephen R.
;           Langlois, Alphonse J.
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-682-8

Query Match          94.1%; Score 177; DB 12; Length 41;
Best Local Similarity 94.7%; Pred. No. 2,5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0,

Qy      1  NNLRRAIDAOQHLLQLTWQIKQLOARILAVERYIKDQ 38
      |||||:|||||:|||||:|||||:|||||:|||||:
Db      4  NNLRRAIEAOQHLLQLTWVGIKQLOARILAVERYIKDQ 41

RESULT 25
US-10-267-748-8
; Sequence 8, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;           Mathews, Thomas J.
;           Wild, Carl T.
;           Barney, Shawn O.

```

```

1 Lambert, Dennis M.
2 Petteway, Stephen R.
3 Langlois, Alphonse J.
4 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
5 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
6 TRANSMISSION
7 NUMBER OF SEQUENCES: 239
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Pennie & Edmonds
10 STREET: 1155 Avenue of the Americas
11 CITY: New York
12 STATE: New York
13 COUNTRY: USA
14 ZIP: 10036-2711
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/10/267,748
22 FILING DATE: 08-Oct-2002
23 CLASSIFICATION: <unknown>
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US/08/484,223A
26 FILING DATE: 07-JUN-1995
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Coruzzi, Laura A.
29 REGISTRATION NUMBER: 30,742
30 REFERENCE/DOCKET NUMBER: 7872-029
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (212) 790-9090
33 TELEFAX: (212) 869-9741/8864
34 TELEX: 66141 PENNIE
35 INFORMATION FOR SEQ ID NO: 8:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 41 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: <Unknown>
40 MOLECULE TYPE: peptide
41 TOPOLOGY: unknown
42 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
43 US-10-267-748-8
44
45 Query Match 94.1%; Score 177; DB 12; Length 41;
46 Best Local Similarity 94.7%; Pred. No. 2.5e-17;
47 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
48
49 QY 1 NNLRRAIDAOOHLQLTWVQIKQLQARILAEVRYKDDQ 38
50 |||||
51 DB 4 NNLRRAIDAOOHLQLTWVQIKQLQARILAEVRYKDDQ 41
52
53 RESULT 26
54 US-10-663-589-30
55 Sequence 30, Application US/10663589
56 Publication No. US20040063637A1
57 GENERAL INFORMATION:
58 APPLICANT: Timeartis, Inc.
59 TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
60 TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
61 FILE REFERENCE: TRN-003
62 CURRENT APPLICATION NUMBER: US/10/663,589
63 CURRENT FILING DATE: 2003-09-16
64 PRIOR APPLICATION NUMBER: US 60/414,441
65 PRIOR FILING DATE: 2002-09-27
66 NUMBER OF SEQ ID NOS: 95
67 SOFTWARE: PatentIn version 3.2
68 SEQ ID NO 30
69 LENGTH: 41
70 TYPE: PRT
71 ORGANISM: Artificial
72 FEATURE:

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OTHER INFORMATION: synthesized
US-10-663-589-30

Query Match	94.1%;	Score 177;	DB 12;	length 41;
Best Local Similarity	94.7%;	Pred. No. 2.5e-17;		
Matches	36;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;

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QY      1 NNILRAIDAQQHLLQLTWQGIQQLQARILANERYLYKDG 38
      |||||:|||||
Db      4 NNILRAIEAQHLLQLTWQGIQQLQARILANERYLYKDG 41

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RESULT 27
US-10-663-589-33

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? Sequence 33 Application US/10663589
? Publication No. US20040063637A1
? GENERAL INFORMATION:
? APPLICANT: Trimetris, Inc.
? TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
? TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
? FILE REFERENCE: TRM-003
? CURRENT APPLICATION NUMBER: US/10/663,589
? CURRENT FILING DATE: 2003-09-16
? PRIOR APPLICATION NUMBER: US 60/414,441
? PRIOR FILING DATE: 2002-09-27
? NUMBER OF SEQ ID NOS: 95
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 33
? LENGTH: 41
? TYPE: PRT
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: synthesized
? US-10-663-589-33

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Query Match	94.1%	Score 177	DB 12	Length 41
Best Local Similarity	94.7%	Pred No. 2.5e-17		
Matches 36	Conservative 1	Mismatches 1	Indels 0	Gaps 0

OY 1 NNLLRAIDAOQHLLQLTWTQICQLQARILAVERYLKDQ 38
| | | | : | | | | | | | | | | | | | | |
D6 4 NNLLRAIEAQGHLLQLTWTGCIQLQARILAVERYLKDQ 41

RESULT 28
US-10-663-589-35

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; sequence 52, application 05/10/2003
; Publication No. US20040063637A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-35

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Query Match      94.1%; Score 177; DB 12; Length 41;
Best Local Similarity 94.7%; Pred. No. 2.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY      1 NNLRAIDAGCHILQUTWQIKOLARILAVRRYLKDQ 38
|||||:|||||||:|||||||:|||||||:|||||||:

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QY 1 NNLLRAIDAQQHLLQLTWQIKQLQARILAVERYLKDQ 38
|||||:|||||

Db 1 NNLRAIEAQOHLLOLTVGCIKOLQARILAVERYLKQ 38

RESULT 29

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: Sequence 8, Application US/10252136
: Publication No. US20030103998A1
: GENERAL INFORMATION:
: APPLICANT: Johnson, M. Ross
: APPLICANT: Lambert, Dennis M.
: TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
: TITLE OF INVENTION: VIRAL INFECTIONS
: TITLE OF INVENTION: USING COMBINATORS THERAPY
: FILE REFERENCE: 7872-036
: CURRENT APPLICATION NUMBER: US/10/252,136
: CURRENT FILING DATE: 2002-09-20
: PRIOR APPLICATION NUMBER: US/08/973,952
: PRIOR FILING DATE: 1998-05-29
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 41
: TYPE: PR1
: ORGANISM: Human immunodeficiency virus
: US-10-252-136-8

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Query Match	94.1%	Score 177	DB 14	Length 41
Best Local Similarity	94.7%	Pred. No. 2.5e-17		
Matches 36	Conservative 1	Mismatches 1	Indels 0	Gaps 0

Qy 1 NNLRRAIDAOQHLLQTLTWQIKQLQARILANVERLYKQ 38
 |||||:|||||
 Db 4 NNLRRAIEAQHQLLQTLTWGIKQLQARILANVERLYKQ 41

RESULT 30
US-10-414-192-3

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STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-414-192-3

Query Match 94.1%; Score 177; DB 14; Length 41;
Best Local Similarity 94.7%; Pred. No. 2.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIDAOQHLLQLTWQIKOQARIILAVERYLKDQ 38
Db 4 NNLRAIDAOQHLLQLTWQIKOQARIILAVERYLKDQ 41

Search completed: June 2, 2004, 12:29:26
Job time : 35.0054 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 47.6033 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-544
Perfect score: 187
Sequence: 1 NMLRAIQAOQHILQITWQIKQLQARILAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	184	98.4	38 2	AAR98408
2	184	98.4	38 4	AAB54785
3	184	98.4	38 4	AAB55005
4	184	98.4	38 4	AAB54970
5	184	98.4	38 4	AAB52244
6	184	98.4	38 4	AAU14011
7	184	98.4	38 5	AAO18771
8	179	95.7	37 3	AAAB14705
9	179	95.7	37 4	AAB54969
10	178	95.2	37 3	AAAB14739
11	178	95.2	37 4	AAB55004
12	177	94.7	38 2	AAR55635
13	177	94.7	38 2	AAR55636
14	177	94.7	38 2	AAAR47216
15	177	94.7	38 2	AAAR27614
16	177	94.7	38 3	AAAY88666
17	177	94.7	38 3	AAAY88730
18	177	94.7	38 3	AAAY88731
19	177	94.7	38 3	AAAY89145
20	177	94.7	38 3	AAAY89146
21	177	94.7	38 3	AAAY89243
22	177	94.7	38 3	AAAB14530
23	177	94.7	38 3	AAAB52824
24	177	94.7	38 3	AAAB52786
25	177	94.7	38 3	AAAB52823

26	177	94.7	38 4	AAAG3858	AAAG3858 Amino aci
27	177	94.7	38 4	AAAB92349	AAAB92349 Virus rel
28	177	94.7	38 4	AAAB77021	AAAB77021 Core poly
29	177	94.7	38 4	AAAB77085	AAAB77085 Core poly
30	177	94.7	38 4	AAAB77086	AAAB77086 Core poly
31	177	94.7	38 4	AAAB77596	AAAB77596 Core poly
32	177	94.7	38 4	AAAB77500	AAAB77500 Core poly
33	177	94.7	38 4	AAAB77624	AAAB77624 Core poly
34	177	94.7	38 4	AAU70185	AAU70185 HIV viral
35	177	94.7	38 4	AAU70184	AAU70184 HIV viral
36	177	94.7	38 4	AAAB55690	AAAB55690 DP107 pep
37	177	94.7	38 4	AAAB01489	AAAB01489 Viral cor
38	177	94.7	38 4	AAAB00505	AAAB00505 Viral DPl
39	177	94.7	38 4	AAAB00090	AAAB00090 Viral DPl
40	177	94.7	38 4	AAAB02077	AAAB02077 Viral cor
41	177	94.7	38 4	AAAB00025	AAAB00025 HIV-1 gp4
42	177	94.7	38 4	AAAB00089	AAAB00089 Viral DPl
43	177	94.7	38 4	AAAB00504	AAAB00504 Viral DPl
44	177	94.7	38 4	AAAB00629	AAAB00629 Viral DPl
45	177	94.7	38 4	AAAB01980	AAAB01980 Viral cor
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47	177	94.7	38 4	AAU13053	AAU13053 DP178-11k
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51	177	94.7	38 4	AAU12639	AAU12639 DP178-11k
52	177	94.7	38 4	AAAB2962	AAAB2962 Anti-HIV
53	177	94.7	38 5	AAE22282	AAE22282 gp41 fusi
54	177	94.7	38 5	AADE02097	AADE02097 Hybrid po
55	177	94.7	38 5	AADE01509	AADE01509 Hybrid po
56	177	94.7	38 6	ABG75976	ABG75976 HIV-1 gp4
57	177	94.7	38 6	ABU09553	ABU09553 Peptide f
58	177	94.7	38 6	ABU010245	ABU010245 HIV-1 gp
59	177	94.7	38 7	ADC939756	ADC939756 DP-107 an
60	177	94.7	38 7	ADE73011	ADE73011 HIV gp41
61	177	94.7	41 2	AAAR52840	AAAR52840 DP-125 -
62	177	94.7	41 2	AAAR98406	AAAR98406 Peptide D
63	177	94.7	41 2	AAW17019	AAW17019 DP-178-11
64	177	94.7	41 2	AAW27616	AAW27616 Human imm
65	177	94.7	41 2	AAW27622	AAW27622 Human imm
66	177	94.7	41 3	AAAY89779	AAAY89779 Core poly
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68	177	94.7	41 3	AAAY89134	AAAY89134 Core poly
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72	177	94.7	41 4	AAAB77489	AAAB77489 Core poly
73	177	94.7	41 4	AAAB02106	AAAB02106 Viral cor
74	177	94.7	41 4	AAAB01187	AAAB01187 Viral DPl
75	177	94.7	41 4	AAAB02636	AAAB02636 Viral cor
76	177	94.7	41 4	AAAB01969	AAAB01969 Viral cor
77	177	94.7	41 4	AAAG67047	AAAG67047 Control p
78	177	94.7	41 4	AAAB02074	AAAB02074 Viral cor
79	177	94.7	41 4	AAAB00598	AAAB00598 Viral DPl
80	177	94.7	41 4	AAU14018	AAU14018 Control p
81	177	94.7	41 4	AAU13733	AAU13733 DP178-11k
82	177	94.7	41 4	AAU13146	AAU13146 DP178-11k
83	177	94.7	41 4	AAU13042	AAU13042 DP178-11k
84	177	94.7	41 5	AAO18828	AAO18828 HIV gp41
85	177	94.7	41 5	AAO18876	AAO18876 HIV gp41
86	177	94.7	41 5	AAO18823	AAO18823 HIV gp41
87	177	94.7	41 5	AADE01989	AADE01989 Hybrid po
88	177	94.7	41 5		
89	177	94.7	41 5		
90	177	94.7	41 5		

ALIGNMENTS

RESULT 1
AAR98408 standard; peptide; 38 AA.

XX AAR98408;
AC 16-OCT-2003 (revised)
XX 17-FEB-1997 (first entry)
DT
XX DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.
DE
XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;
XX influenza virus; hepatitis B virus.
XX Human immunodeficiency virus 1.
OS
XX WO9619495-A1.
PN
XX 27-JUN-1996.
PD
XX 20-DEC-1995; 95WO-US016733.
PF
XX 20-DEC-1994; 94US-00360107.
PR
XX 06-JUN-1995; 95US-00470896.
PS
XX (UYDU-) UNIT DUKE.
PA (TRIM-) TRIMERIS INC.
XX Bolognani DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
PI Petteway SR, Langlois AJ;
XX MPI; 1996-309517/31.
DR
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence
PS search motif.
XX
XX Disclosure; Page 30; 471pp; English.
PS
XX The sequences given in AAR98398-408 represent peptides which exhibit
CC antifusogenic activity, antiviral capability and/or the ability to
CC modulate intracellular processes involving coiled-coil peptide
CC structures. These peptides are recognised by the ALLMOTIS, 107x178x4 and
CC PLZIP search motifs. These peptides may be used to inhibit the
CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 98.4%; Score 184; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,3e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLLRAIQAOQHLLQITWQIQKQARILAVERYLKDQ 38
DB 1 NNLLRAIEHQHLLQITWQIQKQARILAVERYLKDQ 38
RESULT 2
AAB54785
ID AAB54785 standard; peptide; 38 AA.
AC AAB54785;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX HIV antiviral activity exhibiting peptide SEQ ID NO:2.
DE
XX Long laeting fusion peptide inhibitor; viral infection; antiviral;
KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.

XX WO200069902-A1.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US013651.
PF
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONU-) CONUNCHEM INC.
PA
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI MPI; 2001-007496/01.
DR
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
PS
XX Claim 6; Page 173; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidease or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB54783 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 98.4%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,3e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLLRAIQAOQHLLQITWQIQKQARILAVERYLKDQ 38
DB 1 NNLLRAIEHQHLLQITWQIQKQARILAVERYLKDQ 38
RESULT 3
AAB55005
ID AAB55005 standard; peptide; 38 AA.
AC AAB55005;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 amino truncation peptide #35.
DE
XX Long laeting fusion peptide inhibitor; viral infection; antiviral;
KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.

PN MO200069902-A1.
XX
XX 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013651.
XX
XX
PR 17-MAY-1999; 99US-0134406P.
XX
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
XX Briden DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX
XX Disclosure; Page 139; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 98.4%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38
Db 1 NNILRAIEAQHLLQLTWQIQKQARILAVERYLKDQ 38
RESULT 4
AAB54970
ID AAB54970 standard; peptide; 38 AA.
XX
AC AAB54970;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #45.
XX
XX Long laesting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX
XX WO200069902-A1.

XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX
XX 17-MAY-1999; 99US-0134406P.
XX
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Briden DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX
XX Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
Query Match 98.4%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38
Db 1 NNILRAIEAQHLLQLTWQIQKQARILAVERYLKDQ 38
RESULT 5
AAB92244
ID AAB92244 standard; peptide; 38 AA.
XX
AC AAB92244;
XX
DT 22-JUN-2001 (first entry)
DT
XX
XX Virus related peptide SEQ ID NO:1420.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX

XX 17-MAY-2000; 2000WO-US013576.
PF 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX (CONJ-) CONJUCHEM INC.
XX PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX
XX Disclosure; Page 662; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxy/thiol groups on blood components to form a
CC peptidase stabilized therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB9829 to AAB9241 represent peptides which can be used in the
CC exemplification of the present invention
XX
XX SQ Sequence 38 AA;
XX
XX Query Match 98.4%; Score 184; DB 4; Length 38;
XX Best Local Similarity 97.4%; Pred. No. 1,3e-16;
XX Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
XX 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
XX DB
XX
XX RESULT 6
XX AAU14011 standard; peptide; 38 AA.
XX
XX AAU14011;
XX
XX 11-SEP-2003 (revised)
DT 21-NOV-2001 (first entry)
XX
XX DP107 peptide from HIV-1 transmembrane protein gp41.
XX
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
KM antitubercular; antiviral; HIV transmission.
XX
XX Human immunodeficiency virus 1; isolate LAI.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1..35 /note="Amino acids 1-35 can be optionally and serially
XX FT deleted from the N-terminus"
XX FT Misc-difference 4..38 /note="Amino acids 4-38 can be optionally and serially
XX FT deleted from the C-terminus"
XX
XX WO200151673-A2.
XX

PD 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffe P, Lackey JM, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antitubercular, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX
XX
XX Disclosure; Page 33; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antitubercular,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
XX SQ Sequence 38 AA;
XX
XX Query Match 98.4%; Score 184; DB 4; Length 38;
XX Best Local Similarity 97.4%; Pred. No. 1,3e-16;
XX Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
XX 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
XX DB
XX
XX RESULT 7
XX AA018771 standard; peptide; 38 AA.
XX
XX AA018771;
XX
XX 29-OCT-2002 (first entry)
DT
XX
XX HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
DE
XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
KM gp41.
XX
XX Human immunodeficiency virus.
XX
XX WO200256902-A2.
XX
XX 25-JUL-2002.
PD
XX 17-DEC-2001; 2001WO-US048802.
PF
XX 19-DEC-2000; 2000US-0256557P.
PR
XX (SCHER) SCHERING CORP.
XX
XX

PI Baroudy BM;
XX
DR WPI; 2002-636513/58.
XX
PT Treatment of HIV infection in an individual involves administration of a
PT combination of chemokine co-receptor five antagonist and a specified HIV
PT envelope polypeptide.
XX
PS Disclosure; Page 34; 52pp; English.
XX
CC The present invention relates to a method of treating an HIV infection in
CC an individual, which involves administering in combination a chemokine co-
CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
CC derivative. Other viral infections can also be treated using the method.
CC The present sequence is a peptide derived from HIV and useful in the
CC method of the invention
XX
SQ Sequence 38 AA;

Query Match 98.4%; Score 184; DB 5; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,3e-16;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIQKQLQARIILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHHLLQLTWQIQKQLQARIILAVERYLKDQ 38

RESULT 8
AAB14705
ID AAB14705 standard; peptide; 37 AA.
XX
AC AAB14705;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
XX
KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KW humoral response; broad spectrum vaccine; anti-HIV;
KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KW isolate LAI.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200040616-A1.
XX
PD 13-JUL-2000.
XX
PE 10-JAN-2000; 2000WO-US000456.
XX
PR 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
PA (WILD/) WILD C T.
PA (WEIS/) WEIS C D.
XX
PI Wild CT, Weiss CD;
XX
DR WPI; 2000-465959/40.
XX
PT Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
PS Disclosure; Page 36; 97pp; English.
XX
CC Sequence AAB1672-B1473 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralizing antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)

CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond to or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 37 AA;

Query Match 95.7%; Score 179; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIQKQLQARIILAVERYLKD 37
DB 1 NNLLRAIEAQOHHLLQLTWQIQKQLQARIILAVERYLKD 37

RESULT 9
AAB54969
ID AAB54969 standard; peptide; 37 AA.
XX
AC AAB54969;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
XX
KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antitumorigenic; mobile blood component; measles virus; MeV; STV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PE 17-MAY-2000; 2000WO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONF-) CONFUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG,
XX
DR WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

XX PS Disclosure, Page 137, 211pp; English.

CC The present invention describes a modified anti-viral peptide (I)

CC comprising a peptide that exhibits anti-viral activity and a reactive

CC group which is reactive with amino groups, hydroxyl groups, or thiol

CC groups on blood components to form stable covalent bonds. (I) has anti-

CC viral and anti-fusogenic activities. (I) inhibits viral infection of

CC cells by inhibiting cell-cell fusion or free virus infection or to reduce

CC the level of membrane fusion events between two or more entities, e.g.,

CC virus-cell or cell-cell, relative to the level of membrane fusion that

CC occurs in the absence of the peptide. (II) is useful in the treatment of

CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,

CC MeV, and SIV. (I) may be administered prophylactically to previously

CC uninfected individuals. This is useful in cases where an individual has

CC been subjected to a high risk of exposure to a virus. By bonding of long-

CC lived components of the blood, such as immunoglobulin, serum albumin, red

CC blood cells and platelets the activity is extended for days to weeks.

CC This is due to improved stability in vivo and a reduced susceptibility to

CC proteolysis or protease degradation. This minimises the need for more

CC frequent, or even continual, administration of the peptides. AAB54784 to

CC AAB54931 represent peptides used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 37 AA;

XX

Query Match 95.7%; Score 179; DB 4; Length 37;

Best Local Similarity 97.3%; Pred. No. 5.8e-16;

Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLRAIAQOQHLLQLTWQIKQLQARILAVERYLKDQ 37

Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 10

AAB14739

XX AAB14739 standard; peptide; 37 AA.

AC

XX

XX

DT 12-SEP-2003 (revised)

DT 24-NOV-2000 (first entry)

XX

XX

DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.

XX

KM HIV-1: gp41 N-helical domain; gp41 heptad repeat region; coiled coil;

KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;

KM humoral response; broad spectrum vaccine; anti-HIV;

KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;

KM isolate LAI.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200040616-A1.

XX

PD 13-JUL-2000.

XX

PF 10-JAN-2000; 2000WO-US000456.

XX

XX

PR 08-JAN-1999; 99US-0115404P.

PR 07-JAN-2000; 2000US-00480336.

XX

XX

PA (WILD/) WILD C T.

PA (WEIS/) WEISS C D.

XX

XX

PI Wild CT, Weiss CD,

XX

DR WPI, 2000-465959/40.

XX

PT Raising neutralizing antibody response to human immunodeficiency virus,

PT comprises administering a polypeptide capable of forming a stable coiled-

PT coil solution structure.

XX PS Disclosure, Page 38, 97pp; English.

XX

CC Sequences AAB14672-B14739 represent peptides derived from the N-helical

CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,

CC isolate LAI. The invention relates to raising a neutralising antibody

CC response to a broad spectrum of HIV (human immunodeficiency virus)

CC strains and isolates, comprising the administration of a peptide which

CC corresponds to or mimics highly conserved portions of gp41 which are

CC important in mediating the process of viral entry into host cells. Such

CC peptides can correspond to or mimic the coiled coil solution structure of

CC the N-helical domain (the heptad repeat region), or can correspond or

CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-

CC helical segment), or the gp41 core 6-helix bundle, which is formed by the

CC interaction of the N- and C-helical domains of three gp41 proteins. The

CC peptides can be administered either singly or as a combination

CC (particularly a combination of N-helical and C-helical peptides), and can

CC be multimerised. For example, N- and C-helical domain peptides can be

CC alternately linked together to form a peptide which mimics the core 6-

CC helix bundle. Administration of the peptide(s) generates a humoral

CC response, with the production of antibodies against gp41 structures

CC involved in viral entry. As these portions of gp41 are well conserved,

CC such antibodies may be effective against a broad range of HIV strains and

CC isolates. The peptide compositions may be administered as a prophylactic

CC or therapeutic vaccine to generate antibodies which reduce or inhibit the

CC ability of HIV to infect uninfected cells. A composition comprising

CC polyclonal or monoclonal antibodies can be administered to reduce HIV

CC infection of uninfected cells. Antibodies raised against entry-relevant

CC gp41 structures may also be used therapeutically and as tools to further

CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to

CC standardise OS field)

XX

XX

Sequence 37 AA;

XX

Query Match 95.2%; Score 178; DB 3; Length 37;

Best Local Similarity 97.3%; Pred. No. 7.8e-16;

Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNLRAIAQOQHLLQLTWQIKQLQARILAVERYLKDQ 38

Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 11

AAB55004

XX AAB55004 standard; peptide; 37 AA.

AC

XX

XX

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX

XX

DE Anti-HIV peptide DP107 amino truncation peptide #34.

XX

KM Long lasting fusion peptide inhibitor; viral infection; antiviral;

KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;

KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

KM human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200069902-A1.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013651.

XX

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX

XX

PA (CONV-) CONJUCHEM INC.

XX

PI Briden DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.
 DR A modified peptide and a reactive group which is reactive with amino
 XX groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX Sequence 37 AA;
 SQ

Query Match 95.2%; Score 178; DB 4; Length 37;
 Best Local Similarity 97.3%; Pred. No. 7.8e-16;
 Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKQD 38
 |||||:|||||
 DB 1 NLLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQD 37

RESULT 12
 AAR55635
 ID AAR55635 standard; peptide; 38 AA.

XX AAR55635;

XX 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX

DE DP-135 - DP-107 analogue.

XX Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KW antiviral; gp41.
 XX

OS Synthetic.

XX WO9402505-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006769.

XX 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

XX Wild CT, Matthews TJ, Bolognesi DP;

XX WPI; 1994-048790/06.
 DR

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Disclosure; Page 25; 38pp; English.
 XX

CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 38 AA;

Query Match 94.7%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKQD 38
 |||||:|||||
 DB 1 NLLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKQD 38

RESULT 13
 AAR55636
 ID AAR55636 standard; peptide; 38 AA.

XX AAR55636;

XX 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX

DE DP-140 - DP-107 analogue.

XX Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KW antiviral; gp41.
 XX

OS Synthetic.

XX WO9402505-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006769.

XX 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

XX Wild CT, Matthews TJ, Bolognesi DP;

XX WPI; 1994-048790/06.
 DR

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX

PS Disclosure; Page 25; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues

CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 38 AA;

Query Match 94.7%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLLRAIQAOQHLLQITWQIKOQARIILAVERYLKQ 38
 DB 1 NNLLRAIEAOQHLLQITWGIKOLQARIILAVERYLKQ 38

RESULT 14

AAR47216
 ID AAR47216 standard; peptide; 38 AA.

AC AAR47216;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (558-595).

KM Leucine zipper; HIV-1; human immunodeficiency virus;

KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12 /note="residue 12 of the sequence in Fig 1 is H; residue

FT 12 of the sequence in Table 4 is G"

PN W09402505-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93WO-US006769.

PR 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

PA (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

PT New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.

PS Claim 1; Page 27; 38pp; English.

CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 38 AA;

Query Match 94.7%; Score 177; DB 2; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLLRAIQAOQHLLQITWQIKOQARIILAVERYLKQ 38
 DB 1 NNLLRAIEAOQHLLQITWGIKOLQARIILAVERYLKQ 38

RESULT 15

AAW27614
 ID AAW27614 standard; peptide; 38 AA.

AC AAW27614;

DT 25-MAR-2003 (revised)

DT 22-DEC-1997 (first entry)

DE Human immunodeficiency virus gp41 derived peptide DP-107.

KM Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;

OS inhibition; induction; cell fusion; transmembrane; type 1.

XX Human immunodeficiency virus.

PN US5656480-A.

PD 12-AUG-1997.

PF 27-JAN-1995; 95US-00374666.

PR 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

PR 19-JUL-1993; 93WO-US006769.

PA (UYDU-) UNIV DUKE.

PI Bolognesi DP, Wild CT, Matthews TJ;

DR WPI; 1997-414595/38.

PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV

PT syncytia formation and transmembrane.

PS Claim 1; Col 13-14; 18pp; English.

CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein

CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced

CC cell fusion in a culture and cell free HIV transmembrane in a culture to a

CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-

CC MAR-2003 to correct PF field.)

XX Sequence 38 AA;

OY 1 NNLLRAIQAOQHLLQITWQIKOQARIILAVERYLKQ 38
 DB 1 NNLLRAIEAOQHLLQITWGIKOLQARIILAVERYLKQ 38

RESULT 16

AAW88666
 ID AAW88666 standard; peptide; 38 AA.

AC AAW88666;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 21.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;

XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

XX anti-fusogenic; differentiation factor; interleukin; interferon;

XX colony stimulating factor; hormone; angiogenic factor.

OS	Unidentified.
XX	
XX	FN W099559615-A1.
XX	
PD	25-NOV-1999.
XX	
PF	20-MAY-1999; 99WO-US011219.
XX	
PR	20-MAY-1998; 98US-00082279.
XX	(TRIM-) TRIMERIS INC.
PA	
PI	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
DR	WPI; 2000-136792/12.
XX	
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
PT	comprises enhancer sequence.
PS	Disclosure; Page 21; 124pp; English.
CC	The invention relates to hybrid polypeptides comprising enhancer peptide
CC	sequence linked to core polypeptides. The enhancer polypeptides are
CC	derived from various retroviral envelope (gp41) protein sequences,
CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC	pharmacokinetic properties such as increasing the half-life of any core
CC	polypeptide that they are linked to. The core polypeptides are any
CC	polypeptide that may be introduced into a living system and that can
CC	function as a pharmacologically useful peptide for the treatment or
CC	prevention of a disease. The core polypeptides are bioactive peptides
CC	selected from a growth factor, cytokine, differentiation factor,
CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC	factor. The peptides of the invention can be used for inhibiting viral
CC	infection and can be used in anti-viral and anti-fusogenic treatments.
CC	Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC	be used in the invention. Some sequences among those indicated also
CC	comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX	
SQ	Sequence 38 AA;
	Query Match 94.7%; Score 177; DB 3; Length 38;
	Best Local Similarity 94.7%; Pred. No. 1.1e-15;
	Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
QY	1 NNLRLAIQAQHLLQLTVMQIKOLCARILAVERYLKDQ 38 1 NNLRATLEAQHLLQLTWGIGKIQCARILAVERYLKDQ 38
DB	1>NNLRATLEAQHLLQLTWGIGKIQCARILAVERYLKDQ 38
RESULT 17	
AA	AAY86730
ID	AAY86730 standard; peptide; 38 AA.
AC	AAY86730;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	Core polypeptide fragment T No. 85.
KX	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW	anti-fusogenic; differentiation factor; interleukin; interferon;
KM	colony stimulating factor; hormone; angiogenic factor.
XX	
OS	Unidentified.
PN	W099559615-A1.
XX	
PD	25-NOV-1999.
XX	
PF	20-MAY-1999; 99WO-US011219.
XX	
PR	20-MAY-1998; 98US-00082279.
XX	
PA	(TRIM-) TRIMERIS INC.
PI	
DR	WPI; 2000-136792/12.
XX	
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
PT	comprises enhancer sequence.
PS	Disclosure; Page 21; 124pp; English.
CC	The invention relates to hybrid polypeptides comprising enhancer peptide
CC	sequence linked to core polypeptides. The enhancer polypeptides are
CC	derived from various retroviral envelope (gp41) protein sequences,
CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC	pharmacokinetic properties such as increasing the half-life of any core
CC	polypeptide that they are linked to. The core polypeptides are any
CC	polypeptide that may be introduced into a living system and that can
CC	function as a pharmacologically useful peptide for the treatment or
CC	prevention of a disease. The core polypeptides are bioactive peptides
CC	selected from a growth factor, cytokine, differentiation factor,
CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC	factor. The peptides of the invention can be used for inhibiting viral
CC	infection and can be used in anti-viral and anti-fusogenic treatments.
CC	Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC	be used in the invention. Some sequences among those indicated also
CC	comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX	
SQ	Sequence 38 AA;
	Query Match 94.7%; Score 177; DB 3; Length 38;
	Best Local Similarity 94.7%; Pred. No. 1.1e-15;
	Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
QY	1 NNLRLAIQAQHLLQLTVMQIKOLCARILAVERYLKDQ 38 1 NNLRATLEAQHLLQLTWGIGKIQCARILAVERYLKDQ 38
DB	1>NNLRATLEAQHLLQLTWGIGKIQCARILAVERYLKDQ 38
RESULT 17	
AA	AAY86730
ID	AAY86730 standard; peptide; 38 AA.
AC	AAY86730;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	Core polypeptide fragment T No. 85.
KX	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW	anti-fusogenic; differentiation factor; interleukin; interferon;
KM	colony stimulating factor; hormone; angiogenic factor.
XX	
OS	Unidentified.
PN	W099559615-A1.
XX	
PD	25-NOV-1999.
XX	
PF	20-MAY-1999; 99WO-US011219.
XX	
PR	20-MAY-1998; 98US-00082279.
XX	
PA	(TRIM-) TRIMERIS INC.
PI	
DR	WPI; 2000-136792/12.
XX	
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
PT	comprises enhancer sequence.
PS	Disclosure; Page 21; 124pp; English.
CC	The invention relates to hybrid polypeptides comprising enhancer peptide
CC	sequence linked to core polypeptides. The enhancer polypeptides are
CC	derived from various retroviral envelope (gp41) protein sequences,
CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC	pharmacokinetic properties such as increasing the half-life of any core
CC	polypeptide that they are linked to. The core polypeptides are any
CC	polypeptide that may be introduced into a living system and that can
CC	function as a pharmacologically useful peptide for the treatment or
CC	prevention of a disease. The core polypeptides are bioactive peptides
CC	selected from a growth factor, cytokine, differentiation factor,
CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC	factor. The peptides of the invention can be used for inhibiting viral
CC	infection and can be used in anti-viral and anti-fusogenic treatments.
CC	Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC	be used in the invention. Some sequences among those indicated also
CC	comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX	
SQ	Sequence 38 AA;
	Query Match 94.7%; Score 177; DB 3; Length 38;
	Best Local Similarity 94.7%; Pred. No. 1.1e-15;
	Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
QY	1 NNLRLAIQAQHLLQLTVMQIKOLCARILAVERYLKDQ 38 1 NNLRATLEAQHLLQLTWGIGKIQCARILAVERYLKDQ 38
DB	1>NNLRATLEAQHLLQLTWGIGKIQCARILAV

```

XX 20-MAY-1998; 98US-00082279.
PA (TRIM-) TRIMERIS INC.
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
DR
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
PS Disclosure; Page 22; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AA8851-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
XX Sequence 38 AA;
SO
Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 NNLRLATQAOOHLQLTFWMOIKQLOARILAVERYLKDO 38
1 NNLRLATQAOOHLQLTFWMOIKQLOARILAVERYLKDO 38
DB
RESULT 18
AA88731
ID AA88731 standard; peptide; 38 AA.
XX
XX AA88731;
AC
XX 23-MAY-2000 (first entry)
DT
XX Core polypeptide fragment T No. 86.
DE
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX Unidentified.
OS
XX WO959615-A1.
PN
XX 25-NOV-1999.
PD
XX 20-MAY-1999; 99WO-US011219.
XX 20-MAY-1998; 98US-00082279.
XX (TRIM-) TRIMERIS INC.
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT

```

PT comprises enhancer sequence.
 XX
 PS Disclosure; Page 22; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp11) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;
 Query Match 94.7%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIQAOQHLLQITWQIQOLQARILAVERYLKDQ 38
 1 NNLRAIEAQHLLQITWGIKQIQARILAVERYLKDQ 38
 DB 1 NNLRAIEAQHLLQITWGIKQIQARILAVERYLKDQ 38
 RESULT 19
 AAY89145
 ID AAY89145 standard; peptide; 38 AA.
 AC AAY89145;
 XX
 XX 23-MAY-2000 (first entry)
 DT
 XX
 DE Core polypeptide fragment T No. 583.
 XX
 XX Retrovirus; hybrid polypeptide; enhancer; gp11; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 XX WO959615-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 20-MAY-1999; 99WO-US011219.
 PF
 XX 20-MAY-1998; 98US-00082279.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI
 XX WPI; 2000-136792/12.
 DR
 XX A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.
 PS
 XX Disclosure; Page 30; 124pp; English.
 XX
 XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp11) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can

CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;
 Query Match 94.7%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIQAOQHLLQITWQIQOLQARILAVERYLKDQ 38
 1 NNLRAIEAQHLLQITWGIKQIQARILAVERYLKDQ 38
 DB 1 NNLRAIEAQHLLQITWGIKQIQARILAVERYLKDQ 38
 RESULT 20
 AAY89146
 ID AAY89146 standard; peptide; 38 AA.
 AC AAY89146;
 XX
 XX 23-MAY-2000 (first entry)
 DT
 XX
 DE Core polypeptide fragment T No. 583.
 XX
 XX Retrovirus; hybrid polypeptide; enhancer; gp11; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 XX WO959615-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 20-MAY-1999; 99WO-US011219.
 PF
 XX 20-MAY-1998; 98US-00082279.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI
 XX WPI; 2000-136792/12.
 DR
 XX A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.
 PS
 XX Disclosure; Page 30; 124pp; English.
 XX
 XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp11) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can

CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 SQ Sequence 38 AA;

Query Match 94.7%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 21
 AAY89243
 ID AAY89243 standard; peptide; 38 AA.

AC AAY89243;
 XX
 DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 681.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS WO9559615-A1.

PN 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

PS Disclosure; Page 32; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY86651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 SQ Sequence 38 AA;

Query Match 94.7%; Score 177; DB 3; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 22
 AAB14530
 ID AAB14530 standard; peptide; 38 AA.

AC AAB14530;

XX 12-SEP-2003 (revised)

DT 24-NOV-2000 (first entry)

DE HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).

KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy.

XX Human immunodeficiency virus 1.

PN WO200040616-A1.

XX 13-JUL-2000.

XX 10-JAN-2000; 2000WO-US000456.

XX 08-JAN-1999; 99US-0115404P.

XX 07-JAN-2000; 2000US-00480336.

XX (WILD/) WILD C.T.

XX (WEISS/) WEISS C.D.

XX Wild CT, Weiss CD;

XX WPI; 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.

PS Claim 5; Page 56; 97pp; English.

XX Sequences AAB14529-B14531 and AAB14537-B14568 represent specifically
 CC claimed peptides derived from the N-helical domain of the gp41 envelope
 CC glycoprotein from a variety of HIV-1 isolates. The invention relates to
 CC raising a neutralising antibody response to a broad spectrum of HIV
 CC (human immunodeficiency virus) strains and isolates, comprising the
 CC administration of a peptide which corresponds to or mimics highly
 CC conserved portions of gp41 which are important in mediating the process
 CC of viral entry into host cells. Such peptides can correspond to or mimic
 CC the coiled coil solution structure of the N-helical domain (the heptad
 CC repeat region), or can correspond or mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41
 CC core 6-helix bundle, which is formed by the interaction of the N- and C-
 CC helical domains of three gp41 proteins. The peptides can be administered
 CC either singly or as a combination (particularly a combination of N-
 CC helical and C-helical peptides), and can be multimerised. For example, N-
 CC and C-helical domain peptides can be alternately linked together to form
 CC a peptide which mimics the core 6-helix bundle. Administration of the
 CC peptide(s) generates a humoral response, with the production of
 CC antibodies against gp41 structures involved in viral entry. As these
 CC portions of gp41 are well conserved, such antibodies may be effective
 CC against a broad range of HIV strains and isolates. The peptide
 CC compositions may be administered as a prophylactic or therapeutic vaccine
 CC to generate antibodies which reduce or inhibit the ability of HIV to
 CC infect uninfected cells. A composition comprising polyclonal or
 CC monoclonal antibodies can be administered to reduce HIV infection of
 CC uninfected cells. Antibodies raised against entry-relevant gp41
 CC structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to

PN WO20066622-A1.
XX
XX 09-NOV-2000.
XX
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM,
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
XX partial length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
XX is used to modulate inflammation.
XX
XX Claim 15; Page 42; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
XX helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
XX located in the amino terminus of the gp41 ectodomain. gp41 plays a
XX critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
XX interacts with members of the formyl peptide receptor (FPR) family and
XX thereby up-regulates an inflammatory response, and acts as a potent
XX chemottractant and activator of human peripheral blood phagocytes (but
XX not T cells). The present peptide can be used to modulate an inflammatory
XX response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 1.1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIQKQLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARILAVERYLKQ 38

RESULT 26
AAG63858
ID AAG63858 standard; peptide; 38 AA.
XX
XX AAG63858;
XX
XX 11-SEP-2003 (revised)
XX 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of a HIV-1 gp41 peptide fragment.
XX
XX HIV-1; isolate LAI; gp41; viral entry; envelope protein; glycoprotein;
XX viral infection; antiviral.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200159457-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004030.
XX
XX 10-FEB-2000; 2000US-0181543P.
XX 28-SEP-2000; 2000US-02355901P.
XX
XX (PANA-) PANACOS PHARM INC.
XX
XX Wild CT, Allaway GP;
XX
XX WPI; 2001-522493/57.
XX
XX Screening for inhibitors of viral entry structure formation by

PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.
XX
XX Disclosure; Page 23; 68pp; English.
XX
XX
XX The present sequence represents a fragment of a Human immunodeficiency
XX virus type 1 (HIV-1) isolate LAI gp41 protein. The peptide is used to
XX raise antibodies for use in the method of the invention. The
XX specification describes a method of screening for inhibitors of viral
XX entry structure formation. The method comprises contacting a viral
XX envelope protein or glycoprotein (e.g. gp41) with a triggering agent and
XX a candidate compound to form a mixture, and measuring the effect that the
XX candidate compound has on the formation of conformational intermediates.
XX The effect of the candidate compound can be measured by antibody binding
XX to these conformational intermediates. The compounds identified by the
XX method are useful as inhibitors for inhibiting or preventing viral
XX infection and to treat humans infected with HIV-1 or other viruses. This
XX antiviral compounds can also be used to inactivate viruses in body
XX fluids, e.g. blood or blood compounds used for therapeutic purposes. The
XX assay is also useful for detecting antibodies in virus-infected
XX individuals or virus-infected body fluids or tissues that inhibit entry-
XX relevant conformational changes in one or more viral envelope proteins or
XX glycoproteins. The presence of the antibodies in infected individuals or
XX samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
SQ Sequence 38 AA;
Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 1.1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIQKQLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARILAVERYLKQ 38

RESULT 27
AAB92349
ID AAB92349 standard; peptide; 38 AA.
XX
XX AAB92349;
XX
XX 22-JUN-2001 (first entry)
XX
XX Virus related peptide SEQ ID NO:1525.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013576.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity.
XX
XX

XX Disclosure; Page 704; 733pp; English.
 PS
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidease activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 38 AA;
 XX
 Query Match 94.7%; Score 177; DB 4; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARILAVERYLKDQ 38
 XX
 RESULT 28
 AAB77021
 ID AAB77021 standard; peptide; 38 AA.
 XX
 AC AAB77021;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Core polypeptide T21.
 XX
 DE Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KM fusion-related disorder; bacterial infection; viral infection.
 XX
 OS Unidentified.
 XX
 PN WO200103723-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018772.
 XX
 PR 09-JUL-1999; 99US-00350641.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX
 DR WPI, 2001-147136/15.
 XX
 PT New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX
 PS Disclosure; Page 30; 151pp; English.
 XX
 CC The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the

CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used
 CC
 SQ Sequence 38 AA;
 XX
 Query Match 94.7%; Score 177; DB 4; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
 DB 1 NNLLRAIEAQHLLQLTWQIGIKQLQARILAVERYLKDQ 38
 XX
 RESULT 29
 AAB77085
 ID AAB77085 standard; peptide; 38 AA.
 XX
 AC AAB77085;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Core polypeptide T85.
 XX
 DE Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KM fusion-related disorder; bacterial infection; viral infection.
 XX
 OS Unidentified.
 XX
 PN WO200103723-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018772.
 XX
 PR 09-JUL-1999; 99US-00350641.
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 PA (TRIM-) TRIMERIS INC.
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 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX
 DR WPI, 2001-147136/15.
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 PT New hybrid polypeptide, useful for preventing, treating and diagnosing
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 CC coil peptide interactions. Other uses include preventing, treating and/or
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 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
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 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
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 Best Local Similarity 94.7%; Pred. No. 1.1e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38
 DB 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38

RESULT 30
 AAB77086

ID AAB77086 standard; peptide; 38 AA.

XX AAB77086;

DT 19-APR-2001 (first entry)

DE Core polypeptide T86.

KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KW fusion-related disorder; bacterial infection; viral infection.

XX Unidentified.

XX WO200103723-A1.

XX 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US018772.

PR 09-JUL-1999; 99US-00350641.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Mernutka G, Anwer MK, Lambert DM;

XX WPI; 2001-147136/15.

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 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
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 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
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XX Sequence 38 AA;

Query Match 94.7%; Score 177; DB 4; Length 38;
 Best Local Similarity 94.7%; Pred. No. 1.1e-15;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38
 DB 1 NNILRAIQAOQHLLQLTWQIQKQARILAVERYLKDQ 38

Search completed: June 2, 2004, 11:41:46
 Job time : 47.6033 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.3261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336a-544
Perfect score: 187
Sequence: 1 NNLIRAIQAQOHLTLTWQIKQLARILAVERYIKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	94.7	357	2 S21986	envelope protein g
2	177	94.7	851	2 S33995	env polypeptide
3	177	94.7	853	2 S54384	env polypeptide
4	177	94.7	854	2 S13288	env polypeptide - huma
5	177	94.7	855	1 VCLJZR	env polypeptide pr
6	177	94.7	856	1 VCLJH3	env polypeptide pr
7	177	94.7	856	1 VCLJVL	env polypeptide pr
8	177	94.7	861	1 VCLJLV	env polypeptide pr
9	176	94.1	357	2 S22006	envelope protein g
10	176	94.1	357	2 S21994	envelope protein g
11	176	94.1	357	2 S22002	envelope protein g
12	176	94.1	358	2 S22002	envelope protein g
13	176	94.1	358	2 S22000	envelope protein g
14	176	94.1	358	2 S70417	envelope protein g
15	176	94.1	868	1 VCLJH4	env polypeptide
16	174	93.0	357	2 S21990	envelope protein g
17	174	93.0	729	1 VCLJXK	env polypeptide pr
18	174	93.0	859	1 VCLJMN	env polypeptide pr
19	174	93.0	861	1 VCLJKB	env polypeptide pr
20	173	92.5	443	2 C41621	env polypeptide p
21	173	92.5	445	2 A41621	env polypeptide M
22	173	92.5	454	2 B41621	env polypeptide D
23	173	92.5	843	1 H44001	env polypeptide pr
24	173	92.5	846	1 VCLJND	env polypeptide pr
25	173	92.5	852	2 T12016	envelope glycoprote
26	173	92.5	855	1 VCLJAZ	env polypeptide pr
27	173	92.5	856	1 VCLJZW	env polypeptide pr
28	173	92.5	856	1 A44963	env polypeptide pr
29	173	92.5	861	1 VCLJSC	env polypeptide pr

30	172	92.0	859	2 T01672	envelope polypeptide
31	169	90.4	358	2 S21998	envelope protein g
32	168	89.8	357	2 S21992	envelope protein g
33	165	88.2	852	1 VCLJBR	env polypeptide -
34	162	86.6	854	1 VCLJST	env polypeptide pr
35	159	85.0	847	2 T09448	envelope glycoprote
36	159	85.0	847	2 S13289	env polypeptide - huma
37	150	69.5	104	2 S52930	GP41 ENV protein -
38	127	67.9	867	2 S49197	envelope protein p
39	122	65.2	874	1 VCLJG4	env polypeptide -
40	122	65.2	877	2 C46356	env polypeptide -
41	119	63.6	863	2 A53034	gag polypeptide -
42	117	62.6	732	2 S46352	env polypeptide -
43	115	61.5	366	2 B41565	env polypeptide -
44	113	60.4	712	1 VCLJSA	env polypeptide pr
45	113	60.4	851	2 S12159	env polypeptide - huma
46	113	60.4	852	1 VCLJGG	env polypeptide pr
47	113	60.4	859	1 VCLJST	env polypeptide pr
48	112	60.4	869	2 S53098	envelope polypeptide
49	112	59.9	859	1 VCLJCT	env polypeptide pr
50	111	59.4	855	2 A45713	Env transmembrane
51	111	59.4	858	1 VCLJG2	env polypeptide pr
52	111	59.4	881	2 S03068	env polypeptide - huma
53	111	59.4	885	2 S04322	env polypeptide -
54	111	59.4	886	2 T11555	env polypeptide - stim
55	110	58.8	881	1 VCLJG3	env polypeptide -
56	109	58.3	859	2 S24571	env polypeptide - huma
57	109	58.3	869	2 A47665	env polypeptide gp120 (
58	108	57.8	880	1 VCLJST	env polypeptide pr
59	107	57.2	151	2 S30458	env polypeptide - huma
60	107	57.2	889	1 VCLJG5	env polypeptide -
61	106	56.7	887	2 T11566	envelope glycoprote
62	105	56.1	151	2 S30448	env polypeptide - huma
63	105	56.1	151	2 S30453	env polypeptide -
64	105	56.1	151	2 S30452	env polypeptide - huma
65	105	56.1	151	2 S30450	env polypeptide -
66	105	56.1	151	2 S30451	env polypeptide - huma
67	104	55.6	786	2 S28084	env polypeptide -
68	103	55.1	151	2 S30459	env polypeptide - huma
69	103	55.1	151	2 S30457	env polypeptide -
70	103	55.1	151	2 S30456	env polypeptide - huma
71	103	55.1	151	2 S30455	env polypeptide -
72	103	55.1	151	2 S30454	env polypeptide - huma
73	103	55.1	151	2 S60695	env polypeptide -
74	94	50.3	68	2 S60696	env polypeptide - huma
75	94	50.3	68	2 S60705	env polypeptide -
76	94	50.3	68	2 S60707	env polypeptide - huma
77	94	50.3	68	2 S60694	env polypeptide -
78	94	50.3	69	2 S60706	env polypeptide - huma
79	89	47.6	68	2 S60693	env polypeptide -
80	89	47.6	68	2 S60687	env polypeptide - huma
81	87	46.5	68	2 S60692	env polypeptide -
82	86	46.0	68	2 S60688	env polypeptide - huma
83	83	44.4	69	2 S60690	env polypeptide -
84	83	44.4	69	2 S60689	env polypeptide - huma
85	83	44.4	69	2 S60691	env polypeptide -
86	79	42.2	294	2 S60525	envelope polypeptide
87	79	42.2	297	2 S60538	envelope polypeptide
88	72	38.5	372	2 S46344	env polypeptide -
89	72	38.5	375	2 S46345	env polypeptide -
90	70	37.4	294	2 S60545	envelope polypeptide

ALIGNMENTS

RESULT 1
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70422

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129

A:Experimental source: patient 27L

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 94.7%; Score 177; DB 2; Length 357; Best Local Similarity 94.7%; Pred. No. 1.2e-15; Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 38
Db 54 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 91

RESULT 2

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlino, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199

C:Superfamily: type E retrovirus env polypeptide

Query Match 94.7%; Score 177; DB 2; Length 851; Best Local Similarity 94.7%; Pred. No. 1.2e-15; Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 38
Db 548 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 585

RESULT 3

S54384 envelope polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-853 <THE>

A:Cross-references: EMBL:M2639; NID:G329377; PIDN:AAA45370.1; PID:G329385

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 94.7%; Score 177; DB 2; Length 853; Best Local Similarity 94.7%; Pred. No. 1.2e-15; Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 38
Db 550 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 587

RESULT 4

S13288

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; PMID:91043044; PMID:2172833

A:Accession: S13288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 94.7%; Score 177; DB 2; Length 854; Best Local Similarity 94.7%; Pred. No. 1.2e-15; Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 38
Db 551 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 588

RESULT 5

VCLJZR env polypeptide precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus Zr-6

C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C:Accession: D26192

R:Srinivasan, A.; Anand, R.; Ranganathan, P.; Peorino, P.; Schochtmann, G.; Cui

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide

A:Reference number: A26192; PMID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-855/Product: env polypeptide #status predicted <MAT>

F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>

F:501-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 94.7%; Score 177; DB 1; Length 855; Best Local Similarity 94.7%; Pred. No. 1.2e-15; Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 38
Db 552 NNTLRATQAQOHLQTLTWGIRKQARILAVERYLKQ 589

RESULT 6

VCLJH3 env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Joseph, S.F.; Dorar

bernger, J.A.; Papas, T.S.; Garayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; PMID:85111123; PMID:2576615

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domains: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMM>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.7%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 1.2e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIQOQHLLQLTWGIKQARILAVERYLKDD 38
Db 558 NNLLRAIEAQOHLQLTWGIRKQARILAVERYLKDD 590
RESULT 7
env polypotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Meusing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laaky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A:Reference number: A93355; MUID:8511157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domains: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMM>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.7%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 1.2e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIQOQHLLQLTWGIKQARILAVERYLKDD 38
Db 558 NNLLRAIEAQOHLQLTWGIRKQARILAVERYLKDD 590
RESULT 8
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:8509333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C:Genetics:

A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domains: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <TMM>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,146,161,165,191,202,233,246,267,281,294,300,306,337,344,361,391,397,402,411,
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.7%; Score 177; DB 1; Length 861;
Best Local Similarity 94.7%; Pred. No. 1.2e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIQOQHLLQLTWGIKQARILAVERYLKDD 38
Db 558 NNLLRAIEAQOHLQLTWGIRKQARILAVERYLKDD 595
RESULT 9
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S72006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE>
A:Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
A:Experimental source: patient L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypotein
Query Match 94.1%; Score 176; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLLRAIQOQHLLQLTWGIKQARILAVERYLKDD 38
Db 54 NNLLRAIEAQOHLQLTWGIRKQARILAVERYLKDD 91
RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140; 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:G60179
C:Superfamily: type E retrovirus env polypotein
Query Match 94.1%; Score 176; DB 2; Length 357;

Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYLKQ 91

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22004

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 48

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292, 'X', 294-357 <STE2>

A:Cross-references: EMBL:X61353; NID:g60188

C:Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 176; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22002

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 3L

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STE2>

A:Cross-references: EMBL:X61352; NID:g60186

C:Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 55 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYLKQ 92

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22000

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21990

A:Accession: S22000

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 55 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYLKQ 92

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
S70417

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

C:Accession: S70417

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70417

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185

C:Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 176; DB 2; Length 358;
Best Local Similarity 92.1%; Pred. No. 6.5e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 55 NNILRAIEAQOHLQLTWGIKOLQARVLAVERYLKQ 92

RESULT 15

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
VCLJTH4

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C:Accession: C25523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S.

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human ;

A:Reference number: A94136; PMID:8704161; PMID:3490666

A:Accession: C25523

A:Molecule type: DNA

A:Residues: 1-868 <DES>

A:Cross-references: GB:M13137; NID:G326460; PIDN:AAA4311.1; PID:G326467
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F:1-521/Product: coat protein gp120 #status predicted <GPI>
 F:522-868/Product: coat protein gp41 #status predicted <CP2>
 F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459

Query Match 94.1%; Score 176; DB 1; Length 868;
 Best Local Similarity 94.7%; Pred. No. 1.7e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 Db 565 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 602

RESULT 16

S21990
 envelope protein gp120/gp41 - human immunodeficiency virus type 1

A:Variety: isolate 20
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S21990; S70423
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
 A:Reference number: S21990
 A:Accession: S21990

A:Molecule type: DNA
 A:Residues: 1-357 <STE1>
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA3626.1; PID:G60176

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70423

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-332, 'X', 334-357 <STE2>
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA3626.1; PID:G60176
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.0%; Score 174; DB 2; Length 357;
 Best Local Similarity 89.5%; Pred. No. 1.2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 Db 54 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 91

RESULT 17

VCLJXK

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N:Alternate names: coat polyprotein
 N:Contains: coat protein gp120; coat protein gp32
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
 C:Accession: B42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A:Reference number: A42995; MUID:92351552; PMID:1322587
 A:Accession: B42995
 A:Molecule type: mRNA
 A:Residues: 1-729 <SHI>

A:Cross-references: GB:S41266; GB:D01206
 C:Genetics:

A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F:1-689/Domain: extracellular #status predicted <EXT>
 F:1-133/Domain: signal sequence #status predicted <SIG>
 F:17-33/Region: hydrophobic #status predicted
 F:34-517/Product: coat protein gp120 #status predicted <CP1>
 F:514-517/Region: cleavage processing #status predicted <CP1>
 F:518-729/Product: coat protein gp32 #status predicted <CP2>
 F:518-534/Region: hydrophobic #status predicted <CP2>
 F:590-711/Domain: transmembrane #status predicted <TM1>
 F:712-729/Domain: intracellular #status predicted <INT>

F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414,
 Query Match 93.0%; Score 174; DB 1; Length 729;
 Best Local Similarity 92.1%; Pred. No. 2.6e-15;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 Db 559 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 596

RESULT 18

VCLJMN

env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)

N:Alternate names: coat polyprotein
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C:Accession: A28922

R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Scar
 Virology 164, 531-536, 1988
 A:Title: Envelope sequences of two new United States HIV-1 isolates.
 A:Reference number: A28922; MUID:88219542; PMID:3369091
 A:Accession: A28922

A:Molecule type: DNA
 A:Residues: 1-859 <GUR>

C:Genetics:

A:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-859/Product: env polyprotein #status predicted <BP>
 F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401,

Query Match 93.0%; Score 174; DB 1; Length 859;
 Best Local Similarity 89.5%; Pred. No. 3.1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 Db 557 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 594

RESULT 19

VCLJKB

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N:Alternate names: coat polyprotein
 N:Contains: coat protein gp120; coat protein gp41
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
 C:Accession: A42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A:Reference number: A42995; MUID:92351552; PMID:1322587
 A:Accession: A42995
 A:Molecule type: mRNA
 A:Residues: 1-861 <SHI>

A:Cross-references: GB:S41266; GB:D01206
 C:Genetics:

A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F/1-688/Domain: extracellular #status predicted <EXT>
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/17-33/Region: hydrophobic #status predicted
 F/14-517/Region: cleavage processing #status predicted <CP1>
 F/14-517/Region: cleavage processing #status predicted <CP2>
 F/18-861/Product: coat protein gp41 #status predicted
 F/18-534/Region: hydrophobic #status predicted
 F/590-711/Domain: transmembrane #status predicted <TM1>
 F/712-861/Domain: intracellular #status predicted <INT>
 F/756-772/Region: hydrophobic #status predicted
 F/93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.0%; Score 174; DB 1; Length 861;
 Best Local Similarity 92.1%; Pred. No. 3, 1e-15;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 38
 DB 559 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 596

RESULT 20

env polyprotein P - human immunodeficiency virus type 1 (fragment)
 N/Alternate names: coat polyprotein
 N/Contents: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C/Accession: C41621

R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A/Reference number: A41621; MUID:92107924; PMID:11763038

A/Accession: C41621
 A/Molecule type: DNA
 A/Residues: 1-443 <BUR>
 A/Cross-references: GB:M77230; NID:9328631; PIDN:AA03792.1; PID:9555015
 A/Note: this virus was isolated from the mother's sexual partner
 C/Genetics:

A/Genes: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F/1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F/552-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F/424-443/Domain: transmembrane #status predicted <TMN>
 F/9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 92.5%; Score 173; DB 2; Length 443;
 Best Local Similarity 89.5%; Pred. No. 2, 1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 38
 DB 293 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 330

RESULT 21

env polyprotein M - human immunodeficiency virus type 1 (fragment)
 N/Alternate names: coat polyprotein
 N/Contents: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C/Accession: A41621

R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A/Reference number: A41621; MUID:92107924; PMID:11763038

A/Accession: A41621
 A/Molecule type: DNA

A/Residues: 1-445 <BUR>
 A/Cross-references: GB:M77228; NID:9328627; PIDN:AA03790.1; PID:9555013
 A/Note: this virus was isolated from the mother
 C/Genetics:

A/Genes: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F/1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F/554-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F/426-445/Domain: transmembrane #status predicted <TMN>
 F/9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 92.5%; Score 173; DB 2; Length 445;
 Best Local Similarity 89.5%; Pred. No. 2, 1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 38
 DB 295 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 332

RESULT 22

env polyprotein D - human immunodeficiency virus type 1 (fragment)
 N/Alternate names: coat polyprotein
 N/Contents: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
 C/Accession: B41621

R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A/Reference number: A41621; MUID:92107924; PMID:11763038

A/Accession: B41621
 A/Molecule type: DNA
 A/Residues: 1-454 <BUR>
 A/Cross-references: GB:M77279
 A/Note: this virus was isolated from the daughter
 C/Genetics:

A/Genes: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F/1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F/563-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F/435-454/Domain: transmembrane #status predicted <TMN>
 F/9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo

Query Match 92.5%; Score 173; DB 2; Length 454;
 Best Local Similarity 89.5%; Pred. No. 2, 1e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 38
 DB 304 NNILRAIQAOQHLLQLTWQIKOLQARILAVRYLKQ 341

RESULT 23

env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
 N/Alternate names: coat polyprotein
 N/Contents: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
 C/Accession: H44001

R/Li, Y.; Hu, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
 J. Virol. 66, 6587-6600, 1992
 A/Title: Complete nucleotide sequence, genome organization, and biological properties of
 A/Reference number: A44001; MUID:93021387; PMID:1404605

A/Accession: H44001
 A/Molecule type: DNA
 A/Residues: 1-843 <LTY>

A:Cross-references: GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TM>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 92.5%; Score 173; DB 1; Length 843;
Best Local Similarity 89.5%; Pred. No. 4.2e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
DB 340 NNILRAIEAQOHLQLTWGIGIKQLQARVLAVERYLRDQ 577

RESULT 24
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J000066
R:Splice, B.: Site, J.: Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immun
A:Reference number: J000065; MWID:90034200; PMID:2806917
A:Accession: J000066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-846/Product: coat protein gp41 #status predicted <GP2>
F:502-520/Domain: transmembrane #status predicted <TM>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 92.5%; Score 173; DB 1; Length 846;
Best Local Similarity 89.5%; Pred. No. 4.2e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
DB 543 NNILRAIEAQOHLQLTWGIGIKQLQARVLAVERYLRDQ 580

RESULT 25
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12016
R:McCurchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
A:Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: Z17379; MWID:98178716; PMID:9519894
A:Accession: T12016
A:status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.5%; Score 173; DB 2; Length 852;
Best Local Similarity 89.5%; Pred. No. 4.2e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
DB 549 NNILRAIEAQOHLQLTWGIGIKQLQARVLAVERYLRDQ 586

RESULT 26
VCLJAZ
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barry, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MWID:85090453; PMID:2578227
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458/
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.5%; Score 173; DB 1; Length 855;
Best Local Similarity 89.5%; Pred. No. 4.2e-15;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
DB 552 NNILRAIEAQOHLQLTWGIGIKQLQARVLAVERYLRDQ 589

RESULT 27
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774
R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MWID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.5%; Score 173; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 4.2e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 553 NNILRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 590

RESULT 28

A:Accession: A44963
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate Z321)
 N:Alternate names: coat polypeptide
 N:Contains: coat protein gp120; coat protein gp41
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
 C:Accession: A44963
 R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989
 A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
 A:Reference number: A44963; MUID:89228766; PMID:2713163
 A:Accession: A44963
 A:Molecule type: DNA
 A:Residues: 1-856 <SRI>
 A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polypeptide
 C:Keyword: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-520/Product: coat protein gp120 #status predicted <CP1>
 F:521-856/Product: coat protein gp41 #status predicted <CP2>
 F:84-705/Domain: transmembrane #status predicted <TMN>
 F:87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611

Query Match 92.5%; Score 173; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 4.2e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 553 NNILRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 590

RESULT 29

VCLJSC
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)
 N:Alternate names: coat polypeptide
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C:Accession: B28922
 R:Girgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
 Virology 164, 531-536, 1988
 A:Title: Envelope sequences of two new United States HIV-1 isolates.
 A:Reference number: A28922; MUID:88219542; PMID:3369091
 A:Accession: B28922
 A:Molecule type: DNA
 A:Residues: 1-861 <GUR>
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polypeptide
 C:Keyword: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-861/Product: env polypeptide #status predicted <BP>
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 92.5%; Score 173; DB 1; Length 861;
 Best Local Similarity 89.5%; Pred. No. 4.3e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 558 NNILRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 595

RESULT 30

T01672
 envelope polypeptide precursor - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01672
 R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986
 A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
 A:Reference number: Z14389; MUID:86245056; PMID:2424612
 A:Accession: T01672
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-859 <ALI>
 A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
 C:Superfamily: type E retrovirus env polypeptide

Query Match 92.0%; Score 172; DB 2; Length 859;
 Best Local Similarity 89.5%; Pred. No. 5.8e-15;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
 DB 555 NNILRAIEAQOHLQLTWGIKOLQARILAVERYLKQ 592

Search completed: June 2, 2004, 11:50:12
 Job time: 11.3261 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 6.19565 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-544
Perfect score: 187
Sequence: 1 NNILRALIQAOQHLLQLTWQIKOLARILAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	177	94.7	853	1	ENV_HV1EL
2	177	94.7	853	1	ENV_HV1MF
3	177	94.7	853	1	ENV_HV1Z2
4	177	94.7	855	1	ENV_HV1Z6
5	177	94.7	856	1	ENV_HV1B1
6	177	94.7	856	1	ENV_HV1H2
7	177	94.7	856	1	ENV_HV1H3
8	177	94.7	856	1	ENV_HV1LW
9	177	94.7	856	1	ENV_HV1PV
10	177	94.7	861	1	ENV_HV1BR
11	176	94.1	847	1	ENV_HV1S1
12	176	94.1	855	1	ENV_HV1OY
13	176	94.1	868	1	ENV_HV1C4
14	174	93.0	868	1	ENV_HV1X1
15	174	93.0	861	1	ENV_HV1XB
16	174	93.0	861	1	ENV_HV1XN
17	173	92.5	843	1	ENV_HV1Y2
18	173	92.5	846	1	ENV_HV1ND
19	173	92.5	851	1	ENV_HV1B8
20	173	92.5	852	1	ENV_HV1S3
21	173	92.5	855	1	ENV_HV1A2
22	173	92.5	856	1	ENV_HV1SC
23	173	92.5	856	1	ENV_HV1W1
24	173	92.5	856	1	ENV_HV1ZH
25	173	92.5	856	1	ENV_HV1RH
26	173	92.5	867	1	ENV_HV1J3
27	172	92.0	859	1	ENV_HV1M2
28	171	91.4	847	1	ENV_HV1W2
29	168	89.8	863	1	ENV_HV1Z8
30	165	88.2	852	1	ENV_HV1VZ
31	162	86.6	854	1	ENV_SIVZG
32	122	65.2	865	1	ENV_SIVAT
33	122	65.2	877	1	ENV_SIVAG

34	119	63.6	854	1	ENV_SIVAT	002837 simian immu
35	116	62.0	768	1	ENV_SIVAT	P27757 simian immu
36	116	60.4	712	1	ENV_HV2S2	P32536 human immu
37	113	60.4	851	1	ENV_HV2D1	P17755 human immu
38	113	60.4	851	1	ENV_HV2G1	P18040 human immu
39	113	60.4	856	1	ENV_HV2N2	P05883 human immu
40	113	60.4	859	1	ENV_HV2ST	P20872 human immu
41	112	59.9	859	1	ENV_HV2CA	P24105 human immu
42	111	59.4	380	1	ENV_SIVM2	P08810 simian immu
43	111	59.4	858	1	ENV_HV2RO	P04577 human immu
44	111	59.4	885	1	ENV_SIVS4	P12492 simian immu
45	111	59.4	889	1	ENV_SIVSP	P19503 simian immu
46	110	58.8	882	1	ENV_SIVM1	P05885 simian immu
47	109	58.3	859	1	ENV_HV2D2	P15831 human immu
48	108	57.8	880	1	ENV_SIVML	P11267 simian immu
49	107	57.2	846	1	ENV_HV2SB	P12449 human immu
50	107	57.2	881	1	ENV_SIVMK	P05884 simian immu
51	106	56.7	857	1	ENV_HV2BR	Q74126 human immu
52	106	56.7	860	1	ENV_HV2BE	P18094 human immu
53	104	55.6	821	1	ENV_SIVGB	P22380 simian immu
54	55	29.4	1379	1	M3K5_MOUSE	O35099 mus muscucu
55	54	28.9	2564	1	SPCO_HUMAN	Q9h254 homo sapien
56	53	28.6	445	1	EXTL_STRAAM	O995X0 staphylococ
57	53	28.3	1374	1	M3K5_HUMAN	O99583 homo sapien
58	52	27.8	236	1	G16_SCHMA	P46435 schistosoma
59	51.5	27.5	924	1	HXK3_RAT	P27926 rattus norv
60	50	26.7	684	1	RPOC_MARPO	P06273 marchantia
61	49	26.2	286	1	IN35_HUMAN	P80217 homo sapien
62	49	26.2	1756	1	PEPL_HUMAN	O60437 homo sapien
63	49	26.2	1867	1	MOT1_YEAST	P32333 saccharomyc
64	49	26.2	4349	1	DYHC_FUSSO	P78716 fusarium so
65	49	26.2	8797	1	SNEI_HUMAN	O8n191 homo sapien
66	48	25.7	305	1	OTC_SYNP7	Q935Y4 synchococc
67	48	25.7	380	1	OXA4_MYCLE	O50205 mycobacteri
68	48	25.7	551	1	YD25_YEAST	O07657 saccharomyc
69	48	25.7	702	1	AT11_VARY	P34011 varicola vir
70	48	25.7	906	1	CTN1_HUMAN	P35221 homo sapien
71	48	25.7	906	1	CTN1_MOUSE	P26231 mus muscucu
72	48	25.7	1386	1	Y064_MYCPN	P75613 mycoplasma
73	48	25.7	1938	1	MYH4_RABIT	Q28641 cryptolagus
74	47.5	25.4	134	1	Y652_METUA	O58068 methanococc
75	47.5	25.4	962	1	ARVC_HUMAN	O00192 homo sapien
76	47.5	25.4	969	1	ARVC_MOUSE	P98203 mus muscucu
77	47.5	25.4	1319	1	SOS1_MOUSE	Q62245 mus muscucu
78	47.5	25.4	1333	1	SOS1_HUMAN	Q07889 homo sapien
79	47.5	25.4	1411	1	EBA1_HUMAN	O15075 homo sapien
80	47.5	25.4	1955	1	PIIMA_PARIN	O61308 parascaris
81	47	25.1	106	1	Y0CC_HAERIN	O57152 haemophilus
82	47	25.1	256	1	Y0T1_YEAST	P34247 saccharomyc
83	47	25.1	376	1	O43A_DROME	P81317 drosophila
84	47	25.1	418	1	DADI_RHILLO	Q98108 rhicobium 1
85	47	25.1	1081	1	GALY_YEAST	P19659 saccharomyc
86	47	25.1	1938	1	MYG_ABOIR	P24733 aequipecten
87	47	25.1	1939	1	MYH4_HUMAN	O9y623 homo sapien
88	46.5	24.9	132	1	R58_CIOAB	Q97812 clostridium
89	46.5	24.9	159	1	VAT_CAMPV	P19618 cauliiflower
90	46.5	24.9	581	1	FRIZ_DROME	P18537 drosophila

ALIGNMENTS

RESULT 1
ENV_HV1EL
ID ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
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CC -----
CC EMBL; K03454; AAA44329.1; -
DR EMBL; A07108; CA000616.1; -
DR HIV; K03454; ENVSELI.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAAD07A5 CRC64;

Best Local Similarity 94.7%; Pred. No. 8.8e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 NNILRAIQAOHLLQTLTWQIKOQARILAVRYLKDQ 38
Db 550 NNILRAIEAOHLLQTLTWGIGIKOQARILAVRYLKDQ 587
RESULT 2
ENV_HVIMF STANDARD; PRT; 853 AA.
ID ENV_HVIMF
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA Wasilak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";
RL J. Virol. 64:3792-3803(1990).
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M33943; AAA44850.1; -
DR PDB; 1ATK; 16-JUN-97.
DR HIV; M33943; ENVSMFA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 509
FT CHAIN 510 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).


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FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377893BF22ABA CRC64;

Query Match 94.7%; Score 177; DB 1; Length 853;
Best Local Similarity 94.7%; Pred. No. 8.8e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOHLLQLTWQIQOLQARILAVERYLKDQ 38
Db 551 NNILRAIQAOHLLQLTWQIQOLQARILAVERYLKDQ 588

RESULT 3
ENV_HV122 STANDARD; PRT; 853 AA.
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
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CC -----
CC EMBL; M22639; AAA45370.1; -.
DR PIR; S54384; S54384.
DR HIV; M22639; ENV52226.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL. 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.

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FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query Match 94.7%; Score 177; DB 1; Length 853;
Best Local Similarity 94.7%; Pred. No. 8.8e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOHLLQLTWQIQOLQARILAVERYLKDQ 38
Db 550 NNILRAIQAOHLLQLTWQIQOLQARILAVERYLKDQ 587

RESULT 4
ENV_HV126 STANDARD; PRT; 855 AA.
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Srinivasan A., Anand R., York D., Ranganathan P., Peorino P.,
  Sanchez-Pescador R.;
RA Sanchez-Pescador R.;
RA "Molecular characterization of human immunodeficiency virus from
  Zaire: nucleotide sequence analysis identifies conserved and variable
  RT domains in the envelope gene.";
RT Gene 52.71-82(1987).
RL
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CC -----

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[illegible][illegible]

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FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A8931BB27 CRC64;

Query Match 94.7%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 553 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKDQ 590

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87293196; PubMed=3040055;
RA Rather L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Rather L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF03819; AAC82596.1; -
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DLB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
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FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 236 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 166 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
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FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match 94.7%; Score 177; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNILRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 553 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKDQ 590

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11707;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=65226248; PubMed=2986795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-III env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
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 CC -----
 CC EMBL; M14100; AAA44679.1; -
 DR PDB; 1JUV; 17-OCT-01.
 DR HIV; M14100; ENV\$HXB3.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 KW 3D-structure.
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 FT CHAIN 1 30
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 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
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 FT CARBOHYD 88 88
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 FT SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;
 SQ
 Query Match 94.7%; Score 177; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 8.9e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQUTWQIQOLQARILAVERYLKQ 38
 Db 553 NNLLRAIEAQHLLQUTWQIQOLQARILAVERYLKQ 590
 RESULT 8
 ENV_HVILM STANDARD; PRT; 856 AA.
 ID ENV_HVILM
 AC 070626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (TM12.3 isolate) (HIV-1).
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=82834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S., Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type 11B).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12055; AAA76690.1; -
 DR PDB; 1IR3; 02-MAY-01.
 DR GlycoSuiteDB; 070626; -
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 KW 3D-structure.
 FT CHAIN 1 30
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 FT DISULFID 512 856
 FT DISULFID 54 74
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 FT CARBOHYD 301 301
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 FT CARBOHYD 339 339
 FT SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;
 SQ
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 Best Local Similarity 94.7%; Pred. No. 8.9e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNILRAIQAOHLLQLTWQIKQLARILAVERYLKDQ 38
 Db 553 NNILRAIQAOHLLQLTWQIKQLARILAVERYLKDQ 590
 RESULT 9
 ENV_HVLPV STANDARD; PRT; 856 AA.
 AC P03376; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85111157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
 RL Nature 313:450-456(1985).
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 CC -----
 CC EMBL: K02083; AAB59873.1; -;
 CC EMBL: X01762; CA25903.1; ALT_SEQ.
 CC PIR: A03974; VCLJVL.
 CC HIV: K02083; ENVSPV22.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam: PF00517; GP120; 1.
 CC Pfam: PF00517; GP41; 1.
 CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.
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 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
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 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
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 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCBD1DC3C1209B3 CRC64;
 Query Match Score 177; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 8.9e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNILRAIQAOHLLQLTWQIKQLARILAVERYLKDQ 38
 Db 553 NNILRAIQAOHLLQLTWQIKQLARILAVERYLKDQ 590
 RESULT 10
 ENV_HVLPV STANDARD; PRT; 861 AA.
 AC P03377; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85099333; PubMed=2981635;
 RA Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RL Cell 40:9-17(1985).
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 CC -----

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CC -----
DR EMBL; A04321; AAB59751.1; -
DR EMBL; A04321; CA000352.1; -
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV$BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDs; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516
FT CHAIN 517 861
FT DISULFID 54 74
FT DISULFID 119 210
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SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 94.7%; Score 177; DB 1; Length 861;
Best Local Similarity 94.7%; Pred. No. 8.9e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
ON NCBI_TaxId=11691;
RX SEQUENCE FROM N.A.
RP MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398 (1990).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M65024; AAA5072.1; -
DR PDB; 1OBE; 15-MAY-97.
DR HIV; M38428; ENV$SP162.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDs; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT CHAIN 503 847
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SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

Query Match 94.1%; Score 176; DB 1; Length 847;
Best Local Similarity 92.1%; Pred. No. 1.2e-16;
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[illegible]

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FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
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SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

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Best Local Similarity 92.2e-16; Pred. No. 1.2e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      1  NNLLRAIAOQHLLQLTVMQIKOLAAIILAVERYLKDO 38
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        552 >NNLRLRAEOQHLLQLTVMGIIKQLARVLAVERYLKDO 589

RESULT 13
ENV_HY1C4          STANDARD;           PRT;       868 AA.
ID   ENV_HY1C4
AC   P05879;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Envelope polypeptide GP160 precursor [containing: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirinae.
OX   NCBI_TaxId=11687;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87041461; PubMed=3490666;
RA   Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RT   Andersen P.R., Devare S.G.;
RT   "Molecular cloning and primary nucleotide sequence analysis of a
RT   distinct human immunodeficiency virus isolate reveal significant
RT   divergence in its genomic sequences.";
RT   Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
RL   [2]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=90253924; PubMed=2187500;
RA   Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Russo P.,
RA   DeVico A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
RT   "Characterization of the secreted, native gp120 and gp160 of the human
RT   immunodeficiency virus type 1.";
RT   AIDS Res. Hum. Retroviruses 6:371-380(1990).
CC   -----
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CC   entities requires a license agreement (See http://www.isb.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M13137; AAA44311.1; -.
DR   PIR; C25523; VCLJH4.
DR   HIV; M13137; ENVSODC45.
DR   InterPro; IPR000328; Env GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120, 1.
DR   Pfam; PF00517; GP41, 1.
KW   AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW   Signal.
FT SIGNAL         1      33
FT CHAIN          34     522    EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).

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FT CHAIN 522 868 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 55 75 BY SIMILARITY.
FT DISULFID 120 216 BY SIMILARITY.
FT DISULFID 127 207 BY SIMILARITY.
FT DISULFID 132 163 BY SIMILARITY.
FT DISULFID 228 258 BY SIMILARITY.
FT DISULFID 239 250 BY SIMILARITY.
FT DISULFID 307 341 BY SIMILARITY.
FT DISULFID 387 429 BY SIMILARITY.
FT DISULFID 394 429 BY SIMILARITY.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 828 828 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 868 AA; 98698 MW; A11527F52A6F0C8 CRC64;

Query Match 94.1%; Score 176; DB 1; Length 868;
Best Local Similarity 94.7%; Pred. No. 1.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQTLTWGIKQLARILAVERYLKQ 38
Db 565 NNLLRAIKAOQHLLQTLTWGIKQLARILAVERYLKQ 602

RESULT 14
ENV_HV1JR STANDARD; PRT; 848 AA.
ID ENV_HV1JR
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide precursor (Contains: Exterior membrane glycoprotein GP160; Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroviridae; Lentiviridae.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M38429; AAB03749.1; -
DR PDB: 1CB4; 1B-MAR-99.
DR HIV; M38429; ENV5URCSF.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT CHAIN 1 32
FT SIGNAL 33 503
FT CHAIN 504 848
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 154
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 437
FT DISULFID 381 410
FT DISULFID 87 87
FT CARBOHYD 134 134
FT CARBOHYD 137 137
FT CARBOHYD 153 153
FT CARBOHYD 157 157
FT CARBOHYD 185 185
FT CARBOHYD 195 195
FT CARBOHYD 228 228
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 287 287
FT CARBOHYD 293 293
FT CARBOHYD 299 299
FT CARBOHYD 329 329
FT CARBOHYD 336 336
FT CARBOHYD 352 352
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 403 403
FT CARBOHYD 440 440
FT CARBOHYD 453 453
FT CARBOHYD 603 603
FT CARBOHYD 608 608
FT CARBOHYD 617 617
FT CARBOHYD 629 629
FT CARBOHYD 808 808
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;

Query Match 93.0%; Score 174; DB 1; Length 848;
Best Local Similarity 89.5%; Pred. No. 2.3e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQTLTWGIKQLARILAVERYLKQ 38
Db 545 NNLLRAIEAOQHLLQTLTWGIKQLARILAVERYLKQ 582

RESULT 15
ENV_HV1JMN STANDARD; PRT; 856 AA.
ID ENV_HV1JMN
AC P05877;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide precursor (Contains: Exterior membrane

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DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11696;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88219542; PubMed=3369091;
 RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Reltz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates";
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
 CC PATIENT IN 1984.
 CC -----
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 CC -----
 CC EMBL; M17449; AAA44857.1; -.
 DR PDB; LACY; 31-JUL-94.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1N12; 25-FEB-03.
 DR PDB; 1N10; 25-FEB-03.
 DR HIV; M17449; ENV5MN.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 513 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 514 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 210 BY SIMILARITY.
 FT DISULFID 125 201 BY SIMILARITY.
 FT DISULFID 130 162 BY SIMILARITY.
 FT DISULFID 223 252 BY SIMILARITY.
 FT DISULFID 233 244 BY SIMILARITY.
 FT DISULFID 301 335 BY SIMILARITY.
 FT DISULFID 381 445 BY SIMILARITY.
 FT DISULFID 388 418 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97140 MW; D197D80940BE732 CRC64;
 Query Match 93.0%; Score 174; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 2.3e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNILRAIQAOQHLLQITWQIQOLQARILAVRYLKQD 38
 DB 554 NNILRAIEAQHMLQLTWIGIKQLQARILAVRYLKQD 591
 RESULT 16
 ID ENV_HV1KB STANDARD; PRT; 861 AA.
 AC P31819;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92351552; PubMed=1322587;
 RA Shimizu H., Hasebe F., Teuchie H., Morikawa S., Ushijima H.,
 RA Kitamura T.;
 RT "Analysis of a human immunodeficiency virus type 1 isolate carrying a
 RT truncated transmembrane glycoprotein";
 RL Virology 189:534-546(1992).
 CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
 CC THE COONS FOR 729-ALA AND 730-ARG.
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 CC -----
 CC EMBL; D12582; BAA02124.1; ALT_SEQ.
 DR PIR; A42995; VCLJKB.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 518 861 TRANSMEMBRANE GLYCOPROTEIN.
 FT TRANSMEM 690 711 POTENTIAL.
 FT DISULFID 59 79 BY SIMILARITY.
 FT DISULFID 124 212 BY SIMILARITY.
 FT DISULFID 131 203 BY SIMILARITY.
 FT DISULFID 136 160 BY SIMILARITY.
 FT DISULFID 125 254 BY SIMILARITY.
 FT DISULFID 225 246 BY SIMILARITY.
 FT DISULFID 303 337 BY SIMILARITY.
 FT DISULFID 383 446 BY SIMILARITY.
 FT DISULFID 390 419 BY SIMILARITY.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 643 643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 861 AA; 98116 MW; 3C06787658F0C3DA CRC64;

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Query Match 93.0%; Score 174; DB 1; Length 861;
Best Local Similarity 92.1%; Pred. No. 2, 3e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 559 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 596

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RESULT 17
ENV_HV1Y2 STANDARD; PRT; 843 AA.
ID ENV_HV1Y2
AC P35561;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS ENV.
GN Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H., Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation."
RL J. Virol. 66:6587-6600 (1992).

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CC EMBL, M93258; -; NOT_ANNOTATED_CDS.
CC PIR, H44001; H44001.
DR PDB, 1G9N; 27-DEC-00.
DR InterPro, IPR000328; Env_Gp41.

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DR InterPro, IPR000777; GP120.
DR Pfam, PF00516; GP120; 1.
DR Pfam, PF00517; Gp41; 1.
KW Aids; Coat protein; Glycoprotein; Transmembrane; signal; 3d-structure.
FT SIGNAL 1 29
FT CHAIN 30 489
FT TRANSMEM 738 755
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
FT DISULFID 224 235
FT DISULFID 292 326
FT DISULFID 373 432
FT DISULFID 380 405
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
FT CARBOHYD 381 381
FT CARBOHYD 389 389
FT CARBOHYD 395 395
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FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
SQ SEQUENCE 843 AA; 95648 MW; C69DF0971C918B71 CRC64;

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Query Match 92.5%; Score 173; DB 1; Length 843;
Best Local Similarity 89.5%; Pred. No. 3, 1e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 540 NNLLRAIQAOHLLQLTWQIKQLQARILAVERYLKDQ 577

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RESULT 18
ENV_HV1YND STANDARD; PRT; 846 AA.
ID ENV_HV1YND
AC P18759;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS ENV.
GN Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034200; PubMed=2806917;

```

RA Spire B., Site J., Zachar V., Rey F., Baerre-Strauss F., Gallibert F.,
RT Hampe A., Chermann J.C.:
RL "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the
CC human immunodeficiency virus." J.
CC Gene 81:275-284(1989).
CC
CC -I- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
CC
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CC
CC -----
DR EMBL; M27323; AAA44873.1; -.
DR PIR; J00066; VCLIND.
DR HIV; M27323; ENV5NDK.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL. 1 29
FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 502 846 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 200 BY SIMILARITY.
FT DISULFID 125 191 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 213 242 BY SIMILARITY.
FT DISULFID 223 234 BY SIMILARITY.
FT DISULFID 291 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 807 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2E83 CRC64;
Query Match 92.5%; Score 173; DB 1; Length 846;
Best Local Similarity 89.5%; Pred. No. 3, 2e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0
Qy 1>NNLLRAIQAOQHLLQLFTWVQIKQLQARILLAVERYLKQD 38
Db 543>NNLLRAIEAQOHLQLFTWVGIKQLQARVLAVERYLRDQ 580

ID	ENV_HV1B8	STANDARD;	PRT;	851 AA.
AC	P04582;			
AD	ENV_HV1B8			
DT	13-AUG-1987	(Rel. 05, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	ENV.			
GN	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Vitruvius; Retroviral viruses; Retroviridae; Lentivirus.			
OC	NCBI_Taxid=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=65111123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn B.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.,			
RA	Wong-Staal F.,			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.",			
RL	Nature 313:277-284(1985).			
CC	-----			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; K02011; AAA44661.1; -.			
DR	PDB; 1DDH; 13-JAN-89.			
DR	PDB; 1HHG; 31-OCT-93.			
DR	PDB; 1QO3; 02-JAN-00.			
DR	PDB; 1S2T; 24-DEC-97.			
DR	HIV; K02011; ENV5BH8.			
DR	GlycoSiteDB; P04582; -.			
DR	InterPro; IPR00328; Env_GP41.			
DR	InterPro; IPR00777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;			
KW	3D-structure.			
KM				
FT	SIGNAL	1	30	
FT	CHAIN	31	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	301	301	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 92.5%; Score 173; DB 1; Length 851;
 Best Local Similarity 92.1%; Pred. No. 3, 2e-16;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
 Db 548 NNILRAIEGOQHLLQTLTWGIKQLQARILAVERYLKQ 585

RESULT 20
 ENV_HV153 STANDARD; PRT; 852 AA.
 ID ENV_HV153
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=11690;
 RN (1)
 RP MEDLINE=90317906; PubMed=2370688;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome."
 RL J. Virol. 64:4016-4020(1990).

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CC -----
 CC EMBL: AY352275; AA017031.1; -
 CC PDB: 1MEQ; 11-DEC-02.
 CC HIV; M38427; ENVSF33.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam: PF00516; GP120; 1.
 CC DR Pfam: PF00517; GP41; 1.
 CC KW AIDS; Coat protein; Polypeptide; Polypeptide; Transmembrane; Signal;
 CC 3D-structure.
 CC RL SIGNAL 1 31 BY SIMILARITY.
 CC FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 CC FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
 CC FT DISULFID 53 73 BY SIMILARITY.
 CC FT DISULFID 118 206 BY SIMILARITY.
 CC FT DISULFID 125 197 BY SIMILARITY.
 CC FT DISULFID 130 156 BY SIMILARITY.
 CC FT DISULFID 219 248 BY SIMILARITY.
 CC FT DISULFID 229 240 BY SIMILARITY.
 CC FT DISULFID 297 331 BY SIMILARITY.
 CC FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 96663 MW; E7BFBFD2359910D CRC64;

Query Match 92.5%; Score 173; DB 1; Length 852;
 Best Local Similarity 89.5%; Pred. No. 3, 2e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
 Db 549 NNILRAIEGOQHLLQTLTWGIKQLQARILAVERYLKQ 586

RESULT 21
 ENV_HV1A2 STANDARD; PRT; 855 AA.
 ID ENV_HV1A2
 AC P03378;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=11685;
 RN (1)
 RP MEDLINE=85090453; PubMed=2578227;
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
 RA Stempien M.M., Brown-Shiner S.L., Gee W.W., Renard A., Randolph A.,
 RA Levy J.A., Dina D., Luciw P.A.;
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)."
 RL Science 227:484-492(1985).

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CC -----
 CC EMBL: K02007; AAB59882.1; -

DR	Pf1:	A03976;	VCLJAZ.
DR	HIV;	K02007;	ENV\$SE2.
DR	InterPro;	IPR000328;	Env GP41.
DR	InterPro;	IPR000777;	GP120.
DR	Pfam;	PF00516;	GP120; 1.
DR	Pfam;	PF00517;	GP41; 1.
KW	AIDS;	Coat protein;	Polypotein; Glycoprotein; Transmembrane; Signal.
FT	SIGNAL	1	29
FT	CHAIN	30	509
FT	CHAIN	510	855
FT	DISULFID	53	73
FT	DISULFID	118	208
FT	DISULFID	125	199
FT	DISULFID	130	155
FT	DISULFID	221	250
FT	DISULFID	231	242
FT	DISULFID	299	333
FT	DISULFID	380	442
FT	DISULFID	387	415
FT	CARBOHYD	87	87
FT	CARBOHYD	129	129
FT	CARBOHYD	140	140
FT	CARBOHYD	154	154
FT	CARBOHYD	158	158
FT	CARBOHYD	184	184
FT	CARBOHYD	190	190
FT	CARBOHYD	200	200
FT	CARBOHYD	233	233
FT	CARBOHYD	244	244
FT	CARBOHYD	265	265
FT	CARBOHYD	279	279
FT	CARBOHYD	292	292
FT	CARBOHYD	298	298
FT	CARBOHYD	304	304
FT	CARBOHYD	334	334
FT	CARBOHYD	341	341
FT	CARBOHYD	358	358
FT	CARBOHYD	364	364
FT	CARBOHYD	388	388
FT	CARBOHYD	394	394
FT	CARBOHYD	400	400
FT	CARBOHYD	408	408
FT	CARBOHYD	445	445
FT	CARBOHYD	458	458
FT	CARBOHYD	461	461
FT	CARBOHYD	610	610
FT	CARBOHYD	615	615
FT	CARBOHYD	624	624
FT	CARBOHYD	636	636
FT	CARBOHYD	815	815
SO	SEQUENCE	855 AA;	97438 MW; A3BC20573AACG1A2 CRC64;
Query Match			
Best local Similarity			
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
Oy	1	NNLRLAIQAQOHLLDTWTWKQLCARLIAYERYRYKQ	38
Dd	552	NNLRLALAEAQHLLDLTWIGIKQLDARVLAVERLYRDQ	589
RESULT 22			
ID	ENV_HYVISC	STANDARD;	PRT; 856 AA.
AC	P05878;		
DT	01-NOV-1988	(Rel. 09, Created)	
DT	01-NOV-1988	(Rel. 09, Last sequence update)	
DT	15-JUN-1999	(Rel. 38, Last annotation update)	
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
OS	Human immunodeficiency virus type 1 (SC isolate) (HIV-1).		

CC	Vitruves, Retroid vitruves; Retroviridae; Lentivirus.
OK	NCBI TaxID=11702;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=86219542; PubMed=3369091;
RA	Gungo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA	Farrrell K., Wong-Staal F., Gallo R.C., Reitz M.S.Jr.;
RT	"Envelope sequences of two new United States HIV-1 isolates";
RL	Virology 164:531-536(1988).
CC	-I - MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC	1984 IN SOUTHERN CALIFORNIA.
CC	-----
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M17450; -, NOT_ANNOTATED_CDS.
DR	HIV; M17450; ENVSSC.
DR	InterPro; IPR000328; Env GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120; 1.
DR	Pfam; PF00517; GP41; 1.
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW	Signal.
FT	SIGNAL. 1 29
FT	CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT	SITE 760 IN-FRAME TERMINATION CODON.
FT	DISULFID 53 73 BY SIMILARITY.
FT	DISULFID 118 206 BY SIMILARITY.
FT	DISULFID 125 197 BY SIMILARITY.
FT	DISULFID 130 160 BY SIMILARITY.
FT	DISULFID 219 247 BY SIMILARITY.
FT	DISULFID 228 239 BY SIMILARITY.
FT	DISULFID 296 330 BY SIMILARITY.
FT	DISULFID 376 439 BY SIMILARITY.
FT	DISULFID 383 412 BY SIMILARITY.
FT	CARBOHYD 87 87 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 129 129 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 135 135 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 140 140 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 143 143 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 159 159 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 163 163 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 189 189 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 198 198 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 234 234 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 241 241 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 262 262 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 276 276 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 295 295 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 301 301 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 302 302 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 331 331 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 338 338 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 354 354 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 360 360 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 384 384 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 394 394 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 400 400 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 405 405 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 442 442 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 457 457 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 611 611 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 616 616 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 625 625 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 637 637 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 674 674 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 816 816 N-LINKED (GLCNAC . .) (POTENTIAL).

SQ SEQUENCE 856 AA; 97055 MW; DAFADA600BA7A08 CRC64;
 Query Match 92.5%; Score 173; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 3.2e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIAQOQHLLQTLTWGIKQLQARILAVERYLKDQ 38
 DB 553 NNLLRAIAQOQHLLQTLTWGIKQLQARILAVERYLKDQ 590

RESULT 23
 ENV_HV1W1 STANDARD; PRT; 856 AA.
 ID ENV_HV1W1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 DE ENV.
 OS Human immunodeficiency virus type 1 (MMJ1 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6218077; PubMed=2423250;
 RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parke E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HIV-1/HIV/LAV, the retrovirus of AIDS."
 RL Cell 45:637-648(1986).
 CC -1- MISCELLANEOUS: ISOLATES MMJ1, MMJ2, AND MMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC PIR; A24774; VCLJ3W.
 DR PDB; 1LB0; 04-DEC-02.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM
 FT SIGNAL 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 30 510 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 856 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 444 BY SIMILARITY.
 FT DISULFID 383 417 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C40ADE9 CRC64;
 Query Match 92.5%; Score 173; DB 1; Length 856;
 Best Local Similarity 89.5%; Pred. No. 3.2e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIAQOQHLLQTLTWGIKQLQARILAVERYLKDQ 38
 DB 553 NNLLRAIAQOQHLLQTLTWGIKQLQARILAVERYLKDQ 590

RESULT 24
 ENV_HV1ZH STANDARD; PRT; 856 AA.
 ID ENV_HV1ZH
 AC P05881;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 DE ENV.
 OS Human immunodeficiency virus type 1 (Zaire H321 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=11692;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89228766; PubMed=2713163;
 RA Strinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J., McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
 RT "Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence comparison to recent isolates and generation of hybrid HIV-1."
 RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
 CC
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 CC EMBL; M15896; AAB53948.1; -.
 DR PIR; A44963; A44963.
 DR HIV; M15896; ENV52321.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM
 FT SIGNAL 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 30 511 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 856 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 153 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 331 BY SIMILARITY.
 FT DISULFID 379 445 BY SIMILARITY.
 FT DISULFID 386 418 BY SIMILARITY.

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FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 839653F8BBD174E CRC64;

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Query Match 92.5%; Score 173; DB 1; Length 856;
Best Local Similarity 92.1%; Pred. No. 3.2e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 NNLLRAIQAOQHLLQTLTWQIKOLQARILAVERYLNDQ 38
Db 553 NNLLRAIEAQHLLKLTWGIKOLQARILAVERYLNDQ 590

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ENV_HV1RH STANDARD; PRT; 865 AA.
ID ENV_HV1RH
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
regions in the envelope gene of HIV-1/HIV/LAV, the retrovirus of
RT AIDS."
RT Cell 45:637-648(1986).

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M17451; AAA45057.1; -
CC HIV: M17451; ENVSRF.
CC InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane;
KW signal.
FT CHAIN 1 29
FT CHAIN 30 519
FT CHAIN 520 865
FT DISULFID 53 73
FT DISULFID 118 218
FT DISULFID 125 209
FT DISULFID 130 157
FT DISULFID 231 260
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SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADC CRC64;

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Query Match 92.5%; Score 173; DB 1; Length 865;
Best Local Similarity 89.5%; Pred. No. 3.2e-16;
Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 NNLLRAIQAOQHLLQTLTWQIKOLQARILAVERYLNDQ 38
Db 562 NNLLRAIEAQHLLKLTWGIKOLQARILAVERYLNDQ 599

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ENV_HV1J3 STANDARD; PRT; 867 AA.
ID ENV_HV1J3
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RH3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

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FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 SQ SEQUENCE 859 AA; 97109 MW; DBCF9AA5E3ABF29 CRC64;
 Query Match 92.0%; Score 172; DB 1; Length 859;
 Best Local Similarity 89.5%; Pred. No. 4,4e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKDQ 38
 Db 555 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKDQ 592
 RESULT 28
 ENV_HV1W2 STANDARD; PRT; 847 AA.
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.R., Redfield R.R., Markham P.D.,
 RA Salauddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT "Genetic variation in HIV-1/LAV over time in patients with AIDS or at risk for AIDS."
 RL Science 232:1548-1553 (1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC -----
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 CC -----
 CC EMBL: M12507; AAB12990.1; -
 DR HIV; M12507; ENV\$WMJ2.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
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 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73AA5BCAE CRC64;
 Query Match 91.4%; Score 171; DB 1; Length 847;
 Best Local Similarity 89.5%; Pred. No. 6e-16;
 Matches 34; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKDQ 38
 Db 544 NNILRAIQAOQHLLQTLTWQIKQLQARILAVERYLKDQ 581
 RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86281278; PubMed=3395517;
 RA Yourho J., Josephs S.F., Rietz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."
 RL AIDS Res. Hum. Retroviruses 4:165-173 (1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.
 CC -----
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 CC -----

FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB86345DEC915F CRC64;

Query Match
Best Local Similarity 88.2%; Score 165; DB 1; Length 852;

Matches 32; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
DB 549 NNILMAIEAQQHMLBELTWGIGIKQLQARVLAVERYLKDQ 586

Search completed: June 2, 2004, 11:43:00
Job time: 7.19565 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 / Search time 31.9076 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-544
Perfect score: 187
Sequence: 1 NMLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqe, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_Organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	177	94.7	132 15	090052 human immun
2	177	94.7	132 15	07SLI22 human immun
3	177	94.7	143 15	07SM06 human immun
4	177	94.7	144 15	07ZCD7 human immun
5	177	94.7	144 15	07ZCD6 human immun
6	177	94.7	153 15	07SM03 human immun
7	177	94.7	357 15	078119 human immun
8	177	94.7	357 15	0993A8 human immun
9	177	94.7	588 15	0993A7 human immun
10	177	94.7	589 15	0993A7 human immun
11	177	94.7	590 15	0993B1 human immun
12	177	94.7	616 15	0993A9 human immun
13	177	94.7	618 15	0993B0 human immun
14	177	94.7	727 15	0993B2 human immun
15	177	94.7	747 15	09Q723 human immun
16	177	94.7	748 15	070607 human immun

17	177	94.7	752 15	070604 human immun	070604 human immun
18	177	94.7	752 15	070605 human immun	070605 human immun
19	177	94.7	752 15	070608 human immun	070608 human immun
20	177	94.7	757 15	09Q722 human immun	09Q722 human immun
21	177	94.7	811 15	09DVL6 human immun	09dvl6 human immun
22	177	94.7	842 15	073341 human immun	073341 human immun
23	177	94.7	842 15	070895 human immun	070895 human immun
24	177	94.7	842 15	073340 human immun	073340 human immun
25	177	94.7	847 15	069966 human immun	069966 human immun
26	177	94.7	851 15	078243 human immun	078243 human immun
27	177	94.7	854 15	055566 human immun	055566 human immun
28	177	94.7	854 15	085582 human immun	085582 human immun
29	177	94.7	854 15	072502 human immun	072502 human immun
30	177	94.7	854 15	090178 human immun	090178 human immun
31	177	94.7	854 15	078705 human immun	078705 human immun
32	177	94.7	855 15	08A0V7 human immun	08A0V7 human immun
33	177	94.7	855 15	08ADT7 human immun	08ADT7 human immun
34	177	94.7	856 15	074090 human immun	074090 human immun
35	177	94.7	856 15	092877 human immun	092877 human immun
36	177	94.7	856 15	074599 human immun	074599 human immun
37	177	94.7	856 15	041772 human immun	041772 human immun
38	177	94.7	857 15	092822 human immun	092822 human immun
39	177	94.7	857 15	071013 human immun	071013 human immun
40	177	94.7	857 15	089654 human immun	089654 human immun
41	177	94.7	864 15	09YP39 human immun	09YP39 human immun
42	177	94.7	864 15	07ZJC8 human immun	07ZJC8 human immun
43	177	94.1	125 15	091WP9 human immun	091WP9 human immun
44	176	94.1	132 15	061W05 human immun	061w05 human immun
45	176	94.1	133 15	090Q20 human immun	090Q20 human immun
46	176	94.1	137 15	09DQ04 human immun	09dQ04 human immun
47	176	94.1	142 15	091WQ7 human immun	091WQ7 human immun
48	176	94.1	142 15	070207 human immun	070207 human immun
49	176	94.1	144 15	07ZCC6 human immun	07ZCC6 human immun
50	176	94.1	144 15	07ZCC5 human immun	07ZCC5 human immun
51	176	94.1	144 15	07ZCC2 human immun	07ZCC2 human immun
52	176	94.1	144 15	07ZCB1 human immun	07ZCB1 human immun
53	176	94.1	144 15	07ZCB0 human immun	07ZCB0 human immun
54	176	94.1	144 15	07ZC96 human immun	07ZC96 human immun
55	176	94.1	144 15	07ZC95 human immun	07ZC95 human immun
56	176	94.1	144 15	07ZC89 human immun	07ZC89 human immun
57	176	94.1	144 15	07ZC88 human immun	07ZC88 human immun
58	176	94.1	144 15	07ZC71 human immun	07ZC71 human immun
59	176	94.1	144 15	07ZC70 human immun	07ZC70 human immun
60	176	94.1	145 15	07ZC57 human immun	07ZC57 human immun
61	176	94.1	145 15	07ZC40 human immun	07ZC40 human immun
62	176	94.1	145 15	07ZC35 human immun	07ZC35 human immun
63	176	94.1	145 15	07ZC31 human immun	07ZC31 human immun
64	176	94.1	146 15	07SM37 human immun	07SM37 human immun
65	176	94.1	155 15	08J3P2 human immun	08J3P2 human immun
66	176	94.1	155 15	08J3Q3 human immun	08J3Q3 human immun
67	176	94.1	155 15	08J3Q1 human immun	08J3Q1 human immun
68	176	94.1	156 15	08JAL7 human immun	08Jal7 human immun
69	176	94.1	174 15	08JED8 human immun	08Jed8 human immun
70	176	94.1	192 15	08JAL2 human immun	08Jal2 human immun
71	176	94.1	219 15	08JAJ4 human immun	08Jaj4 human immun
72	176	94.1	225 15	0991C1 human immun	0991C1 human immun
73	176	94.1	225 15	0991B9 human immun	0991B9 human immun
74	176	94.1	225 15	0991C5 human immun	0991C5 human immun
75	176	94.1	225 15	0991C0 human immun	0991C0 human immun
76	176	94.1	357 15	078118 human immun	078118 human immun
77	176	94.1	357 15	078116 human immun	078116 human immun
78	176	94.1	357 15	078155 human immun	078155 human immun
79	176	94.1	358 15	078140 human immun	078140 human immun
80	176	94.1	358 15	078141 human immun	078141 human immun
81	176	94.1	360 15	08QDX2 human immun	08Qdx2 human immun
82	176	94.1	362 15	08QDX1 human immun	08Qdx1 human immun
83	176	94.1	398 15	072603 human immun	072603 human immun
84	176	94.1	421 15	08J514 human immun	08J514 human immun
85	176	94.1	606 15	09Q6V8 human immun	09Q6V8 human immun
86	176	94.1	679 15	091K02 human immun	091K02 human immun
87	176	94.1	797 15	003808 human immun	003808 human immun
88	176	94.1	797 15	003810 human immun	003810 human immun
89	176	94.1	799 15	003807 human immun	003807 human immun

90 176 94.1 801 15 Q03809 human immu

ALIGNMENTS

RESULT 1

Q09052 PRELIMINARY; PRT; 132 AA.

AC Q90052; 01-DEC-2001 (T-EMBLrel. 19, last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=99ES-MOI496;

RX MEDLINE=21322034; Pubmed=11429126;

RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E., Garcia-Saiz A.;

RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."

RL AIDs Res. Hum. Retroviruses 17:851-855(2001).

DR EMBL; AF31089; AK92300.1; -

DR GO; GO:0016021; C:viral envelope; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; Gp41; 1.

KM Transmembrane.

FT NON_TER 1

FT NON_TER 132

SQ SEQUENCE 132 AA; 15708 MW; 51D9DB8AED574FAE CRC64;

Query Match 94.7%; Score 177; DB 15; Length 132;
Best Local Similarity 94.7%; Pred. No. 7.6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQTLTWGIKQLQARILAVERYLKQ 38

Db 10 NNILRAIEAQHLLQTLTWGIKQLQARILAVERYLKQ 47

RESULT 2

Q7SLZ2 PRELIMINARY; PRT; 132 AA.

AC Q7SLZ2; 01-OCT-2003 (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GT970;

RA Gonzalez Perez M.P., Garcia Saiz A.;

RT "Epidemiological and molecular characteristics of HIV and HTLV infection in Equatorial Guinea, 1996-1998."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF30024; AAP87755.1; -

DR Pfam; PF00517; Gp41; 1.

KM Envelope protein.

FT NON_TER 1

FT NON_TER 132

SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 132;
Best Local Similarity 94.7%; Pred. No. 7.6e-17;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQTLTWGIKQLQARILAVERYLKQ 38

Db 11 NNILRAIEAQHLLQTLTWGIKQLQARILAVERYLKQ 48

RESULT 3

Q7SM06 PRELIMINARY; PRT; 143 AA.

AC Q7SM06; 01-OCT-2003 (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GT1138;

RA Gonzalez Perez M.P., Garcia Saiz A.;

RT "Epidemiological and molecular characteristics of HIV and HTLV infection in Equatorial Guinea, 1996-1998."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF30010; AAP87741.1; -

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; Gp41; 1.

KM Envelope protein.

FT NON_TER 1

FT NON_TER 143

SQ SEQUENCE 143 AA; 17210 MW; 415F5E738F876BE0 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 143;
Best Local Similarity 94.7%; Pred. No. 8.2e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQTLTWGIKQLQARILAVERYLKQ 38

Db 11 NNILRAIEAQHLLQTLTWGIKQLQARILAVERYLKQ 48

RESULT 4

Q7ZCD7 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD7; 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX3-1;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boule R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;

RT "Phocom mutations at residue positions critical for envelope (T-20) resistance in enfuvirtide-naïve patients infected with subtype B and non-B HIV-1."

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY185383; AA065658.1; -

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_Gp41.

DR Pfam; PF00517; Gp41; 1.

KM Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318B8E CRC64;

Query Match 94.7%; Score 177; DB 15; Length 144;

Best Local Similarity 94.7%; Pred. No. 8.3e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIQKOLQARIILAVERYLKQ 38
DB 24 NNILRAIEAQHLLQLTWQIGIKOLQARIILAVERYLKQ 61

RESULT 5

07ZCD6 PRELIMINARY; PRT; 144 AA.

AC 07ZCD6; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, last annotation update)
ENVELOPE glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185384; AA065659.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EBB CRC64;

Query Match 94.7%; Score 177; DB 15; Length 144;
Best Local Similarity 94.7%; Pred. No. 8.3e-17;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIQKOLQARIILAVERYLKQ 38
DB 24 NNILRAIEAQHLLQLTWQIGIKOLQARIILAVERYLKQ 61

RESULT 6

07SMO3 PRELIMINARY; PRT; 153 AA.

AC 07SMO3; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, last annotation update)
ENVELOPE glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CR598;
RA Gonzalez Perez M.P., Garcia Saiz A.,
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530013; AAP87744.1; -
KM Envelope protein.
FT NON_TER 1
FT NON_TER 153
SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1FFEC035 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 153;
Best Local Similarity 94.7%; Pred. No. 8.8e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIQKOLQARIILAVERYLKQ 38
DB 11 NNILRAIEAQHLLQLTWQIGIKOLQARIILAVERYLKQ 48

RESULT 7

078119 PRELIMINARY; PRT; 357 AA.

AC 078119; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, last annotation update)
ENVELOPE protein, gp120 /gp41 (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.,
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid."
RL AIDS Res. Hum. Retroviruses 8:53-59 (1992).
DR EMBL; X61356; CAA43624.1; -
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 357 AA; 41118 MW; FE4CA7E122A886 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 357;
Best Local Similarity 94.7%; Pred. No. 2.1e-16;

Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIQKOLQARIILAVERYLKQ 38
DB 54 NNILRAIEAQHLLQLTWQIGIKOLQARIILAVERYLKQ 91

RESULT 8

0993A8 PRELIMINARY; PRT; 588 AA.

AC 0993A8; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, last annotation update)
ENVELOPE glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Dcosta S.S., Hurtwitz J.L.,
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240AE8 CRC64;

Query Match
Best Local Similarity 94.7%; Score 177; DB 15; Length 588;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
Db 496 NNLLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 533

RESULT 9
Qy 0993A7 PRELIMINARY; PRT; 588 AA.
AC 0993A7;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt1;
RA Dcostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321148; AAK20296.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match
Best Local Similarity 94.7%; Score 177; DB 15; Length 588;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
Db 496 NNLLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 533

RESULT 10
Qy 0993B1 PRELIMINARY; PRT; 589 AA.
AC 0993B1;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=1F8;
RA Dcostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321144; AAK20292.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 589 589
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match
Best Local Similarity 94.7%; Score 177; DB 15; Length 589;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
Db 496 NNLLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 533

RESULT 11
Qy 0993A9 PRELIMINARY; PRT; 590 AA.
AC 0993A9;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA Dcostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321146; AAK20294.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 590 590
SQ SEQUENCE 590 AA; 65902 MW; 91ED899C8BF91CAF CRC64;

Query Match
Best Local Similarity 94.7%; Score 177; DB 15; Length 590;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKQ 38
Db 497 NNLLRAIEAQOHLQLTWGIRKQLQARILAVERYLKQ 534

RESULT 12
Qy 0993B0 PRELIMINARY; PRT; 616 AA.
ID 0993B0

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AC 0993B0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321145; AAK20293.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 616 AA; 616 616
SQ 616 AA; 616 616
Query Match 94.7%; Score 177; DB 15; Length 616;
Best Local Similarity 94.7%; Pred. No. 3,7e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 497 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 534

RESULT 13
Q993B2 PRELIMINARY; PRT; 618 AA.
AC 0993B2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCostra S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321143; AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 618 AA; 618 618
SQ 618 AA; 618 618
Query Match 94.7%; Score 177; DB 15; Length 618;
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Best Local Similarity 94.7%; Pred. No. 3.8e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 499 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 536

RESULT 14
Q90723 PRELIMINARY; PRT; 727 AA.
AC 090723;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11IBx;
RA MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein."
RT Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=11IBx;
RA MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity."
RT J. Virol. 73:10310-10319(1999).
RL EMBL; AF189158; AAF25627.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD626D26B9566 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 727;
Best Local Similarity 94.7%; Pred. No. 4.4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 548 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 585

RESULT 15
Q70607 PRELIMINARY; PRT; 747 AA.
AC 070607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RA REITZ M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA SHAW G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AAA76669.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;
Query Match 94.7%; Score 177; DB 15; Length 747;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 548 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 585
RESULT 16
QY 070606 PRELIMINARY; PRT; 748 AA.
ID 070606;
AC 070606;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12033; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;
Query Match 94.7%; Score 177; DB 15; Length 748;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 549 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 586
RESULT 17
QY 070604 PRELIMINARY; PRT; 752 AA.
ID 070604;
AC 070604;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM851;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30A8B94013B45A CRC64;
Query Match 94.7%; Score 177; DB 15; Length 752;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 553 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 590
RESULT 18
QY 070605 PRELIMINARY; PRT; 752 AA.
ID 070605;
AC 070605;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AAA7667.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 94.7%; Score 177; DB 15; Length 752;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 553 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 590

RESULT 19
ID Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AAA76670.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.


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DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 752;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 553 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 590

RESULT 20
ID Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBx;
RX MEDLINE=9272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
  Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
  HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBx;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
  Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
  type 1 variant map outside regions required for coreceptor
  specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0042025; C: host cell nucleus; IEA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR GO: GO:0003700; F: transcription factor activity; IEA.
DR GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR InterPro: IPR00625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 757
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BD2E CRC64;

Query Match 94.7%; Score 177; DB 15; Length 757;
Best Local Similarity 94.7%; Pred. No. 4.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 548 NNTLRATQAQOHLQLTWQIKQLQARILAVERYLKQ 585

RESULT 21

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Q9DVL6
ID Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; Pubmed=11044094;
RA Vinda N., Peeters M., Mulenga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507(2000).
DR EMBL; AJ401037; CAC15045.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
FT NON_TER 811 811
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 811;
Best Local Similarity 94.7%; Pred. No. 5e-16; 1; Indels 0; Gaps 0;
Matches 36; Conservative 1; Mismatches 1;

QY 1 NNLRAIQAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
Db 557 NNLRAIEAQHLLQTLTWGIGIKQLQARILAVERYLKQ 594

RESULT 22
Q73341 PRELIMINARY; PRT; 842 AA.
ID Q73341;
AC Q73341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=66303593; Pubmed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RA Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization.";
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39236; AAB37173.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1E9F1 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 842;
Best Local Similarity 94.7%; Pred. No. 5.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIQAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
Db 539 NNLRAIEAQHLLQTLTWGIGIKQLQARILAVERYLKQ 576

RESULT 23
Q70895 PRELIMINARY; PRT; 842 AA.
ID Q70895;
AC Q70895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RX MEDLINE=98285725; Pubmed=9621027;
RA Gao F., Robertson D.L., Carruthers C.D., Morrison S.G., Jian B.,
RA Chen Y., Barre-Sinoussi F., Girard M., Srinivasan A., Abiniku A.G.,
RA Shaw G.M., Sharp P.M., Hahn B.H.;
RT "A comprehensive panel of near-full-length clones and reference
RT sequences for non-subtype B isolates of human immunodeficiency virus
RT type 1.";
RL J. Virol. 72:5680-5698(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Gao F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005495; AAD03179.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94810 MW; F82041B1D932DCAD CRC64;

Query Match 94.7%; Score 177; DB 15; Length 842;
Best Local Similarity 94.7%; Pred. No. 5.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIQAOQHLLQTLTWQIKQLQARILAVERYLKQ 38
Db 539 NNLRAIEAQHLLQTLTWGIGIKQLQARILAVERYLKQ 576

RESULT 24
Q73340 PRELIMINARY; PRT; 842 AA.
ID Q73340;
AC Q73340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
 Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization.";
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL; U39235; AAB37172.1;
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 60784F2A47B791EB CRC64;

Query Match 94.7%; Score 177; DB 15; Length 842;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATGAGHLLQTLTWGIRKQLQARILAVRYLKQ 38
 DB 539 NNTLRATGAGHLLQTLTWGIRKQLQARILAVRYLKQ 576

RESULT 25
 ID 069996 PRELIMINARY; PRT; 847 AA.
 AC 069996;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
 Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
 von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1657(1996).
 DR [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX NIAID/NIH AIDS Variation Program;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MCEVILLY M.M.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U08445; AAB04071.1; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 847 AA; 95602 MW; FCBCEA7AF446FB20 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 847;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATGAGHLLQTLTWGIRKQLQARILAVRYLKQ 38
 DB 544 NNTLRATGAGHLLQTLTWGIRKQLQARILAVRYLKQ 581

RESULT 26
 ID 078243 PRELIMINARY; PRT; 851 AA.
 AC 078243;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Env polyprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,
 RA Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer
 RT chronically infected HUT-78 cellular clone.";
 RL J. Viral Diseases 1:40-55(1992).
 DR [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352106; PubMed=2765297;
 RA Federic M., Ratti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Macchi B., Mangiano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non
 RT producer clones from HUT-78 infected with a patient HIV isolate.";
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ratti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Borsetti A., Saggio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not
 RT productive clone.";
 RL Int. J. Immunopharmacol. 3:17-23(1990).
 DR EMBL; Z11530; CAA77628.1; -.
 DR PIR; A53591; A53591.
 DR PIR; S13288; S13288.
 DR PIR; S33985; S33985.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 851;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 DB 548 NNTLRRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 585

RESULT 27
 O56566 PRELIMINARY; PRT; 854 AA.
 AC O56566;
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 RT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PIH309;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Altman-Onal Y., Collier C., Giraud A., Babic-Ercce A., Biron F.,
 RA Verrier B.;
 RT "Comparison of complete env gene sequences from individuals with
 RT symptomatic primary HIV type 1 infection."
 RT AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL: AF041132; AAC02523.1; -
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97062 MW; 58B012C83A0C3D2 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 854;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 DB 551 NNTLRRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 588

RESULT 28
 O85582 PRELIMINARY; PRT; 854 AA.
 AC O85582;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 RT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone."
 RT J. Virol. 59:284-291(1986).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.,
 RA Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.

RN (3)
 RP SEQUENCE FROM N.A.
 RA Buckler C.E.;
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92219406; PubMed=1373204;
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
 RT GP41 results in loss of killing by CD8+ A24-restricted cytotoxic T
 RT lymphocytes."
 RT J. Virol. 66:3151-3154(1992).
 DR EMBL: M1992; AAA44992.1; -
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D555A CRC64;

Query Match 94.7%; Score 177; DB 15; Length 854;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
 DB 551 NNTLRRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 588

RESULT 29
 Q72502 PRELIMINARY; PRT; 854 AA.
 AC Q72502;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 RT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=N14-3;
 RX MEDLINE=96036482; PubMed=7483282;
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
 RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
 RT from primary virus cultures using the polymerase chain reaction."
 RT Virology 213:80-86(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone."
 RT J. Virol. 59:284-291(1986).
 DR EMBL: U26942; AAB60578.1; -
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.

DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT CONFLICT 214 214 H -> L (IN REF. 2).
 FT CONFLICT 530 530 A -> S (IN REF. 2).
 FT CONFLICT 739 739 G -> D (IN REF. 2).
 SQ SEQUENCE 854 AA; 97005 MW; FF226483841D1220 CRC64;

Query Match 94.7%; Score 177; DB 15; Length 854;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKQ 38
 DB 551 NNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKQ 588

RESULT 30

ID 090178 PRELIMINARY; PRT; 854 AA.
 AC 090178;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074930; PubMed=7983770;
 RA Fang H., Pincus S.H.;
 RT "Unique insertion sequence and pattern of CD4 expression in variants
 RT selected with immunotoxins from human immunodeficiency virus type 1-
 RT infected T cells."
 RL J. Virol. 69:75-81(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Fang H., Pincus S.H.;
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an
 RT immunotoxin-resistant variant T cell line."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF070521; AAC28452.1; -.
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 94.7%; Score 177; DB 15; Length 854;
 Best Local Similarity 94.7%; Pred. No. 5.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKQ 38
 DB 551 NNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKQ 588

Search completed: June 2, 2004, 11:48:25
 Job time : 32.9076 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 14.0435 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-544

Perfect score: 187
Sequence: 1 NNLRRAIQAOCHLQLTWQIKQARILVERVYKDKQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	98.4	38	4	US-08-973-952-82
2	177	94.7	38	1	US-08-374-666-1
3	177	94.7	38	3	US-08-486-099-89
4	177	94.7	38	3	US-08-360-107A-99
5	177	94.7	38	3	US-08-360-107A-99
6	177	94.7	38	3	US-08-484-223B-89
7	177	94.7	38	3	US-08-919-597-89
8	177	94.7	38	3	US-08-475-668A-89
9	177	94.7	38	3	US-08-485-551A-89
10	177	94.7	38	3	US-08-471-913A-89
11	177	94.7	38	3	US-08-485-264A-89
12	177	94.7	38	3	US-09-082-279B-16
13	177	94.7	38	3	US-09-082-279B-507
14	177	94.7	38	3	US-09-082-279B-604
15	177	94.7	38	4	US-08-474-349A-89
16	177	94.7	38	4	US-08-474-349A-89
17	177	94.7	38	4	US-09-315-304B-16
18	177	94.7	38	4	US-09-315-304B-507
19	177	94.7	38	4	US-09-315-304B-604
20	177	94.7	38	4	US-08-255-208A-25
21	177	94.7	38	4	US-08-470-896-89
22	177	94.7	38	4	US-08-485-546A-89
23	177	94.7	38	4	US-09-796-202-11
24	177	94.7	38	4	US-09-834-784-16
25	177	94.7	38	4	US-09-834-784-507
26	177	94.7	38	4	US-09-834-784-604
27	177	94.7	38	4	US-08-464-003-1

28	177	94.7	38	4	US-09-779-451-2	Sequence 2, Appl1
29	177	94.7	38	4	US-09-515-965A-16	Sequence 16, Appl1
30	177	94.7	38	4	US-09-515-965A-507	Sequence 507, Appl1
31	177	94.7	38	4	US-09-515-965A-604	Sequence 604, Appl1
32	177	94.7	38	4	US-09-350-641C-16	Sequence 16, Appl1
33	177	94.7	38	4	US-09-350-641C-607	Sequence 507, Appl1
34	177	94.7	38	4	US-09-350-641C-604	Sequence 604, Appl1
35	177	94.7	41	1	US-08-073-028-8	Sequence 8, Appl1
36	177	94.7	41	1	US-08-374-666-3	Sequence 3, Appl1
37	177	94.7	41	1	US-08-484-223B-243	Sequence 243, Appl1
38	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
39	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
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43	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
44	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
45	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
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48	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
49	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
50	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
51	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
52	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
53	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
54	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
55	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
56	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
57	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
58	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
59	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
60	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
61	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
62	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
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64	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
65	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
66	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
67	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
68	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
69	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
70	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
71	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
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73	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
74	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
75	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
76	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
77	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
78	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
79	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
80	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
81	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
82	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
83	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
84	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
85	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
86	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
87	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
88	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
89	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1
90	177	94.7	41	3	US-08-484-223B-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 98.4%; Score 184; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 6,4e-19;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRRAIQAOHLLQLTWQIKOQARILAVERYLKQ 38
DB 1 NNLRRAIEAQHLLQLTWQIKOQARILAVERYLKQ 38

RESULT 2
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1

Query Match 94.7%; Score 177; DB 1; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIQAOHLLQLTWQIKOQARILAVERYLKQ 38
DB 1 NNLRRAIEAQHLLQLTWQIKOQARILAVERYLKQ 38

RESULT 3
US-08-486-099-89
Sequence 89, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIQAOHLLQLTWQIKOQARILAVERYLKQ 38
DB 1 NNLRRAIEAQHLLQLTWQIKOQARILAVERYLKQ 38

RESULT 4
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIQQLQARILAVERYLKDQ 38

RESULT 5
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIQQLQARILAVERYLKDQ 38

RESULT 6
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89;
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 7
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8664
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89;
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 8
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 606065

GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8664
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89;
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 9
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWGIKQIQLARILLAVERYLKDQ 38
DB 1 NNILRAIQOQHLLQLTWGIKQIQLARILLAVERYLKDQ 38

RESULT 10
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWGIKQIQLARILLAVERYLKDQ 38
DB 1 NNILRAIQOQHLLQLTWGIKQIQLARILLAVERYLKDQ 38

RESULT 11
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 12
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 13
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 14
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match 94.7%; Score 177; DB 3; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIEAQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 15
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 633395

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULAR TYPE: peptide
US-08-474-349A-89

Query Match
Best Local Similarity 94.7%; Score 177; DB 4; Length 38;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 16
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Biolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown
MOLECULAR TYPE: peptide
US-08-474-349A-441

Query Match
Best Local Similarity 94.7%; Score 177; DB 4; Length 38;
Matches 36; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 17
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M. D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match
Best Local Similarity 94.7%; Score 177; DB 4; Length 38;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38

RESULT 18
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M. D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-507

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 19
US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 20
US-08-255-208A-25
Sequence 25, Application US/08255208A
Patent No. 6440656
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,208A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6.4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 21
US-08-470-896-89
Sequence 89, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKOLQARILAVERYLKQ 38
DB 1 NNILRAIEAOQHLLQLTWGIKOLQARILAVERYLKQ 38

RESULT 22

US-08-485-546A-89
Sequence 89, Application US/08485546A
Patent No. 6518013

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKOLQARILAVERYLKQ 38
DB 1 NNILRAIEAOQHLLQLTWGIKOLQARILAVERYLKQ 38

RESULT 23
US-09-796-202-11
Sequence 11, Application US/09796202
Patent No. 6548636

GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38

TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(38)
OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKOLQARILAVERYLKQ 38
DB 1 NNILRAIEAOQHLLQLTWGIKOLQARILAVERYLKQ 38

RESULT 24

US-09-834-784-16
Sequence 16, Application US/09834784
Patent No. 6562787

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Nerutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQAOQHLLQLTWGIKOLQARILAVERYLKQ 38
DB 1 NNILRAIEAOQHLLQLTWGIKOLQARILAVERYLKQ 38

RESULT 25
US-09-834-784-507
Sequence 507, Application US/09834784
Patent No. 6562787

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-507

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 26
US-09-834-784-604
Sequence 604, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-604

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 27
US-08-464-003-1
Sequence 1, Application US/08464003
Patent No. 6573078
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Daniel P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,003
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-464-003-1

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 28
US-09-779-451-2
Sequence 2, Application US/09779451
Patent No. 6605427
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 94.7%; Score 177; DB 4; Length 38;
Best Local Similarity 94.7%; Pred. No. 6,4e-18;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Dy 1 NNLLRRAIQAQOHHLTWTWQIKQLQARILAVERYLKDQ 38
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 1 NNLLRRAIAEQHHLTQTWTWGKIQKLQARRILAVERYLKDQ 38

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RESULT 29
US-09-515-965A-16
: Sequence 16, Application US/09515965A
: Patent No. 6623741
: GENERAL INFORMATION:
: APPLICANT: Antczak, J.
: APPLICANT: Delmedico, M.
: APPLICANT: Erickson, J.
: APPLICANT: Lambert, D.
: APPLICANT: Sista, P.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION
: TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
: FILE REFERENCE: 7872-073
: CURRENT APPLICATION NUMBER: US/09/515,965A
: CURRENT FILING DATE: 2000-02-29
: PRIOR APPLICATION NUMBER: 09/315,304
: PRIOR FILING DATE: 1999-05-20
: PRIOR APPLICATION NUMBER: 09/082,279
: PRIOR FILING DATE: 1998-05-20
: NUMBER OF SEQ ID NOS: 1994
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 16
: LENGTH: 38
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Core polypeptide
US-09-515-965A-16

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Query Match	94.7%;	Score 177;	DB 4;	Length 38;
Best Local Similarity	94.7%;	Pred. No. 6.4e-18;		
Matches 36;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;

QY . 1 NNILRRAIQAQQHLLQLTWGKIQOLQARI LAVERYLEKDQ 38
| | | | | : | | | | | | | | | | | | | | |
Db 1 NNILRRAIQAQQHLLQLTWGKIQOLQARI LAVERYLEKDQ 38

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1 RESULT 30
2 US-09-515-965A-507
3 Sequence 507, Application US/09515965A
4 Patent No. 6623741
5 GENERAL INFORMATION:
6 APPLICANT: Antczak, J.
7 APPLICANT: Delmedico, M.
8 APPLICANT: Erickson, J.
9 APPLICANT: Lambert, D.
10 APPLICANT: Sista, P.
11 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION
12 TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
13 FILE REFERENCE: 7872-073
14 CURRENT APPLICATION NUMBER: US/09/515,965A
15 CURRENT FILING DATE: 2000-02-29
16 PRIOR APPLICATION NUMBER: 09/315,304
17 PRIOR FILING DATE: 1999-05-20
18 PRIOR APPLICATION NUMBER: 09/082,279
19 PRIOR FILING DATE: 1998-05-20
20 NUMBER OF SEQ ID NOS: 1994
21 SOFTWARE: FastSeq for Windows Version 3.0
22 SEQ ID NO 507
23 LENGTH: 38
24 TYPE: PRT
25 ORGANISM: Artificial Sequence
26 FEATURE:
27 OTHER INFORMATION: Core polypeptide
28 US-09-515-965A-507

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Query Match 94.7%; Score 177; DB 4; Length 38;
 Best Local Similarity 94.7%; Pred. No. 6.4e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNILKRAIQAOOHLLQLTWMOIKQIAARLIVERTKQ 38
 |||||:|||||
 Db 1 NNILKRAIEAOQHLLQLTWVGKIKQIAARLIVERTKQ 38

Search completed: June 2, 2004, 11:52:40
Job time : 14.0435 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 35.0054 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-544
Perfect score: 187
Sequence: 1 NNILFRAIQOQHILQLTWQIKQLARILVERYLKQD 38

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

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Published Applications_AA.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	184	98.4	38	14	US-10-252-136-82	Sequence 82, Appl
2	177	94.7	38	9	US-09-796-202-11	Sequence 11, Appl
3	177	94.7	38	9	US-09-779-451-2	Sequence 2, Appl
4	177	94.7	38	10	US-09-493-346-2	Sequence 2, Appl
5	177	94.7	38	12	US-10-267-682-89	Sequence 89, Appl
6	177	94.7	38	12	US-10-267-748-89	Sequence 89, Appl
7	177	94.7	38	12	US-09-809-060-6	Sequence 6, Appl
8	177	94.7	38	12	US-09-809-060-7	Sequence 7, Appl
9	177	94.7	38	12	US-10-663-589-3	Sequence 3, Appl
10	177	94.7	38	12	US-10-681-879-2	Sequence 2, Appl
11	177	94.7	38	12	US-09-828-615-2	Sequence 2, Appl
12	177	94.7	38	14	US-10-116-797-2	Sequence 2, Appl
13	177	94.7	38	14	US-10-323-314-11	Sequence 11, Appl
14	177	94.7	38	14	US-10-414-192-1	Sequence 1, Appl
15	177	94.7	38	14	US-10-351-641-16	Sequence 16, Appl

16	177	94.7	38	14	US-10-351-641-507	Sequence 507, App
17	177	94.7	38	14	US-10-351-641-604	Sequence 604, App
18	177	94.7	38	15	US-10-005-305-165	Sequence 165, App
19	177	94.7	38	15	US-10-005-305-202	Sequence 202, App
20	177	94.7	38	15	US-10-005-305-203	Sequence 203, App
21	177	94.7	38	15	US-10-420-194-1234	Sequence 1234, App
22	177	94.7	38	16	US-10-664-021-2	Sequence 2, Appl
23	177	94.7	38	16	US-10-671-316-2	Sequence 2, Appl
24	177	94.7	41	12	US-10-267-682-8	Sequence 8, Appl
25	177	94.7	41	12	US-10-267-748-8	Sequence 8, Appl
26	177	94.7	41	12	US-10-663-589-30	Sequence 30, Appl
27	177	94.7	41	12	US-10-663-589-33	Sequence 33, Appl
28	177	94.7	41	12	US-10-663-589-35	Sequence 35, Appl
29	177	94.7	41	14	US-10-252-136-8	Sequence 8, Appl
30	177	94.7	41	14	US-10-414-192-3	Sequence 3, Appl
31	177	94.7	41	14	US-10-414-192-9	Sequence 9, Appl
32	177	94.7	41	14	US-10-351-641-496	Sequence 496, App
33	177	94.7	41	14	US-10-351-641-601	Sequence 601, App
34	177	94.7	41	14	US-10-351-641-633	Sequence 633, App
35	177	94.7	41	14	US-10-351-641-1163	Sequence 1163, App
36	177	94.7	41	16	US-10-664-021-27	Sequence 27, Appl
37	177	94.7	41	16	US-10-671-316-27	Sequence 27, Appl
38	177	94.7	44	12	US-10-663-589-36	Sequence 36, Appl
39	177	94.7	44	12	US-10-663-589-36	Sequence 36, Appl
40	177	94.7	45	9	US-10-414-192-10	Sequence 10, Appl
41	177	94.7	45	9	US-09-779-451-9	Sequence 9, Appl
42	177	94.7	45	12	US-09-809-060-50	Sequence 50, Appl
43	177	94.7	45	12	US-10-663-589-29	Sequence 29, Appl
44	177	94.7	45	14	US-10-351-641-1164	Sequence 1164, App
45	177	94.7	45	16	US-10-664-021-26	Sequence 26, Appl
46	177	94.7	45	16	US-10-671-316-26	Sequence 26, Appl
47	177	94.7	49	9	US-09-796-202-3	Sequence 3, Appl
48	177	94.7	49	14	US-10-323-314-3	Sequence 3, Appl
49	177	94.7	51	12	US-10-663-589-27	Sequence 27, Appl
50	177	94.7	51	12	US-10-351-641-745	Sequence 745, App
51	177	94.7	51	16	US-10-664-021-24	Sequence 24, Appl
52	177	94.7	51	16	US-10-671-316-24	Sequence 24, Appl
53	177	94.7	52	14	US-10-351-641-1119	Sequence 1119, App
54	177	94.7	53	14	US-10-351-641-955	Sequence 955, App
55	177	94.7	53	14	US-10-351-641-1062	Sequence 1062, App
56	177	94.7	55	12	US-09-779-451-1	Sequence 1, Appl
57	177	94.7	55	12	US-09-809-060-14	Sequence 14, Appl
58	177	94.7	57	15	US-10-438-631-1	Sequence 1, Appl
59	177	94.7	59	16	US-10-664-021-1	Sequence 1, Appl
60	177	94.7	59	16	US-10-671-316-1	Sequence 1, Appl
61	177	94.7	60	12	US-10-663-589-1	Sequence 1, Appl
62	177	94.7	63	12	US-10-267-682-201	Sequence 201, App
63	177	94.7	63	12	US-10-267-748-201	Sequence 201, App
64	177	94.7	63	14	US-10-252-136-54	Sequence 54, Appl
65	177	94.7	103	14	US-10-263-103-29	Sequence 29, Appl
66	177	94.7	103	15	US-10-438-631-3	Sequence 3, Appl
67	177	94.7	113	15	US-10-438-631-4	Sequence 4, Appl
68	177	94.7	177	14	US-10-040-3498-2	Sequence 2, Appl
69	177	94.7	198	9	US-09-854-816-88	Sequence 88, Appl
70	177	94.7	198	9	US-09-854-816-89	Sequence 89, Appl
71	177	94.7	200	14	US-10-263-103-25	Sequence 25, Appl
72	177	94.7	200	15	US-10-438-631-8	Sequence 8, Appl
73	177	94.7	232	14	US-10-059-271-81	Sequence 81, Appl
74	177	94.7	252	14	US-10-059-271-82	Sequence 82, Appl
75	177	94.7	256	14	US-10-059-271-97	Sequence 97, Appl
76	177	94.7	268	9	US-09-854-816-16	Sequence 16, Appl
77	177	94.7	268	9	US-09-854-816-17	Sequence 17, Appl
78	177	94.7	268	9	US-09-854-816-18	Sequence 18, Appl
79	177	94.7	269	9	US-09-854-816-19	Sequence 19, Appl
80	177	94.7	269	9	US-09-854-816-43	Sequence 43, Appl
81	177	94.7	338	12	US-10-267-682-90	Sequence 90, Appl
82	177	94.7	338	12	US-10-267-748-90	Sequence 90, Appl
83	177	94.7	344	14	US-10-040-3498-1	Sequence 1, Appl
84	177	94.7	345	9	US-09-779-451-8	Sequence 8, Appl
85	177	94.7	345	14	US-10-026-741-49	Sequence 49, Appl
86	177	94.7	391	14	US-10-214-670-58	Sequence 58, Appl
87	177	94.7	488	8	US-10-059-271-93	Sequence 93, Appl
88	177	94.7	491	8	US-08-911-824-95	Sequence 95, Appl
					US-08-911-824-56	Sequence 56, Appl

ALIGNMENTS

89 177 94.7 519 9 US-09-756-551A-8 Sequence 8, Appli
90 177 94.7 599 8 US-08-911-824-108 Sequence 108, App

RESULT 1

US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 98.4%; Score 184; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 5, 1e-17;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNNLRAIEAQOHLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 2

US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBSTITUTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 94.7%; Score 177; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 5, 1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNNLRAIEAQOHLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 3
US-09-779-451-2

; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 94.7%; Score 177; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 5, 1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNNLRAIEAQOHLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 4
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 94.7%; Score 177; DB 10; Length 38;
Best Local Similarity 94.7%; Pred. No. 5, 1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNNLRAIQAOQHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNNLRAIEAQOHLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 5

US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petterway, Stephen R.
; APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89
Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 0; Gaps 0;
QY 1 NNLRRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRRAIEAQOHLQLTWGIRKQLQARILAVERYLKDQ 38
RESULT 6
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petreway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89
Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRRAIEAQOHLQLTWGIRKQLQARILAVERYLKDQ 38
RESULT 7
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6
Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRRAIQAOQHLLQLTWGIKQLQARILAVERYLKDQ 38
DB 1 NNLRRAIEAQOHLQLTWGIRKQLQARILAVERYLKDQ 38
RESULT 8
US-09-809-060-7

; Sequence 7, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQITWGIKQLOARILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHLQITWGIKQLOARILAVERYLKDQ 38

RESULT 9
US-10-663-589-3
; Sequence 3, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Timetris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQITWGIKQLOARILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHLQITWGIKQLOARILAVERYLKDQ 38

RESULT 10
US-10-681-879-2
; Sequence 2, Application US/10681879
; Publication No. US20040062767A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/10/681,879

; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/493,346
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQITWGIKQLOARILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHLQITWGIKQLOARILAVERYLKDQ 38

RESULT 11
US-09-828-615-2
; Sequence 2, Application US/09828615
; Publication No. US20020146415A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672
; CURRENT APPLICATION NUMBER: US/09/828,615
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 94.7%; Score 177; DB 12; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQITWGIKQLOARILAVERYLKDQ 38
DB 1 NNLLRAIEAQOHLQITWGIKQLOARILAVERYLKDQ 38

RESULT 12
US-10-116-797-2
; Sequence 2, Application US/10116797
; Publication No. US2003004411A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5.1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 13
US-10-323-314-11
; Sequence 11, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-10-323-314-11.

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 14
US-10-414-192-1
; Sequence 1, Application US/10414192
; Publication No. US20030181382A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Bolognesi, Dani P.
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/414,192
; FILING DATE: 15-Apr-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 15
US-10-351-641-16
; Sequence 16, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKOLQARILAVERYLKQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKOLQARILAVERYLKQ 38

RESULT 16
US-10-351-641-507
; Sequence 507, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Amer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641

;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1257
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 507
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
;; US-10-351-641-507

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKDQ 38

RESULT 17
US-10-351-641-604
;; Sequence 604, Application US/10351641
;; Publication No. US20030186874A1
;; GENERAL INFORMATION:
;; APPLICANT: Barney, S.
;; APPLICANT: Guthe, K.
;; APPLICANT: Merutka, G.
;; APPLICANT: Anwer, M.
;; APPLICANT: Lambert, D.
;; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;; TITLE OF INVENTION: PROPERTIES
;; FILE REFERENCE: 7872-100
;; CURRENT APPLICATION NUMBER: US/10/351,641
;; CURRENT FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: 09/350,641
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/315,304
;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1257
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 604
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
;; US-10-351-641-604

Query Match 94.7%; Score 177; DB 14; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKDQ 38

RESULT 18
US-10-005-305-165
;; Sequence 165, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE

;; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 165
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
;; US-10-005-305-165

Query Match 94.7%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKDQ 38

RESULT 19
US-10-005-305-202
;; Sequence 202, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
;; FILE REFERENCE: NIH171.001C1
;; CURRENT APPLICATION NUMBER: US/10/005,305
;; CURRENT FILING DATE: 2001-11-02
;; PRIOR APPLICATION NUMBER: PCT/US00/12371
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,686
;; PRIOR FILING DATE: 1999-05-05
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 202
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
;; US-10-005-305-202

Query Match 94.7%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIQAOQHLLQLTWQIKQLQARIILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKDQ 38

RESULT 20
US-10-005-305-203
;; Sequence 203, Application US/10005305
;; Publication No. US20030203841A1
;; GENERAL INFORMATION:
;; APPLICANT: The Government of the United States of America, represented by the
;; APPLICANT: Secretary, Department of Health and Human Services
;; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
;; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
;; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS

FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 94.7%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKOLQARIILAVERYLKDQ 38

RESULT 21
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US20040006035A1
GENERAL INFORMATION:
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: MCSwigen, Jim
APPLICANT: Blatt, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
FILE REFERENCE: MHB02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match 94.7%; Score 177; DB 15; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKOLQARIILAVERYLKDQ 38

RESULT 22
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US20040076637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and Their Use in Therapy to Inhibit Transmission of Human
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 94.7%; Score 177; DB 16; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKOLQARIILAVERYLKDQ 38

RESULT 23
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match 94.7%; Score 177; DB 16; Length 38;
Best Local Similarity 94.7%; Pred. No. 5,1e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIQOQHLLQLTWQIKOLQARIILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLQLTWGIGIKOLQARIILAVERYLKDQ 38

RESULT 24
US-10-267-682-8
; Sequence 8, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Biolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-682-8
Query Match 94.7%; Score 177; DB 12; Length 41;
Best Local Similarity 94.7%; Pred. No. 5.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKQLQARIIVAVRYLKDQ 38
DB 4 NNLLRAIEAQHLLQLTWGIGIKQLQARIIVAVRYLKDQ 41

RESULT 25
US-10-267-748-8
; Sequence 8, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Biolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.

Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-748-8
Query Match 94.7%; Score 177; DB 12; Length 41;
Best Local Similarity 94.7%; Pred. No. 5.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIQAOQHLLQLTWQIKQLQARIIVAVRYLKDQ 38
DB 4 NNLLRAIEAQHLLQLTWGIGIKQLQARIIVAVRYLKDQ 41

RESULT 26
US-10-663-589-30
; Sequence 30, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial

STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-414-192-3

Query Match 94.7%; Score 177; DB 14; Length 41;
Best Local Similarity 94.7%; Pred. No. 5.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 NNILRAIQAOQHLLQLTWQIKOLQARILAVERYLKDQ 38
4 NNILRAIEHQHLLQLTWGIKOLQARILAVERYLKDQ 41

Search completed: June 2, 2004, 12:29:27
Job time : 36.0054 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.3261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336a-2

Perfect score: 187

Sequence: 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database :

1: PIR 78: *
2: p1r1: *
3: p1r2: *
4: p1r3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	96.3	357	2 S21996	envelope protein g
2	180	96.3	851	2 S33985	env polypeptide
3	180	96.3	853	2 S54384	envelope glycoprote
4	180	96.3	854	2 S13288	env protein - huma
5	180	96.3	855	1 VCLJZR	env polypeptide pr
6	180	96.3	856	1 VCLJH3	env polypeptide pr
7	180	96.3	856	1 VCLJVL	env polypeptide pr
8	180	96.3	861	1 VCLJLV	env polypeptide pr
9	179	95.7	357	2 S22006	envelope protein g
10	179	95.7	357	2 S21994	envelope protein g
11	179	95.7	357	2 S22002	envelope protein g
12	179	95.7	358	2 S22000	envelope protein g
13	179	95.7	358	2 S22000	envelope protein g
14	179	95.7	358	2 S22000	envelope protein g
15	179	95.7	358	2 S22000	envelope protein g
16	177	94.7	357	2 S21990	envelope protein g
17	176	94.1	443	2 C41621	env polypeptide pr
18	176	94.1	445	2 C41621	env polypeptide pr
19	176	94.1	445	2 A41621	env polypeptide pr
20	176	94.1	445	2 A41621	env polypeptide pr
21	176	94.1	445	2 A41621	env polypeptide pr
22	176	94.1	445	2 A41621	env polypeptide pr
23	176	94.1	445	2 A41621	env polypeptide pr
24	176	94.1	445	2 A41621	env polypeptide pr
25	176	94.1	445	2 A41621	env polypeptide pr
26	176	94.1	445	2 A41621	env polypeptide pr
27	176	94.1	445	2 A41621	env polypeptide pr
28	176	94.1	445	2 A41621	env polypeptide pr
29	176	94.1	445	2 A41621	env polypeptide pr

30	175	93.6	859	2 T01672	envelope polypeptide
31	172	92.0	358	2 S21998	envelope protein g
32	171	91.4	357	2 S21992	envelope protein g
33	168	89.8	852	1 VCLJBR	env polypeptide
34	165	88.2	854	1 VCLJST	env polypeptide pr
35	162	86.6	847	2 T09448	envelope glycoprote
36	162	86.6	847	2 S13289	env protein - huma
37	127	67.9	104	2 S52930	GP41 ENV protein -
38	125	66.8	864	1 VCLJG4	env polypeptide
39	125	66.8	877	2 C46356	env polypeptide
40	124	66.3	877	2 S49197	env polypeptide
41	120	64.2	732	2 S46352	envelope protein p
42	116	62.0	863	2 A53034	env polypeptide
43	115	60.4	366	2 B41655	env polypeptide
44	113	60.4	712	1 VCLJSA	env polypeptide pr
45	113	60.4	851	2 S12159	env protein - huma
46	113	60.4	852	1 VCLJGG	env polypeptide pr
47	113	60.4	859	1 VCLJST	env polypeptide pr
48	113	60.4	859	1 S53098	envelope polypeptide
49	112	59.9	859	1 VCLJCT	env polypeptide pr
50	111	59.4	855	2 A45713	Env transmembrane
51	111	59.4	858	1 VCLJG2	env polypeptide pr
52	111	59.4	861	2 S03068	env protein - huma
53	111	59.4	885	2 S04322	env polypeptide
54	111	59.4	886	2 T11555	env protein - simi
55	110	58.8	881	1 VCLJG3	env polypeptide
56	109	58.3	859	2 S24571	env protein - huma
57	109	58.3	869	2 A47665	env protein gp120(
58	108	57.8	880	1 VCLJST	env polypeptide pr
59	107	57.2	151	2 S30458	env protein - huma
60	107	57.2	786	2 S28084	env polypeptide
61	107	57.2	889	1 VCLJG5	env polypeptide
62	106	56.7	887	2 T11566	envelope glycoprote
63	105	56.1	151	2 S30453	env protein - huma
64	105	56.1	151	2 S30453	env protein - huma
65	105	56.1	151	2 S30452	env protein - huma
66	105	56.1	151	2 S30450	env protein - huma
67	105	56.1	151	2 S30451	env protein - huma
68	103	55.1	151	2 S30459	env protein - huma
69	103	55.1	151	2 S30457	env protein - huma
70	103	55.1	151	2 S30456	env protein - huma
71	103	55.1	151	2 S30455	env protein - huma
72	103	55.1	151	2 S30454	env protein - huma
73	97	51.9	68	2 S60695	env protein - huma
74	97	51.9	68	2 S60696	env protein - huma
75	97	51.9	68	2 S60705	env protein - huma
76	97	51.9	68	2 S60707	env protein - huma
77	97	51.9	68	2 S60694	env protein - huma
78	97	51.9	69	2 S60706	env protein - huma
79	92	49.2	68	2 S60693	env protein - huma
80	92	49.2	68	2 S60687	env protein - huma
81	90	48.1	68	2 S60692	env protein - huma
82	89	47.6	68	2 S60688	env protein - huma
83	86	46.0	69	2 S60690	env protein - huma
84	86	46.0	69	2 S60689	env protein - huma
85	86	46.0	69	2 S60691	env protein - huma
86	82	43.9	294	2 S60525	env protein - huma
87	82	43.9	297	2 S60538	envelope polypeptide
88	75	40.1	372	2 S46344	env polypeptide
89	75	40.1	375	2 S46345	env polypeptide
90	73	39.0	294	2 S60545	envelope polypeptide

ALIGNMENTS

RESULT 1
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_1
C:Accession: S70422, S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <S72>
A/Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:g1067129
A/Experimental source: patient 27L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.3%; Score 180; DB 2; Length 357;
Best Local Similarity 97.4%; Pred. No. 2,4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 54 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 91

RESULT 2

S33985
env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C/Accession: S33985
R/Carlini, F.
Submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33985
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-851 <CAR>
A/Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:g60199
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.3%; Score 180; DB 2; Length 851;
Best Local Similarity 97.4%; Pred. No. 6,2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 548 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 585

RESULT 3

S54384
envelope polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1995
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <THR>
A/Cross-references: EMBL:M22639; NID:9329377; PIDN:AAA45370.1; PID:g329385
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 96.3%; Score 180; DB 2; Length 853;
Best Local Similarity 97.4%; Pred. No. 6,2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 550 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 587

RESULT 4

S13288
env protease - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C/Accession: S13288
R/O'Brien, W.A.; Koyangi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; MUID:91043044; PMID:2172833
A/Accession: S13288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OBR>
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.3%; Score 180; DB 2; Length 854;
Best Local Similarity 97.4%; Pred. No. 6,2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 551 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 588

RESULT 5

VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cui
Gene 52, 71-82, 1987
A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <SRI>
A/Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:g329403
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-85/Domain: signal sequence #status predicted <SIG>
F:20-85/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,166,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 96.3%; Score 180; DB 1; Length 855;
Best Local Similarity 97.4%; Pred. No. 6,2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 552 NNLRRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 589

RESULT 6

VCLH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03973
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar
nberger, J.A.; Papas, T.S.; Ghayab, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93353; MUID:85111123; PMID:2578615
A/Accession: A03973
A/Molecule type: DNA

A;Residues: 1-856 <BAT>
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g3326383; PIDN:AAA442
C;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <TM>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 6.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03974
R;Meising, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A;Reference number: A93355; MUID:5511157; PMID:2982104
A;Accession: A03974
A;Molecule type: DNA
A;Residues: 1-856 <MOE>
A;Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 6.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <NAI>
A;Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C;Gene: env

A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 96.3%; Score 180; DB 1; Length 861;
Best Local Similarity 97.4%; Pred. No. 6.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.3%; Score 180; DB 1; Length 861;
Best Local Similarity 97.4%; Pred. No. 6.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

env polyprotein precursor - human immunodeficiency virus type 1 (patient 4L)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S70420; S22006
R;Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <ST2>
A;Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A;Experimental source: patient L
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type B retrovirus env polyprotein

Query Match 95.7%; Score 179; DB 2; Length 357;
Best Local Similarity 94.7%; Pred. No. 3.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.7%; Score 179; DB 2; Length 357;
Best Local Similarity 94.7%; Pred. No. 3.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10

env polyprotein precursor - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 27B
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C;Accession: S21994; S70421
R;Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A;Reference number: S21990
A;Accession: S21994
A;Molecule type: DNA
A;Residues: 1-357 <ST2>
A;Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R;Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <ST2>
A;Cross-references: EMBL:X61355; NID:g60179
C;Superfamily: type B retrovirus env polyprotein

Query Match 95.7%; Score 179; DB 2; Length 357;

Best Local Similarity 94.7%; Pred. No. 3.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 91

RESULT 11

S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 48
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:G60186; PIDN:CAA43618.1; PID:G60189
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:G60188
C/Superfamily: type E retrovirus env polypotein

Query Match 95.7%; Score 179; DB 2; Length 357;
Best Local Similarity 94.7%; Pred. No. 3.2e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 91

RESULT 12

S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:G60186
C/Superfamily: type E retrovirus env polypotein

Query Match 95.7%; Score 179; DB 2; Length 358;
Best Local Similarity 94.7%; Pred. No. 3.3e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 38
Db 55 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 92

RESULT 13

S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polypotein

Query Match 95.7%; Score 179; DB 2; Length 358;
Best Local Similarity 94.7%; Pred. No. 3.3e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 38
Db 55 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 92

RESULT 14

S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: patient 3B
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
C/Superfamily: type E retrovirus env polypotein

Query Match 95.7%; Score 179; DB 2; Length 358;
Best Local Similarity 94.7%; Pred. No. 3.3e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 38
Db 55 NNLRAIEAQOHLQLTWGKIQOLQARVLAVERYLKQ 92

RESULT 15

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: Isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A;Reference number: S70417; MUID:92144209; PMID:11736940
A;Accession: S70423
A>Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332, 'X', 334-357 <STE2>
A;Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C;Superfamily: type E retrovirus env polyprotein

Query Match 94.7%; Score 177; DB 2; Length 357;
Best Local Similarity 92.1%; Pred. No. 6e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 91

RESULT 16

VCLMN

env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
R;Gurgio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-St
Virology 164, 531-536, 1988
A>Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Accession: A28922
A;Molecule type: DNA
A;Residues: 1-859 <GUR>
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/DNA: signal sequence #status predicted <SIG>
F;30-659/Product: env polyprotein #status predicted <PPP>
F;67,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.7%; Score 177; DB 1; Length 859;
Best Local Similarity 92.1%; Pred. No. 1.6e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 557 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 594

RESULT 17

C41621

env polyprotein P - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: C41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: C41621
A;Molecule type: DNA
A;Residues: 1-443 <BUR>
A;Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015
A;Note: this virus was isolated from the mother's sexual partner
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;444-443/DNA: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,186,200,203,351,356,365,377/Binding site: cap

Query Match 94.1%; Score 176; DB 2; Length 443;
Best Local Similarity 92.1%; Pred. No. 1e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 293 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 330

RESULT 18

A41621

env polyprotein M - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: A41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: A41621
A;Molecule type: DNA
A;Residues: 1-445 <BUR>
A;Cross-references: GB:M77228; NID:9328627; PIDN:AAB03790.1; PID:9555013
A;Note: this virus was isolated from the mother
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;446-445/DNA: transmembrane #status predicted <TMN>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 94.1%; Score 176; DB 2; Length 445;
Best Local Similarity 92.1%; Pred. No. 1e-15;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 295 NNTLRRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 332

RESULT 19

B41621

env polyprotein D - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C;Accession: B41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: B41621
A;Molecule type: DNA
A;Residues: 1-454 <BUR>
A;Cross-references: GB:M77279
A;Note: this virus was isolated from the daughter
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F;1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F;263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F;435-454/Domin: transmembrane #status predicted <TM>
 F;9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carb

Query Match 94.1%; Score 176; DB 2; Length 454;
 Best Local Similarity 92.1%; Pred. No. 1,1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
 Db 304 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 341

RESULT 20
 VCLJXK
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N;Alternate names: coat polyprotein
 N;Contains: coat protein gp120; coat protein gp32
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
 C;Accession: B42995
 R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
 A;Reference number: A42995; MUID:92351552; PMID:1322587
 A;Accession: B42995
 A;Molecule type: mRNA
 A;Residues: 1-729 <SH1>
 A;Cross-references: GB:S41266; GB:D01206
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-689/Domin: extracellular #status predicted <EXT>
 F;1-33/Domin: signal sequence #status predicted <SIG>
 F;1-33/Region: hydrophobic #status predicted <CP1>
 F;34-517/Product: coat protein gp120 #status predicted <CP2>
 F;514-517/Region: cleavage processing #status predicted <CP2>
 F;518-729/Product: coat protein gp32 #status predicted <CP2>
 F;518-534/Region: hydrophobic #status predicted <TM1>
 F;690-711/Domin: transmembrane #status predicted <INT>
 F;712-729/Domin: intracellular #status predicted <INT>
 F;93,141,145,146,163,191,192,237,241,248,269,283,308,338,345,361,367,397,403,408,414

Query Match 94.1%; Score 176; DB 1; Length 729;
 Best Local Similarity 92.1%; Pred. No. 1,1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
 Db 559 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 596

RESULT 21
 H44001
 env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)

N;Alternate names: coat polyprotein
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
 C;Accession: H44001
 R;Li, Y.; Hui, H.; Burgees, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
 J. Virol. 66, 6587-6600, 1992
 A;Title: Complete nucleotide sequence, genome organization, and biological properties of
 A;Reference number: A44001; MUID:93021387; PMID:1404605
 A;Accession: H44001
 A;Molecule type: DNA
 A;Residues: 1-843 <LTY>
 A;Cross-references: GB:M93258
 C;Genetics:

A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-29/Domin: signal sequence #status predicted <SIG>
 F;1-35/Region: hydrophobic
 F;30-489/Product: coat protein gp120 #status predicted <GP1>
 F;490-493/Product: coat protein gp41 #status predicted <GP2>
 F;499-515/Region: hydrophobic
 F;673-689/Region: hydrophobic
 F;738-755/Domin: transmembrane #status predicted <TM>
 F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,

Query Match 94.1%; Score 176; DB 1; Length 843;
 Best Local Similarity 92.1%; Pred. No. 2,1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
 Db 540 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 577

RESULT 22
 VCLJND
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N;Alternate names: coat polyprotein
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
 C;Accession: U00066
 R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
 Gene 81, 275-284, 1989
 A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunoc
 A;Reference number: J00065; MUID:90034200; PMID:2806917
 A;Accession: J00066
 A;Molecule type: DNA
 A;Residues: 1-846 <SH1>
 A;Cross-references: GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162
 A;Note: the authors translated the codon GCG for residue 523 as Arg
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F;1-29/Domin: signal sequence #status predicted <SIG>
 F;30-501/Product: coat protein gp120 #status predicted <CP1>
 F;502-846/Product: coat protein gp41 #status predicted <CP2>
 F;502-520/Domin: transmembrane #status predicted <TM1>
 F;674-692/Domin: transmembrane #status predicted <TM2>
 F;87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606,

Query Match 94.1%; Score 176; DB 1; Length 846;
 Best Local Similarity 92.1%; Pred. No. 2,1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 38
 Db 543 NNTLRATIAEQOHLLQTLTWGKIQOLARVLAVERYLKQ 580

RESULT 23
 T12016
 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T12016
 R;McCuchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
 AIDS Res. Hum. Retroviruses 14, 329-337, 1998
 A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
 A;Reference number: Z17379; MUID:9818716; PMID:9519894
 A;Accession: T12016
 A;Status: preliminary; translated from GB/EMBL/DBD
 A;Molecule type: DNA
 A;Residues: 1-852 <MCC>

A;Cross-references: EMBL:U90934; NID:g2351783; PIDN:AA059271.1; PID:g2351784
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

Query Match 94.1%; Score 176; DB 1; Length 852;
 Best Local Similarity 92.1%; Pred. No. 2.1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 38
 Db 549 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 586

RESULT 24
 VCLJ2
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N;Alternate names: coat polyprotein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C;Accession: A03976
 R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sch
 Science 227, 484-492, 1985
 A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
 A;Reference number: A04003; MUID:85090453; PMID:2578227
 A;Accession: A03976
 A;Molecule type: DNA
 A;Residues: 1-855
 A;Cross-references: GB:X02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;51-509/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;510-855/Product: transmembrane glycoprotein #status predicted <TM>
 F;87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
 F;610,624,636,815/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 94.1%; Score 176; DB 1; Length 855;
 Best Local Similarity 92.1%; Pred. No. 2.1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 38
 Db 552 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 589

RESULT 25
 VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
 C;Accession: A24774
 R;Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986
 A;Title: Identification and characterization of conserved and variable regions in the en
 A;Reference number: A24774; MUID:86218077; PMID:2423250
 A;Accession: A24774
 A;Molecule type: DNA
 A;Residues: 1-856 <STR>
 A;Cross-references: GB:K03455; GB:M38432; NID:g1906382
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-501/Product: coat protein gp120 #status predicted <GP1>
 F;502-847/Product: coat protein gp41 #status predicted <GP2>
 F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 94.1%; Score 176; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 2.1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 38
 Db 553 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 590

RESULT 26

A44963
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)

N;Alternate names: coat polyprotein
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
 C;Accession: A44963
 R;Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989
 A;Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc
 A;Reference number: A44963; MUID:89228766; PMID:2713163
 A;Accession: A44963
 A;Molecule type: DNA
 A;Residues: 1-856 <GBI>
 A;Cross-references: GB:M15896; NID:g329392; PIDN:AAB59394.1; PID:g329394
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-520/Product: coat protein gp120 #status predicted <CP1>
 F;521-856/Product: coat protein gp41 #status predicted <CP2>
 F;64-705/Domain: transmembrane #status predicted <TM>
 F;87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,
 Query Match 94.1%; Score 176; DB 1; Length 856;
 Best Local Similarity 94.7%; Pred. No. 2.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 38
 Db 553 NNTLRRAIEAOQHLLQTLTWGIKOLQARILAVERYLKDO 590

RESULT 27

VCLJXB
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N;Alternate names: coat polyprotein
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
 C;Accession: A42995
 R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t
 A;Reference number: A42995; MUID:92351552; PMID:1322587
 A;Accession: A42995
 A;Molecule type: mRNA
 A;Residues: 1-861 <SHI>
 A;Cross-references: GB:S41266; GB:D01206
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-689/Domain: extracellular #status predicted <EXT>
 F;1-33/Domain: signal sequence #status predicted <SIG>
 F;34-517/Region: hydrophobic #status predicted
 F;514-517/Region: cleavage processing #status predicted <CP1>
 F;518-861/Product: coat protein gp41 #status predicted <CP2>
 F;518-534/Region: hydrophobic #status predicted

F;690-711/Domain: transmembrane #status predicted <TM>
 F;712-861/Domain: intracellular #status predicted <INT>
 F;756-772/Region: hydrophobic #status predicted
 F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 94.1%; Score 176; DB 1; Length 861;
 Best Local Similarity 92.1%; Pred. No. 2.1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
 Db 559 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 596

RESULT 28
 VCLJSC
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C/Accession: B28922
 R/Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
 Virology 164, 531-536, 1988
 A/Title: Envelope sequences of two new United States HIV-1 isolates.
 A/Reference number: A28922; MUID:88219542; PMID:3369091

A/Accession: B28922
 A/Molecule type: DNA
 A/Residues: 1-861 <GUR>
 C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-861/Product: env polyprotein #status predicted <EP>
 F;87,129,135,140,143,159,163,167,198,234,241,262,276,285,301,302,333,340,356,362,386,396

Query Match 94.1%; Score 176; DB 1; Length 861;
 Best Local Similarity 92.1%; Pred. No. 2.1e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
 Db 558 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 595

RESULT 29

VCLJH4
 env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N/Alternate names: coat polyprotein
 N/Contains: coat protein gp120; coat protein gp41
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
 C/Accession: C25523
 R/Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
 Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A/Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
 A/Reference number: A94136; MUID:87041461; PMID:3490666
 A/Accession: C25523

A/Molecule type: DNA
 A/Residues: 1-868 <DESS>
 A/Cross-references: GB:M13137; NID:g326460; PIDN:AAA44311.1; PID:g326467
 C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein
 C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F;1-521/Product: coat protein gp120 #status predicted <GP1>
 F;522-868/Product: coat protein gp41 #status predicted <GP2>
 F;89,138,139,142,166,195,196,208,245,252,273,287,300,312,342,349,365,371,395,405,409,455

Query Match 94.1%; Score 176; DB 1; Length 868;
 Best Local Similarity 94.7%; Pred. No. 2.1e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
 Db 565 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 602

RESULT 30
 T01672
 envelope polyprotein precursor - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
 C/Accession: T01672
 R/Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986

A/Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
 A/Reference number: Z14389; MUID:86245056; PMID:2424612
 A/Accession: T01672

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-859 <ALIT>
 A/Cross-references: EMBL:X03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
 C/Superfamily: type E retrovirus env polyprotein

Query Match 93.6%; Score 175; DB 2; Length 859;
 Best Local Similarity 92.1%; Pred. No. 2.9e-15;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
 Db 555 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 592

Search completed: June 2, 2004, 11:50:08
 Job time: 11.3261 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 6.19565 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336A-2
Perfect score: 187
Sequence: 1 NMLRAIEAQOHLQLTWQIKOLQARILAVERYLKQD 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	180	96.3	853	1	ENV_HV1EL
2	180	96.3	853	1	ENV_HV1MF
3	180	96.3	853	1	ENV_HV122
4	180	96.3	856	1	ENV_HV126
5	180	96.3	856	1	ENV_HV1B1
6	180	96.3	856	1	ENV_HV1H2
7	180	96.3	856	1	ENV_HV1H3
8	180	96.3	856	1	ENV_HV1H4
9	180	96.3	856	1	ENV_HV1H5
10	180	96.3	856	1	ENV_HV1H6
11	179	95.7	855	1	ENV_HV1H7
12	179	95.7	855	1	ENV_HV1H8
13	177	94.7	848	1	ENV_HV1H9
14	177	94.7	848	1	ENV_HV1H10
15	176	94.1	843	1	ENV_HV1H11
16	176	94.1	846	1	ENV_HV1H12
17	176	94.1	851	1	ENV_HV1H13
18	176	94.1	852	1	ENV_HV1H14
19	176	94.1	855	1	ENV_HV1H15
20	176	94.1	856	1	ENV_HV1H16
21	176	94.1	856	1	ENV_HV1H17
22	176	94.1	856	1	ENV_HV1H18
23	176	94.1	861	1	ENV_HV1H19
24	176	94.1	865	1	ENV_HV1H20
25	176	94.1	867	1	ENV_HV1H21
26	176	94.1	868	1	ENV_HV1H22
27	175	93.6	849	1	ENV_HV1H23
28	173	92.5	847	1	ENV_HV1H24
29	171	91.4	863	1	ENV_HV1H25
30	168	89.8	852	1	ENV_HV1H26
31	165	88.2	854	1	ENV_HV1H27
32	125	66.8	865	1	ENV_HV1H28
33	125	66.8	877	1	ENV_HV1H29

34	122	65.2	854	1	ENV_HV1H30
35	116	62.0	768	1	ENV_HV1H31
36	113	60.4	712	1	ENV_HV1H32
37	113	60.4	851	1	ENV_HV1H33
38	113	60.4	851	1	ENV_HV1H34
39	113	60.4	856	1	ENV_HV1H35
40	113	60.4	856	1	ENV_HV1H36
41	113	60.4	859	1	ENV_HV1H37
42	111	59.9	859	1	ENV_HV1H38
43	111	59.4	858	1	ENV_HV1H39
44	111	59.4	885	1	ENV_HV1H40
45	111	59.4	889	1	ENV_HV1H41
46	111	59.4	889	1	ENV_HV1H42
47	109	58.3	859	1	ENV_HV1H43
48	108	57.8	880	1	ENV_HV1H44
49	107	57.2	821	1	ENV_HV1H45
50	107	57.2	846	1	ENV_HV1H46
51	107	57.2	881	1	ENV_HV1H47
52	106	56.7	860	1	ENV_HV1H48
53	106	56.7	860	1	ENV_HV1H49
54	53	28.3	2564	1	SPCQ_HUMAN
55	52	27.8	1379	1	M3K5_MOUSE
56	52	27.5	924	1	HXK3_RAT
57	51.5	27.3	1938	1	MYH4_RABIT
58	50.5	27.0	445	1	EX7L_STAM
59	50.5	27.0	1411	1	BEA1_HUMAN
60	50	26.7	1374	1	M3K5_HUMAN
61	50	26.7	1938	1	MYS_ABOIR
62	50	26.7	1939	1	MYH4_HUMAN
63	49.5	26.5	581	1	FRIZ_DROME
64	49.5	26.5	583	1	FRIZ_DROVI
65	49	26.2	236	1	GT6_SCHMA
66	49	26.2	1756	1	PEPL_HUMAN
67	49	26.2	1459	1	DYHC_FUSO
68	49	26.2	8797	1	SNE1_HUMAN
69	48.5	25.9	790	1	BEA1_MOUSE
70	48	25.7	213	1	Y914_THEMA
71	48	25.7	305	1	OTC_SYNP7
72	48	25.7	314	1	SEHL_HUMAN
73	48	25.7	551	1	YD25_YEAST
74	48	25.7	702	1	ATT1_VARV
75	48	25.7	906	1	CTN1_HUMAN
76	48	25.7	906	1	CTN1_MOUSE
77	48	25.7	1935	1	MYS_CYPCA
78	47.5	25.4	253	1	CYSH_VIBCH
79	47.5	25.4	303	1	ALB3_MALZE
80	47.5	25.4	467	1	EUTE_ECOLI
81	47.5	25.4	467	1	EUTE_SALTY
82	47.5	25.4	962	1	ARVC_HUMAN
83	47.5	25.4	969	1	ARVC_MOUSE
84	47.5	25.4	1319	1	SOS1_MOUSE
85	47.5	25.4	1333	1	SOS1_HUMAN
86	47.5	25.4	1955	1	PUMA_PARUN
87	47	25.1	376	1	O43A_DROME
88	47	25.1	380	1	OXAA_MYCLE
89	47	25.1	418	1	DADI_RHIO
90	47	25.1	684	1	RPOC_MARPO

ALIGNMENTS

RESULT 1
ENV_HV1EL
ID ENV_HV1EL
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).

CC	NCBI_TaxID=11689;
OX	Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=86245056; PubMed=2424612;
RA	Allison M., Main-Hobson S., Montagnier L., Sonigo P.;
RT	"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients."
RL	Cell 46:63-74(1986).
CC	-----
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CC	modified and this statement is not removed. Usage by, and for commercial
CC	entities requires a license agreement (see http://www.ibt-sib.ch/announce/)
CC	or send an email to license@ibt-sib.ch .
CC	-----
DR	EMBL; K03454; AAA44329.1; ?
DR	EMBL; A07108; CAA00616.1; ?
DR	HIV; K03454; ENVSEL1.
DR	InterPro; IPR000328; Env_GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120.1.
DR	Pfam; PF00517; GP41.1.
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
FT	SIGNAL 1 31 BY SIMILARITY.
FT	CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID 53 73 BY SIMILARITY.
FT	DISULFID 118 206 BY SIMILARITY.
FT	DISULFID 125 197 BY SIMILARITY.
FT	DISULFID 130 154 BY SIMILARITY.
FT	DISULFID 219 248 BY SIMILARITY.
FT	DISULFID 229 240 BY SIMILARITY.
FT	DISULFID 297 330 BY SIMILARITY.
FT	DISULFID 376 442 BY SIMILARITY.
FT	DISULFID 383 416 BY SIMILARITY.
FT	CARBOHYD 87 87 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 129 129 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 137 137 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 143 143 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 153 153 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 157 157 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 183 183 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 188 188 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 198 198 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 235 235 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 242 242 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 263 263 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 277 277 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 280 290 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 331 331 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 353 353 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 384 384 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 390 390 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 394 394 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 400 400 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 405 405 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 406 406 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 411 411 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 445 445 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 458 458 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 459 459 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 462 462 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 608 608 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 613 613 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 622 622 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 634 634 N-LINKED (GLCNAC . .) (POTENTIAL).
SQ	SEQUENCE 853 AA; 96721 MW; F9CD864DDAA00D7A5 CRC64;
Query Match	96.3%; Score 180; DB 1; Length 853;

Qy	1	NNLRATEAOOHLLQLTWVQIKQALILAVERYLKDQ	38	
Db	550	NNLRATEAOOHLLQLTWVQIKQALILAVERYLKDQ	587	
Match	37	Conservative	0	Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity	97.4%	Pred. No. 5.2e-17		

FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 96.3%; Score 180; DB 1; Length 853;
 Best Local Similarity 97.4%; Pred. No. 5.2e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 38
 Db 551 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 588

RESULT 3
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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 CC -----
 CC EMBL; M22639; AAA45370.1; -
 DR PIR; S54384; S54384.
 DR HIV; M22639; ENV52226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR00777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT SIGNAL 1 31 BY SIMILARITY
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.

FT DISULFID 383 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query Match 96.3%; Score 180; DB 1; Length 853;
 Best Local Similarity 97.4%; Pred. No. 5.2e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 38
 Db 550 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKDQ 587

RESULT 4
 ID ENV_HV126 STANDARD; PRT; 855 AA.
 AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87248097; PubMed=3036660;
 RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
 RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
 RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
 RT Gene 52:71-82 (1987).
 RL Gene 52:71-82 (1987).
 CC -----
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[illegible]

DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41).	
GN	ENV.	
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).	
CC	Viruses; Retrovirdae; Retroviridae; Lentivirinae.	
OK	NCBI_TaxID=11678;	
RP	[1]	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE=8511123; PubMed=2578615;	
RA	Ratner L., Hesselbline W., Patarca R., Livak K.J., Starcich B.R.,	
RA	Josephs S.F., Doran E.R., Rafalecki J.A., Whitehorn E.A.,	
RA	Laemmlester K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,	
RA	Laemmleberger J.A., Papas T.S., Graybe S.J., Chang N.T., Gallo R.C.,	
RA	Wong-Staal F.;	
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III."	
RL	Nature 313:277-284(1985).	
RN	[2]	
RN	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.	
RX	MEDLINE=9028515; PubMed=2355006;	
RA	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,	
RA	Gregory T.J.;	
RT	"Assignment of intrachain disulfide bonds and characterization of	
RT	potential glycosylation sites of the type 1 recombinant human	
RT	immunodeficiency virus envelope glycoprotein (GP120) expressed in	
RL	Chinese hamster ovary cells."	
RL	J. Biol. Chem. 265:10373-10382(1990).	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb.ch/announce/	
CC	or send an email to license@isb.ch).	
CC	-----	
DR	EMBL; M15654; AAA4205.1; -.	
DR	PIR; A03973; VCLJH3.	
DR	HIV; M15654; ENV5BH102.	
DR	InterPro; IPR000328; Env GP41.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00516; GP41.1.	
DR	Pfam; PF00517; GP41.1.	
KM	AIDS; Coat protein; Polypotein; Glycopotein; Transmembrane;	
KM	Signal.	
FT	SIGNAL.	1 30
FT	CHAIN	31 511
FT	CHAIN	512 856
FT	DISULFID	54 74
FT	DISULFID	119 205
FT	DISULFID	126 196
FT	DISULFID	131 157
FT	DISULFID	218 247
FT	DISULFID	228 239
FT	DISULFID	296 331
FT	DISULFID	378 445
FT	DISULFID	385 418
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FT	CARBOHD	160 160
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FT	CARBOHD	197 197
FT	CARBOHD	230 230
FT	CARBOHD	234 234
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FT	EXTERIOR MEMBRANE GLYCOPOTEIN.	
FT	TRANSMEMBRANE GLYCOPOTEIN.	
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FT	DISULFID	126 196
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FT	DISULFID	218 247
FT	DISULFID	228 239
FT	DISULFID	296 331
FT	DISULFID	378 445
FT	DISULFID	385 418
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FT	EXTERIOR MEMBRANE GLYCOPOTEIN.	
FT	TRANSMEMBRANE GLYCOPOTEIN.	
FT	DISULFID	54 74
FT	DISULFID	119 205
FT	DISULFID	126 196
FT	DISULFID	131 157
FT	DISULFID	218 247
FT	DISULFID	228 239
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FT	DISULFID	378 445
FT	DISULFID	385 418
FT	CARBOHD	88 88
FT	CARBOHD	136 136
FT	CARBOHD	141 141
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FT	CARBOHD	186 186
FT	CARBOHD	197 197
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FT	CARBOHD	276 276
FT	CARBOHD	289 289
FT	CARBOHD	295 295
FT	CARBOHD	301 301
FT	CARBOHD	332 332
FT	CARBOHD	

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FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931B27 CRC64;

Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 5,3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 38
Db 553 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 590

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; O09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF033819; AAC82596.1; -
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DEB; 02-APR-00.
DR PDB; 1G9W; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120, 1.
DR Pfam; PF00517; GP41, 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 511
FT 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
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FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 5,3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 38
Db 553 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQD 590

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
ID ENV_HV1H3
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=8528248; PubMed=2988795;
 RA Crow R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-III env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
 CC -----
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 CC -----
 DR EMBL; M14100; AAA44679.1; -;
 DR PDB; 1JAN; 17-OCT-01.
 DR PDB; 1JAN; 17-OCT-01.
 DR HIV; M14100; ENVSHXB3.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 1 511
 FT DISULFID 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 333 333
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT CARBOHYD 856 AA;
 SO SEQUENCE 856 AA; 97188 MM; 33730688B84C1A9C CRC64;
 Query Match 96.3%; Score 180; DB 1; Length 856;
 Best Local Similarity 97.4%; Pred. No. 5.3e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NMLRAIEAOQHLLQTTWQIKOLARILLAVERYLKDQ 38
 Db 553 NMLRAIEAOQHLLQTTWQIKOLARILLAVERYLKDQ 590
 RESULT 8
 ENV_HVILW STANDARD; PRT; 856 AA.
 ID ENV_HVILW
 AC Q70626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (TM12.3 isolate) (HIV-1).
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.;
 RT "viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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 CC -----
 DR EMBL; U12055; AAA76690.1; -;
 DR PDB; 1IF3; 02-MAY-01.
 DR GlycoStableDB; Q70626; -;
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 1 511
 FT DISULFID 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
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 FT CARBOHYD 230 230
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 FT CARBOHYD 276 276
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 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
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 FT CARBOHYD 356 356
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 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
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 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT CARBOHYD 856 AA;
 SO SEQUENCE 856 AA; 97188 MM; 33730688B84C1A9C CRC64;
 Query Match 96.3%; Score 180; DB 1; Length 856;
 Best Local Similarity 97.4%; Pred. No. 5.3e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 38
Db 553 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 590

RESULT 9
ENV_HV1PV STANDARD; PRT; 856 AA.
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP MEDLINE=85111157; PubMed=2982104;
RX Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).

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DR EMBL; K02083; AAB59873.1; -
DR EMBL; X01762; CAA25903.1; ALT_SEQ.
DR PIR; A03974; VCLJVL.
DR HIV; K02083; ENVSPV22.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; polypeptide; Glycoprotein; Transmembrane;
KM Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.

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FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCB1DC3C1209B3 CRC64;

Query Match 96.3%; Score 180; DB 1; Length 856;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 38
Db 553 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLKQ 590

RESULT 10
ENV_HV1PV STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP MEDLINE=85099333; PubMed=2981635;
RX Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.,
RA "Nucleotide sequence of the AIDS virus, LAV.";
RT Cell 40:9-17(1985).

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CC -----
DR EMBL: A02013; AAB59751.1; -.
DR EMBL: A04321; CA00352.1; -.
DR PIR: A03975; VCLJLV.
DR PDB: 1ERF; 20-FEB-02.
DR HIV: K02013; ENV5BRU.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS: Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516
FT CHAIN 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88 88
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FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4D63A CRC64;

Query Match 96.3%; Score 180; DB 1; Length 861;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 NNTLRATEAOOHLQTLVWQIKQARILAVERYLKQD 38
558 NNTLRATEAOOHLQTLVWQIKQARILAVERYLKQD 595

RESULT 11
ENV_HYV1S1
ID ENV_HYV1S1 STANDARD; PRT; 847 AA.
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RX Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.;
RA "viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RU J. Virol. 64:4390-4398(1990).
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CC -----
DR EMBL: M65024; AAA45072.1; -.
DR PDB: IOBE; 15-MAY-97.
DR HIV: M38428; ENV5SF162.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS: Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT CHAIN 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT DISULFID 87 87
FT CARBOHYD 135 135
FT CARBOHYD 154 154
FT CARBOHYD 186 186
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FT CARBOHYD 274 274
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FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

Query Match 95.7%; Score 179; DB 1; Length 847;
Best Local Similarity 94.7%; Pred. No. 7.1e-17;

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Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQHLLQLTWGIKOLQARVLAVERYLKQ 38
 DB 544 NNLRAIEAQHLLQLTWGIKOLQARVLAVERYLKQ 581

RESULT 12
 ENV_HV10Y STANDARD; PRT; 855 AA.

AC P20888;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Hueb T., Daza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot."
 RL AIDS 3:707-715(1989).
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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 CC EMBL: M26727; AAA83397.1; -.
 DR HIV; M26727; ENV50YI.
 DR InterPro: IPR000328; Env GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM Signal.
 FT 1 29
 FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 118 210 BY SIMILARITY.
 FT DISULFID 125 201 BY SIMILARITY.
 FT DISULFID 130 162 BY SIMILARITY.
 FT DISULFID 223 252 BY SIMILARITY.
 FT DISULFID 233 244 BY SIMILARITY.
 FT DISULFID 301 335 BY SIMILARITY.
 FT DISULFID 381 442 BY SIMILARITY.
 FT DISULFID 388 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 95.7%; Score 179; DB 1; Length 855;
 Best Local Similarity 94.7%; Pred. No. 7.2e-17;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQHLLQLTWGIKOLQARVLAVERYLKQ 38
 DB 552 NNLRAIEAQHLLQLTWGIKOLQARVLAVERYLKQ 589

RESULT 13
 ENV_HV10Y STANDARD; PRT; 848 AA.

AC P20871;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11688;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koyanagi S., Chen I.S.Y.;
 RL Submitted (DEC-1988) to the HIV data bank.
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 CC EMBL: M38429; AAB03749.1; -.
 CC PDB: 1CE4; 18-MAR-99.
 DR HIV; M38429; ENV5URCSF.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 503 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 118 203 BY SIMILARITY.
 FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 328 BY SIMILARITY.
 FT DISULFID 374 437 BY SIMILARITY.
 FT DISULFID 381 410 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 848 AA; 96475 MW; 20767512727EC33 CRC64;

Query Match 94.7%; Score 177; DB 1; Length 848;
 Best Local Similarity 92.1%; Pred. No. 1.4e-16;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQ 38
 Db 545 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQ 582

RESULT 14
 ENV_HV1MN STANDARD; PRT; 856 AA.
 AC POS877;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11696;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8219542; PubMed=3369091;
 RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal P., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS PATIENT IN 1984.
 CC
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 CC
 CC EMBL: M17449; AAA44857.1; -
 DR PDB: 1ACJ; 31-JUL-94.
 DR PDB: 1F58; 29-DEC-99.
 DR PDB: 1NTZ; 25-FEB-03.
 DR PDB: 1NU0; 25-FEB-03.
 DR HIV; M17449; ENVSMN.

DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 445
 FT DISULFID 388 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 141 141
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT CARBOHYD 202 202
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 336 336
 FT CARBOHYD 343 343
 FT CARBOHYD 359 359
 FT CARBOHYD 365 365
 FT CARBOHYD 395 395
 FT CARBOHYD 401 401
 FT CARBOHYD 405 405
 FT CARBOHYD 406 406
 FT CARBOHYD 413 413
 FT CARBOHYD 448 448
 FT CARBOHYD 465 465
 FT CARBOHYD 612 612
 FT CARBOHYD 617 617
 FT CARBOHYD 626 626
 FT CARBOHYD 638 638
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97140 MW; D197D809940B8732 CRC64;

Query Match 94.7%; Score 177; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 1.4e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQ 38
 Db 554 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKQ 591

RESULT 15
 ENV_HV1Y2 STANDARD; PRT; 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;

FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2B83 CRC64;
 Query Match 94.1%; Score 176; DB 1; Length 846;
 Best Local Similarity 92.1%; Pred. No. 1.9e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRATEAQOHLQLTWQIKQARILAVERYLKDQ 38
 DB 543 NNLRATEAQOHLQLTWQIKQARILAVERYLKDQ 580
 RESULT 17
 ENV_HV1B8 STANDARD; PRT; 851 AA.
 ID _ENV_HV1B8
 AC P04582;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11684;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6511123; PubMed=2578615;
 RA Ratner L., Hesselink W., Patarca R., Liyak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalson J.A., Whitehorn E.A.,
 RA Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Chrayeb J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RL "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 Nature 313:277-284(1985).
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 CC -----
 CC EMBL; K02011; AAA44661.1; .
 DR PDB; 1DDH; 13-JAN-99.
 DR PDB; 1HHG; 31-OCT-93.
 DR PDB; 1QO3; 02-JAN-97.
 DR PDB; 1S2T; 24-DEC-97.
 DR HIV; K02011; ENV5B8.
 DR GLYCOSULEDB; P04582; .
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.

FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 440 BY SIMILARITY.
 FT DISULFID 385 413 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
 Query Match 94.1%; Score 176; DB 1; Length 851;
 Best Local Similarity 94.7%; Pred. No. 1.9e-16;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NNLRATEAQOHLQLTWQIKQARILAVERYLKDQ 38
 DB 548 NNLRATEAQOHLQLTWQIKQARILAVERYLKDQ 585
 RESULT 18
 ENV_HV1S3 STANDARD; PRT; 852 AA.
 ID _ENV_HV1S3
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF73 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317906; PubMed=2370688;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RA "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";
 RL J. Virol. 64:4016-4020(1990).
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 CC -----

CC or send an email to license@lsb-sib.ch.

CC EMBL; AY52275; A017031.1; -

DR PDB; 1ME0; 11-DEC-02.

DR HIV; M38427; ENVSSR33.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;

KM 3D-structure.

FT SIGNAL 1 31

FT CHAIN 32 506

FT CHAIN 507 852

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 156

FT DISULFID 219 248

FT DISULFID 229 240

FT DISULFID 297 331

FT DISULFID 377 439

FT DISULFID 384 412

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 142 142

FT CARBOHYD 155 155

FT CARBOHYD 159 159

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 242 242

FT CARBOHYD 263 263

FT CARBOHYD 277 277

FT CARBOHYD 290 290

FT CARBOHYD 296 296

FT CARBOHYD 332 332

FT CARBOHYD 339 339

FT CARBOHYD 355 355

FT CARBOHYD 385 385

FT CARBOHYD 391 391

FT CARBOHYD 397 397

FT CARBOHYD 401 401

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 607 607

FT CARBOHYD 612 612

FT CARBOHYD 621 621

FT CARBOHYD 633 633

FT CARBOHYD 812 812

FT CARBOHYD 852 AA; 96663 MW; E57B8F8D3C9910D CRC64;

SO SEQUENCE

Query Match 94.1%; Score 176; DB 1; Length 852;

Best Local Similarity 92.1%; Pred. No. 1.9e-16;

Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAOQHLLQITVWQIKOLARILAVERYLKQ 38

DB 549 NNILRAIEAOQHLLQITVWQIKOLARILAVERYLKQ 586

RESULT 19

ID ENV_HV1A2 STANDARD; PRT; 855 AA.

AC P03378;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor (contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SP2 isolate) (HIV-1).

OC Viruses; Retrovirus; Retroviridae; Lentivirus.

OX NCBI TaxID=11685;

RN [1] -

RP SEQUENCE FROM N.A.

RX MEDLINE=85090453; PubMed=2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,

RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)." ;

RU Science 227:484-492 (1985).

CC -----

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CC EMBL; K02007; AAB59882.1; -

DR PIR; A03976; VCLJ22.

DR HIV; K02007; ENVSSR2.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KM 3D-structure.

FT SIGNAL 1 29

FT CHAIN 30 509

FT CHAIN 510 855

FT DISULFID 53 73

FT DISULFID 118 208

FT DISULFID 125 199

FT DISULFID 130 155

FT DISULFID 221 250

FT DISULFID 231 242

FT DISULFID 299 333

FT DISULFID 380 442

FT DISULFID 387 415

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 140 140

FT CARBOHYD 154 154

FT CARBOHYD 158 158

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 200 200

FT CARBOHYD 233 233

FT CARBOHYD 244 244

FT CARBOHYD 265 265

FT CARBOHYD 279 279

FT CARBOHYD 292 292

FT CARBOHYD 298 298

FT CARBOHYD 304 304

FT CARBOHYD 334 334

FT CARBOHYD 341 341

FT CARBOHYD 358 358

FT CARBOHYD 364 364

FT CARBOHYD 388 388

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 408 408

FT CARBOHYD 445 445

FT CARBOHYD 458 458

FT CARBOHYD 461 461

FT CARBOHYD 610 610

FT CARBOHYD 615 615

FT CARBOHYD 624 624

FT CARBOHYD 636 636

FT CARBOHYD 815 815

FT CARBOHYD 852 AA; 96663 MW; E57B8F8D3C9910D CRC64;

SO SEQUENCE

Query Match 94.1%; Score 176; DB 1; Length 852;

Best Local Similarity 92.1%; Pred. No. 1.9e-16;

Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAOQHLLQITVWQIKOLARILAVERYLKQ 38

DB 549 NNILRAIEAOQHLLQITVWQIKOLARILAVERYLKQ 586

RESULT 19

ID ENV_HV1A2 STANDARD; PRT; 855 AA.

AC P03378;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor (contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

GN ENV.

SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
 Query Match 94.1%; Score 176; DB 1; Length 855;
 Best Local Similarity 92.1%; Pred. No. 1.9e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYLKQ 38
 DB 552 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYLKQ 589

RESULT 20
 ENV_HV1SC STANDARD; PRT; 856 AA.
 ID ENV_HV1SC
 AC P05878;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 NC Viruses; Retroviridae; Retroviridae; Lentivirus.
 NC NCBI_Taxid=11702;
 RX MEDLINE=68219542; PubMed=3369091;
 RA Gargro C., Guo H.-G., Franchini G., Aldrovini A., Collalti E.,
 RA Farrel K., Wong-Staal F., Gallo R.C., Rietz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536 (1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
 CC 1984 IN SOUTHERN CALIFORNIA.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL; M17450; -; NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL. 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 856 AA; 97055 MW; DAF4DA608EA7A08 CRC64;
 Query Match 94.1%; Score 176; DB 1; Length 856;
 Best Local Similarity 92.1%; Pred. No. 1.9e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYLKQ 38
 DB 553 NNLRAIEAOQHLLQTLTWQIKOLARILAVERYLKQ 590

RESULT 21
 ENV_HV1M1 STANDARD; PRT; 856 AA.
 ID ENV_HV1M1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 OS Human immunodeficiency virus type 1 (MMU1 isolate) (HIV-1).
 NC Viruses; Retroviridae; Retroviridae; Lentivirus.
 NC NCBI_Taxid=31678;
 RX MEDLINE=66218077; PubMed=2423250;
 RA Scarfich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 RT AIDS."
 RT Cell 45:637-648 (1986).
 CC -1- MISCELLANEOUS: ISOLATES MMU1, MMU2, AND MMU3 WERE OBTAINED FROM
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 CC WAS PERINATALLY INFECTED BY HER MOTHER.
 DR PIR; A24774; VCLJ3W.
 DR PDB; 1LB0; 04-DEC-02.
 DR PDB; 1LXK; 04-DEC-02.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL. 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.

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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404D9B CRC64;

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Query Match 94.1%; Score 176; DB 1; Length 856;
Best Local Similarity 92.1%; Pred. No. 1.9e-16;
Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NNTLRATEAQOHLTLTWGKIQOLARILAVERYLKDQ 38
553 NNTLRATEAQOHLTLTWGKIQOLARILAVERYLKDQ 590

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RESULT 22
ENV_HV1ZH STANDARD; PRT; 856 AA.
AC P05881;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11692;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D., Jannoun-Nasr R., Getchell J.,
RT McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of Hybrid HIV-1."
RT AIDS Res. Hum. Retroviruses 5:121-129 (1989).
RL AIDS Res. Hum. Retroviruses 5:121-129 (1989).
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CC -----
DR EMBL; M15896; AAB53948.1; -
DR PIR; A44963; A44963.
DR HIV; M15896; ENV52321.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Aids; Coat protein, Polypeptide, Glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 29
FT CHAIN 30 511
FT DISULFID 512 856
FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 153
FT DISULFID 219 248
FT DISULFID 229 240
FT DISULFID 297 331
FT DISULFID 379 445
FT DISULFID 386 418
FT CARBOHYD 87 87
FT CARBOHYD 132 132
FT CARBOHYD 138 138
FT CARBOHYD 152 152
FT CARBOHYD 156 156
FT CARBOHYD 183 183
FT CARBOHYD 198 198
FT CARBOHYD 242 242
FT CARBOHYD 263 263
FT CARBOHYD 277 277
FT CARBOHYD 294 294
FT CARBOHYD 302 302
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 355 355
FT CARBOHYD 364 364
FT CARBOHYD 387 387
FT CARBOHYD 393 393
FT CARBOHYD 398 398
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 448 448
FT CARBOHYD 461 461
FT CARBOHYD 462 462
FT CARBOHYD 465 465
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 637 637
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;

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Query Match 94.1%; Score 176; DB 1; Length 856;
Best Local Similarity 94.7%; Pred. No. 1.9e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NNTLRATEAQOHLTLTWGKIQOLARILAVERYLKDQ 38
553 NNTLRATEAQOHLTLTWGKIQOLARILAVERYLKDQ 590

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RESULT 23
ENV_HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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RX	NCB1_TaxID=36375;
RA	[1]
RP	SEQUENCE FROM N.A.
RM	MEDLINE=92351552; PubMed=1322587;
RS	Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
RT	Kitamura T.;
RL	"Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated transmembrane glycoprotein."
CC	- I MISCELLANEOUS: READTHROUGH OF THE TERMINATOR TAG OCCURS BETWEEN THE CODONS FOR 729-ALA AND 730-ARG.
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CC	-----
DR	EMBL; D12582; BA402124.1; ALT_SEQ.
DR	PIR; A42995; VCLJKB.
DR	InterPro; IPRO00328; Env GP41.
DR	InterPro; IPR00777; GP120.
DR	Pfam; PF00516; GP120.1.
DR	Pfam; PF00517; GP41.1.
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
KW	SIGNAL.
FT	CHAIN 1 35 POTENTIAL.
FT	TRANSMEM 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	TRANSMEM 661 TRANSMEMBRANE GLYCOPROTEIN.
FT	TRANSMEM 680 711 POTENTIAL.
FT	D1SULFID 59 79 BY SIMILARITY.
FT	D1SULFID 124 212 BY SIMILARITY.
FT	D1SULFID 131 203 BY SIMILARITY.
FT	D1SULFID 136 160 BY SIMILARITY.
FT	D1SULFID 225 254 BY SIMILARITY.
FT	D1SULFID 235 246 BY SIMILARITY.
FT	D1SULFID 303 337 BY SIMILARITY.
FT	D1SULFID 383 446 BY SIMILARITY.
FT	D1SULFID 390 419 BY SIMILARITY.
FT	CARBOHYD 93 93 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 141 141 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 145 145 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 146 146 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 159 159 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 163 163 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 191 191 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 192 192 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 237 237 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 241 241 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 248 248 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 269 269 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 283 283 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 296 296 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 308 308 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 338 338 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 345 345 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 361 361 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 367 367 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 397 397 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 403 403 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 408 408 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 414 414 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 449 449 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 465 465 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 468 468 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 617 617 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 622 622 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 631 631 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 643 643 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD 821 821 N-LINKED (GLCNAC . .) (POTENTIAL).
SO	861 AA; 98116 MW; 3C06787650FC93DA CRC64;

[illegible]

FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 94.1%; Score 176; DB 1; Length 865;
 Best Local Similarity 92.1%; Pred. No. 1.9e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRRAEQOHLTLTWGIGKOLARILAVERYLKDQ 38
 Db 562 NNTLRRAEQOHLTLTWGIGKOLARILAVERYLKDQ 599

RESULT 25
 ID ENV_HV1J3 STANDARD; PRT; 867 AA.
 AC P12489;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11694;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352108; PubMed=2669897;
 RA Komiya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria";
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
 CC -----
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 CC EMBL; M21138; AAB03526.1; -;
 DR HIV; M21138; ENV.S13.
 DR InterPro; IPR000328; ENV_GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 RT Signal.
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 FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
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 FT DISUFID 53 73 BY SIMILARITY.

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Query Match 94.1%; Score 176; DB 1; Length 867;
 Best Local Similarity 94.7%; Pred. No. 1.9e-16;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNTLRRAEQOHLTLTWGIGKOLARILAVERYLKDQ 38
 Db 564 NNTLRRAEQOHLTLTWGIGKOLARILAVERYLKDQ 601

RESULT 26
 ID ENV_HV1C4 STANDARD; PRT; 868 AA.
 AC P05879;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041461; PubMed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
 RA Andersen P.R., Devare S.G.;
 RT "Molecular cloning and primary nucleotide sequence analysis of a RT distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RN [2]
 RP SEQUENCE OF 34-43.

RX MEDLINE=90253924; PubMed=2187500;
 RA Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
 RA Devito A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
 RT "Characterization of the secreted, native gp120 and gp160 of the human
 immunodeficiency virus type 1.";
 RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).
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 DR PIR; C25523; VCLJH4.
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 DR InterPro; IPR000328; Env GP41.
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 KM Signal.
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 Query March 94.1%; Score 176; DB 1; Length 868;
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 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATEAOCHTLOITWMOIKOLQARILAVERYLDDQ 38
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 RESULT 27
 ENV_HV1MA STANDARD; PRT; 859 AA.
 ID ENV_HV1MA
 AC P4583;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
 glycoprotein (gp120); Transmembrane glycoprotein (gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MNL isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11697;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6245056; PubMed=2424612;
 RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 RT of two isolates from African patients.";
 RL Cell 46:63-74 (1986).
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 DR EMBL; A07116; CAA00623.1; -;
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 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
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 KM Signal.
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 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 193 193
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 306 306
 FT CARBOHYD 337 337
 FT CARBOHYD 357 357
 ENV_HV1MA
 FT SIGNAL. 1 30
 FT CHAIN 31 513
 FT DISULFID 514 859
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 334
 FT DISULFID 380 445
 FT DISULFID 387 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 134 134
 FT CARBOHYD 139 139
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 193 193
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 306 306
 FT CARBOHYD 337 337
 FT CARBOHYD 357 357
 ENV_HV1MA
 FT SIGNAL. 1 30
 FT CHAIN 31 513
 FT DISULFID 514 859
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 334
 FT DISULFID 380 445
 FT DISULFID 387 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 134 134
 FT CARBOHYD 139 139
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 193 193
 FT CARBOHYD 202 202
 FT CARBOHYD 239 239
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 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
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 FT CARBOHYD 337 337
 FT CARBOHYD 357 357
 ENV_HV1MA
 FT SIGNAL. 1 30
 FT CHAIN 31 513
 FT DISULFID 514 859
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 334
 FT DISULFID 380 445
 FT DISULFID 387 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 134

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 859 AA; 97109 MW; DBCF9A52B3ABF29 CRC64;
 Query Match 93.6%; Score 175; DB 1; Length 859;
 Best Local Similarity 92.1%; Pred. No. 2.6e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRAIEAQOHLQLTWGIKQIQAARILAVERYLKDQ 38
 Db 555 NNLRAIEAQOHLQLTWGIKQIQAARILAVERYLKDQ 592
 RESULT 28
 ENV HV1W2 STANDARD; PRT; 847 AA.
 ID ENV HV1W2
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.B., Redfield R.R., Markham P.D.,
 RA Salunuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT "Genetic variation in HIV-1/II over time in patients with AIDS or at risk for AIDS."
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC -----
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 CC -----
 CC EMBL: M12507; AAB12990.1; -
 DR HIV; M12507; ENV:WMJ2.
 DR InterPro: IPR000328; Env:GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
 FT DISULFID 379 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73A5B5CAE CRC64;
 Query Match 92.5%; Score 173; DB 1; Length 847;
 Best Local Similarity 89.5%; Pred. No. 4.8e-16;
 Matches 34; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLRAIEAQOHLQLTWGIKQIQAARILAVERYLKDQ 38
 Db 544 NNLRAIEAQOHLQLTWGIKQIQAARILAVERYLKDQ 581
 RESULT 29
 ENV HV1Z8 STANDARD; PRT; 863 AA.
 ID ENV HV1Z8
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; PubMed=3395517;
 RA Youniss J., Josephs S.F., Reltz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.
 CC -----
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 CC -----

FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match
Best Local Similarity 89.8%; Score 168; DB 1; Length 852;

Matches 33; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 549 NNLLMAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 586

Search completed: June 2, 2004, 11:42:54
Job time : 8.19565 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 / Search time 31.9076 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-2
Perfect score: 187
Sequence: 1 NNILRAIEAQHLLQLTWQIKQLQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	96.3	132	15	Q90Q52 human immun
2	180	96.3	132	15	Q7SLZ2 human immun
3	180	96.3	143	15	Q7SM06 human immun
4	180	96.3	144	15	Q7ZCD7 human immun
5	180	96.3	144	15	Q7ZCD6 human immun
6	180	96.3	153	15	Q7SM03 human immun
7	180	96.3	357	15	Q78119 human immun
8	180	96.3	588	15	Q993A8 human immun
9	180	96.3	589	15	Q993A7 human immun
10	180	96.3	590	15	Q993A9 human immun
11	180	96.3	616	15	Q993B0 human immun
12	180	96.3	618	15	Q993B2 human immun
13	180	96.3	727	15	Q9Q723 human immun
14	180	96.3	747	15	Q70607 human immun
15	180	96.3	748	15	Q70606 human immun

17	180	96.3	752	15	Q70604 human immun
18	180	96.3	752	15	Q70605 human immun
19	180	96.3	752	15	Q70608 human immun
20	180	96.3	757	15	Q9Q722 human immun
21	180	96.3	811	15	Q9DVL6 human immun
22	180	96.3	842	15	Q73341 human immun
23	180	96.3	842	15	Q70895 human immun
24	180	96.3	842	15	Q73340 human immun
25	180	96.3	847	15	Q69996 human immun
26	180	96.3	851	15	Q78243 human immun
27	180	96.3	854	15	Q56566 human immun
28	180	96.3	854	15	Q85582 human immun
29	180	96.3	854	15	Q72502 human immun
30	180	96.3	854	15	Q90178 human immun
31	180	96.3	854	15	Q78705 human immun
32	180	96.3	855	15	Q8A0V7 human immun
33	180	96.3	855	15	Q8ADT7 human immun
34	180	96.3	856	15	Q74090 human immun
35	180	96.3	856	15	Q92877 human immun
36	180	96.3	856	15	Q74599 human immun
37	180	96.3	856	15	Q41772 human immun
38	180	96.3	857	15	Q92822 human immun
39	180	96.3	857	15	Q71013 human immun
40	180	96.3	857	15	Q89654 human immun
41	180	96.3	864	15	Q9YP39 human immun
42	180	96.3	864	15	Q7ZJC8 human immun
43	179	95.7	125	15	Q91WP9 human immun
44	179	95.7	132	15	Q91W05 human immun
45	179	95.7	133	15	Q9Q020 human immun
46	179	95.7	137	15	Q9DQ04 human immun
47	179	95.7	142	15	Q91W07 human immun
48	179	95.7	144	15	Q70207 human immun
49	179	95.7	144	15	Q7ZCC6 human immun
50	179	95.7	144	15	Q7ZCC5 human immun
51	179	95.7	144	15	Q7ZCC2 human immun
52	179	95.7	144	15	Q7ZCB1 human immun
53	179	95.7	144	15	Q7ZCB0 human immun
54	179	95.7	144	15	Q7ZC96 human immun
55	179	95.7	144	15	Q7ZC95 human immun
56	179	95.7	144	15	Q7ZC89 human immun
57	179	95.7	144	15	Q7ZC88 human immun
58	179	95.7	144	15	Q7ZC71 human immun
59	179	95.7	144	15	Q7ZC70 human immun
60	179	95.7	145	15	Q7ZC57 human immun
61	179	95.7	145	15	Q7ZC40 human immun
62	179	95.7	145	15	Q7ZC35 human immun
63	179	95.7	145	15	Q7ZC31 human immun
64	179	95.7	146	15	Q7SM37 human immun
65	179	95.7	155	15	Q8J3P2 human immun
66	179	95.7	155	15	Q8J3Q3 human immun
67	179	95.7	155	15	Q8J3Q1 human immun
68	179	95.7	156	15	Q8JAL7 human immun
69	179	95.7	174	15	Q8JEB8 human immun
70	179	95.7	192	15	Q8JAL2 human immun
71	179	95.7	219	15	Q8JAJ4 human immun
72	179	95.7	225	15	Q991C1 human immun
73	179	95.7	225	15	Q991B9 human immun
74	179	95.7	225	15	Q991C5 human immun
75	179	95.7	225	15	Q991C0 human immun
76	179	95.7	357	15	Q78118 human immun
77	179	95.7	357	15	Q78156 human immun
78	179	95.7	357	15	Q78155 human immun
79	179	95.7	358	15	Q78140 human immun
80	179	95.7	358	15	Q78141 human immun
81	179	95.7	360	15	Q8QDX2 human immun
82	179	95.7	392	15	Q8J511 human immun
83	179	95.7	421	15	Q72603 human immun
84	179	95.7	421	15	Q8J514 human immun
85	179	95.7	606	15	Q9Q6V8 human immun
86	179	95.7	629	15	Q91K02 human immun
87	179	95.7	797	15	Q03808 human immun
88	179	95.7	797	15	Q03810 human immun
89	179	95.7	799	15	Q03807 human immun

90 179 95.7 801 15 Q03809 Q03809 human immun
ALIGNMENTS

RESULT 1

Q09052 PRELIMINARY; PRT; 132 AA.
AC Q09052;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MOI496;
RX MEDLINE=2132034; Pubmed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea,"
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF31089; AK92300.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 132 132
SQ 132 AA; 15708 MW; 5199DBAED574FAB CRC64;
Query Match 96.3%; Score 180; DB 15; Length 132;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
Db 10 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 47
RESULT 2
Q7SLZ2 PRELIMINARY; PRT; 132 AA.
AC Q7SLZ2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT970;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998,"
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF330024; AAP87755.1; -.
DR Envelope protein.
FT NON_TER 1 1
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949B33 CRC64;
Query Match 96.3%; Score 180; DB 15; Length 132;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
Db 11 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 48

RESULT 3

Q7SM06 PRELIMINARY; PRT; 143 AA.
AC Q7SM06;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998,"
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF330010; AAP87741.1; -.
KM Envelope protein.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BE0 CRC64;
Query Match 96.3%; Score 180; DB 15; Length 143;
Best Local Similarity 97.4%; Pred. No. 3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 38
Db 11 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKDQ 48
RESULT 4
Q7ZCD7 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Derou S., Fischer A., Baurith T.,
RA Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1,"
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185383; AA065658.1; -.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318BE8 CRC64;
Query Match 96.3%; Score 180; DB 15; Length 144;

Best Local Similarity 97.4%; Pred. No. 3.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 24 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 61

RESULT 5

Q7ZCD6 PRELIMINARY; PRT; 144 AA.

AC 07ZCD6; (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HRLX53-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Bouline R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; A185384; A065659.1; -;
DR GO; GO:0019031; C:Viral envelope; IEA.

DR InterPro; IPR000328; F:Structural molecule activity; IEA.

DR Pfam; PF00517; GP41; 1.

KM Envelope protein.

FT NON_TER 1 144

FT NON_TER 144 144

SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EBB CRC64;

Query Match 96.3%; Score 180; DB 15; Length 144;
Best Local Similarity 97.4%; Pred. No. 3.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 24 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 61

RESULT 6

Q7SMO3 PRELIMINARY; PRT; 153 AA.

AC 07SMO3; (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GT598;

RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF530013; AAP87744.1; -;
KM Envelope protein.

FT NON_TER 1 153

FT NON_TER 153 153

SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1FEFC035 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 153;
Best Local Similarity 97.4%; Pred. No. 3.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 11 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 48

RESULT 7

Q78119 PRELIMINARY; PRT; 357 AA.

AC 078119; (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid";
RL AIDS Res. Hum. Retroviruses 8:53-59 (1992).

DR EMBL; X61356; CAA43624.1; -;
DR PIR; A53591; A53591.

DR PIR; S70422; S21996.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0019031; C:Viral envelope; IEA.

DR InterPro; IPR000328; F:Structural molecule activity; IEA.

DR Pfam; PF00517; GP41; 1.

KM Transmembrane.

FT NON_TER 1 1

FT NON_TER 1 1

SQ SEQUENCE 357 AA; 41118 MW; FE4CA7B122AB8E6 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 357;
Best Local Similarity 97.4%; Pred. No. 7.9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 38
Db 54 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKQ 91

RESULT 8

Q993A8 PRELIMINARY; PRT; 588 AA.

AC 0993A8; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.

RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF21147; AAK20295.1; -;
DR PIR; A53591; A53591.

DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240AEB CRC64;
Query Match 96.3%; Score 180; DB 15; Length 588;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 496 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 533
RESULT 9
Q993A7 PRELIMINARY; PRT; 588 AA.
ID Q993A7
AC Q993A7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt1;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RU Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AKK20296.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B5928FC6D CRC64;
Query Match 96.3%; Score 180; DB 15; Length 588;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 496 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 533
RESULT 10
Q993B1 PRELIMINARY; PRT; 589 AA.
ID Q993B1
AC Q993B1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=1F8;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RU Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AKK20292.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;
Query Match 96.3%; Score 180; DB 15; Length 589;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 496 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 533
RESULT 11
Q993A9 PRELIMINARY; PRT; 590 AA.
ID Q993A9
AC Q993A9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RU Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321146; AKK20294.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;
Query Match 96.3%; Score 180; DB 15; Length 590;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 497 NNTLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 534
RESULT 12
Q993B0 PRELIMINARY; PRT; 616 AA.
ID Q993B0

AC Q993E0; 0993E0; 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
RT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA Docosa S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF221145; AAK20293.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 616 AA; 69189 MW; 57A8E20F9A560AFC CRC64;

Query Match 96.3%; Score 180; DB 15; Length 616;
Best Local Similarity 97.4%; Pred. No. 1.4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 38
Db 497 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 534

RESULT 13
Q993B2 PRELIMINARY; PRT; 618 AA.
ID Q993B2;
AC Q993B2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
RT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA Docosa S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF221143; AAK20291.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;

Query Match 96.3%; Score 180; DB 15; Length 618;

Best Local Similarity 97.4%; Pred. No. 1.4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 38
Db 499 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 536

RESULT 14
Q99723 PRELIMINARY; PRT; 727 AA.
ID Q99723;
AC Q99723;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
RT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RA MEDLINE=9272698; Pubmed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein."
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RA MEDLINE=20027260; Pubmed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity."
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189158; AAF25627.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD62ED26B9E66 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 727;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 38
Db 548 NNTLRALIAOQHLLQTLTWGKIQOLQARILAVERYLKQ 585

RESULT 15
Q70607 PRELIMINARY; PRT; 747 AA.
ID Q70607;
AC Q70607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
RT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12034; AAA76669.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 747
 SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;
 Query Match 96.3%; Score 180; DB 15; Length 747;
 Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
 Db 548 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 585
 RESULT 16
 ID 070606 PRELIMINARY; PRT; 748 AA.
 AC 070606;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12032; AAA76668.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 748
 SQ SEQUENCE 748 AA; 84224 MW; 56BDF186C67694B CRC64;
 Query Match 96.3%; Score 180; DB 15; Length 748;
 Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
 Db 549 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 586
 RESULT 17
 ID 070604 PRELIMINARY; PRT; 752 AA.
 AC 070604;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12030; AAA76666.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 752
 SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
 Query Match 96.3%; Score 180; DB 15; Length 752;
 Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
 Db 553 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 590
 RESULT 18
 ID 070605 PRELIMINARY; PRT; 752 AA.
 AC 070605;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner M.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AA476667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.3%; Score 180; DB 15; Length 752;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 38
Db 553 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 590

RESULT 19
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner M.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AA476670.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.

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DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 752;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 38
Db 553 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 590

RESULT 20
Q9Q722 PRELIMINARY; PRT; 757 AA.
AC Q9Q722;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBx;
RX MEDLINE=9272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
  Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
  HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIIBx;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
  Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
  type 1 variant map outside regions required for coreceptor
  specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL; AF189159; AAF25628.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D263BD2E CRC64;

Query Match 96.3%; Score 180; DB 15; Length 757;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 38
Db 548 NNTLRATIAQOHLQTLTWQIKQLQARILAVERYLKQD 585

RESULT 21

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Q9DVU6          PRELIMINARY;      PRT;      811 AA.
ID Q9DVU6
AC Q9DVU6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; PubMed=11044094;
RA Vilanga N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RT HIV-1 pandemic originated in Central Africa."
RT "unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa."
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ401037; CAC15045.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR006625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER
FT 1
FT NON_TER
FT 1
SQ SEQUENCE 811 AA; 90894 MW; 13A2B13246117541 CRC64;

Query Match          96.3%; Score 180; DB 15; Length 811;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 557 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 594

RESULT 22
Q73341          PRELIMINARY;      PRT;      842 AA.
ID Q73341
AC Q73341;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96305593; PubMed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization."
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL: U39236; AAB37173.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.

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DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1E9F1 CRC64;

Query Match          96.3%; Score 180; DB 15; Length 842;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 539 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 576

RESULT 23
Q70895          PRELIMINARY;      PRT;      842 AA.
ID Q70895
AC Q70895;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RX MEDLINE=98285725; PubMed=9621027;
RA Geo F., Robertson D.L., Carnuthers C.D., Morrison S.G., Jian B.,
RT "A comprehensive panel of near-full-length clones and reference
RT sequences for non-subtype B isolates of human immunodeficiency virus
RT type 1."
RT J. Virol. 72:5680-5698(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Geo F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005495; AAD03179.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 842 AA; 94810 MW; F82041B1D932DCAD CRC64;

Query Match          96.3%; Score 180; DB 15; Length 842;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
Db 539 NNTLRATIEAQOHLQLTWQIKQLQARILAVERYLKDQ 576

RESULT 24
Q73340          PRELIMINARY;      PRT;      842 AA.
ID Q73340
AC Q73340;
DT 01-NOV-1996 (TReMBLrel. 01, Created)

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DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.T., Douglas N.W., Ranbar S., Holmes H., Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C, RT D, E, and F obtained from the World Health Organization Network for HIV Isolation and Characterization";
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL, U39235; AAB37172.1; -;
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 607BAF2A47B791B CRC64;

Query Match 96.3%; Score 180; DB 15; Length 842;
 Best Local Similarity 97.4%; Pred. No. 1.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAOQHLLQTLTWQIKOLQARILAVERYLKDQ 38
 Db 539 NNILRAIEAOQHLLQTLTWQIKOLQARILAVERYLKDQ 576

RESULT 25
 ID 069996 PRELIMINARY; PRT; 847 AA.
 AC 069996;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S., Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M., Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. The human and NIAID Networks for HIV Isolation and Characterization";
 RL J. Virol. 70:1651-1657(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA NIAID/NIH AIDS Variation Program;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA McEvilly M.M.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL, U08445; AAB04071.1; -.

DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 847 AA; 95602 MW; FCBCBA7AF446FB20 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 847;
 Best Local Similarity 97.4%; Pred. No. 2e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAOQHLLQTLTWQIKOLQARILAVERYLKDQ 38
 Db 544 NNILRAIEAOQHLLQTLTWQIKOLQARILAVERYLKDQ 581

RESULT 26
 ID 078243 PRELIMINARY; PRT; 851 AA.
 AC 078243;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Env polypotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carlini F., Federici M., Equestre M., Ricci S., Ratti G., Zibai Q., Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer RT chronically infected HUT-78 cellular clone-";
 RL J. Viral Diseases 1:40-55(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352106; PubMed=2765297;
 RA Federici M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B., Macchi B., Mangiano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non producer clones from HUT-78 infected with a patient HIV isolate";
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Titti F., Federici M., Butto S., Orecchia A., Carlini F., Taddeo B., Borsetti A., Saggio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not productive clone-";
 RL Int. J. Immunopharmacol. 3:17-23(1990).
 DR EMBL, Z11530; CAAT7628.1; -;
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR PIR: S33985; S33985.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A376B9B7E98027 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 851;
 Best Local Similarity 97.4%; Pred. No. 2e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT CONFLICT 214 214 H -> L (IN REF. 2).
 FT CONFLICT 530 530 A -> S (IN REF. 2).
 FT CONFLICT 739 739 G -> D (IN REF. 2).
 SQ SEQUENCE 854 AA; 97005 MW; FF264B3841D1220 CRC64;

Query Match 96.3%; Score 180; DB 15; Length 854;
 Best Local Similarity 97.4%; Pred. No. 2e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAQOHLQITVWQIKQLQARI LAVERYLKQ 38
 DB 551 NNLRAIEAQOHLQITVWQIKQLQARI LAVERYLKQ 588

RESULT 30

ID 090178 PRELIMINARY; PRT; 854 AA.
 AC 090178;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074930; PubMed=7983770;
 RA Fang H., Pincus S.H.;
 RT "Unique insertion sequence and pattern of CD4 expression in variants
 RT selected with immunotoxins from human immunodeficiency virus type 1-
 RT infected T cells."
 RL J. Virol. 69:75-81(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RA Fang H., Pincus S.H.;
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an
 RT immunotoxin-resistant variant T cell line."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070521; AAC28452.1; -.
 DR PIR; A53591; A53591.
 DR PIR; S13288; S13288.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 96.3%; Score 180; DB 15; Length 854;
 Best Local Similarity 97.4%; Pred. No. 2e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAQOHLQITVWQIKQLQARI LAVERYLKQ 38
 DB 551 NNLRAIEAQOHLQITVWQIKQLQARI LAVERYLKQ 588

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 Job time : 35.9076 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 35.0054 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-2
Perfect score: 187
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 28138677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

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- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	187	100.0	38	14	US-10-252-136-82	Sequence 82, Appl
2	180	96.3	38	9	US-09-796-202-11	Sequence 11, Appl
3	180	96.3	38	9	US-09-779-451-2	Sequence 2, Appl
4	180	96.3	38	10	US-09-493-346-2	Sequence 2, Appl
5	180	96.3	38	12	US-10-267-682-89	Sequence 89, Appl
6	180	96.3	38	12	US-10-267-748-89	Sequence 89, Appl
7	180	96.3	38	12	US-09-809-060-6	Sequence 6, Appl
8	180	96.3	38	12	US-09-809-060-7	Sequence 7, Appl
9	180	96.3	38	12	US-10-663-589-3	Sequence 3, Appl
10	180	96.3	38	12	US-10-681-879-2	Sequence 2, Appl
11	180	96.3	38	12	US-09-828-615-2	Sequence 2, Appl
12	180	96.3	38	14	US-10-116-797-2	Sequence 2, Appl
13	180	96.3	38	14	US-10-323-314-11	Sequence 11, Appl
14	180	96.3	38	14	US-10-414-192-1	Sequence 1, Appl
15	180	96.3	38	14	US-10-351-641-16	Sequence 16, Appl

16	180	96.3	38	14	US-10-351-641-507	Sequence 507, App
17	180	96.3	38	14	US-10-351-641-604	Sequence 604, App
18	180	96.3	38	15	US-10-005-305-165	Sequence 165, App
19	180	96.3	38	15	US-10-005-305-202	Sequence 202, App
20	180	96.3	38	15	US-10-005-305-203	Sequence 203, App
21	180	96.3	38	15	US-10-420-194-1234	Sequence 1234, Ap
22	180	96.3	38	16	US-10-664-021-2	Sequence 2, Appl
23	180	96.3	38	16	US-10-671-316-2	Sequence 2, Appl
24	180	96.3	41	12	US-10-267-748-8	Sequence 8, Appl
25	180	96.3	41	12	US-10-267-748-8	Sequence 8, Appl
26	180	96.3	41	12	US-10-663-589-30	Sequence 30, Appl
27	180	96.3	41	12	US-10-663-589-33	Sequence 33, Appl
28	180	96.3	41	12	US-10-663-589-35	Sequence 35, Appl
29	180	96.3	41	14	US-10-252-136-8	Sequence 8, Appl
30	180	96.3	41	14	US-10-414-192-3	Sequence 3, Appl
31	180	96.3	41	14	US-10-414-192-9	Sequence 9, Appl
32	180	96.3	41	14	US-10-351-641-486	Sequence 486, App
33	180	96.3	41	14	US-10-351-641-601	Sequence 601, App
34	180	96.3	41	14	US-10-351-641-633	Sequence 633, App
35	180	96.3	41	14	US-10-351-641-1163	Sequence 1163, Ap
36	180	96.3	41	16	US-10-664-021-27	Sequence 27, Appl
37	180	96.3	41	16	US-10-671-316-27	Sequence 27, Appl
38	180	96.3	44	12	US-10-663-589-36	Sequence 36, Appl
39	180	96.3	44	14	US-10-414-192-10	Sequence 10, Appl
40	180	96.3	45	9	US-09-779-451-9	Sequence 9, Appl
41	180	96.3	45	12	US-09-809-060-50	Sequence 50, Appl
42	180	96.3	45	12	US-10-663-589-29	Sequence 29, Appl
43	180	96.3	45	14	US-10-351-641-1164	Sequence 1164, Ap
44	180	96.3	45	16	US-10-664-021-26	Sequence 26, Appl
45	180	96.3	45	16	US-10-671-316-26	Sequence 26, Appl
46	180	96.3	49	9	US-09-796-202-3	Sequence 3, Appl
47	180	96.3	49	12	US-10-323-313-3	Sequence 3, Appl
48	180	96.3	51	12	US-10-663-589-27	Sequence 27, Appl
49	180	96.3	51	14	US-10-351-641-745	Sequence 745, App
50	180	96.3	51	16	US-10-664-021-24	Sequence 24, Appl
51	180	96.3	51	16	US-10-671-316-24	Sequence 24, Appl
52	180	96.3	52	14	US-10-351-641-1119	Sequence 1119, Ap
53	180	96.3	53	14	US-10-351-641-955	Sequence 955, App
54	180	96.3	53	14	US-10-351-641-1062	Sequence 1062, Ap
55	180	96.3	55	9	US-09-779-451-1	Sequence 1, Appl
56	180	96.3	55	12	US-09-809-060-14	Sequence 14, Appl
57	180	96.3	57	15	US-10-438-691-1	Sequence 1, Appl
58	180	96.3	59	16	US-10-664-021-1	Sequence 1, Appl
59	180	96.3	59	16	US-10-671-316-1	Sequence 1, Appl
60	180	96.3	60	12	US-10-663-589-1	Sequence 1, Appl
61	180	96.3	63	12	US-10-267-682-201	Sequence 201, App
62	180	96.3	63	12	US-10-267-748-201	Sequence 201, App
63	180	96.3	63	14	US-10-252-136-54	Sequence 54, Appl
64	180	96.3	103	14	US-10-263-103-29	Sequence 29, Appl
65	180	96.3	103	15	US-10-438-691-3	Sequence 3, Appl
66	180	96.3	113	15	US-10-438-691-4	Sequence 4, Appl
67	180	96.3	177	14	US-10-040-3498-2	Sequence 2, Appl
68	180	96.3	198	9	US-09-854-816-88	Sequence 88, Appl
69	180	96.3	198	9	US-09-854-816-89	Sequence 89, Appl
70	180	96.3	200	14	US-10-263-103-25	Sequence 25, Appl
71	180	96.3	200	15	US-10-438-691-8	Sequence 8, Appl
72	180	96.3	232	14	US-10-059-271-81	Sequence 81, Appl
73	180	96.3	254	14	US-10-059-271-82	Sequence 82, Appl
74	180	96.3	256	14	US-10-059-271-97	Sequence 97, Appl
75	180	96.3	268	9	US-09-854-816-16	Sequence 16, Appl
76	180	96.3	268	9	US-09-854-816-17	Sequence 17, Appl
77	180	96.3	268	9	US-09-854-816-18	Sequence 18, Appl
78	180	96.3	268	9	US-09-854-816-19	Sequence 19, Appl
79	180	96.3	269	9	US-09-854-816-43	Sequence 43, Appl
80	180	96.3	338	12	US-10-267-682-90	Sequence 90, Appl
81	180	96.3	338	12	US-10-267-748-90	Sequence 90, Appl
82	180	96.3	344	14	US-10-040-3498-1	Sequence 1, Appl
83	180	96.3	345	9	US-09-779-451-8	Sequence 8, Appl
84	180	96.3	359	14	US-10-026-741-49	Sequence 49, Appl
85	180	96.3	359	14	US-10-214-670-58	Sequence 58, Appl
86	180	96.3	391	14	US-10-059-271-93	Sequence 93, Appl
87	180	96.3	488	8	US-08-911-824-95	Sequence 95, Appl
88	180	96.3	491	8	US-08-911-824-56	Sequence 56, Appl

ALIGNMENTS

89 180 96.3 519 9 US-09-756-551A-8
90 180 96.3 539 8 US-08-911-824-108

Sequence 8, Appli
Sequence 108, App

RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 187, DB 14, Length 38;
Best Local Similarity 100.0%; Pred. No. 1, 9e-18;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 2
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUPPATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.3%; Score 180, DB 9, Length 38;
Best Local Similarity 97.4%; Pred. No. 1, 7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 3
US-09-779-451-2

; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 96.3%; Score 180, DB 9, Length 38;
Best Local Similarity 97.4%; Pred. No. 1, 7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 4
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 96.3%; Score 180, DB 10, Length 38;
Best Local Similarity 97.4%; Pred. No. 1, 7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38

RESULT 5
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.

Query Match 96.3%; Score 180, DB 10, Length 38;
Best Local Similarity 97.4%; Pred. No. 1, 7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
;
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match          96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38

RESULT 6
US-10-267-748-89
; Sequence 89, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;           Mathews, Thomas J.
;           Wild, Carl T.
;           Barney, Shawn O.
;           Lambert, Dennis M.
;           Petleway, Stephen R.
;           Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
;
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89
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Query Match          96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
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RESULT 7
US-09-809-060-6
; Sequence 6, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6
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Query Match          96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
Db 1 NNILRAIEAQOHLQLTWGKIKQLQARILAVERYLKQ 38
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RESULT 8
US-09-809-060-7
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Sequence 7, Application US/09809060
Publication No. US2002010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies against Fusion-Active
Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 9
US-10-663-589-3
Sequence 3, Application US/10663589
Publication No. US200400637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 10
US-10-681-879-2
Sequence 2, Application US/10681879
Publication No. US20040062767A1
GENERAL INFORMATION:
APPLICANT: Oleon, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
INFECTION
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/10/681,879

CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/493,346
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 11
US-09-828-615-2
Sequence 2, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Oleon, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 96.3%; Score 180; DB 12; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 12
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Oleon, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 13
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 14
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Mathews, Thomas J.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 15
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Metucka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTVMQIKOLQARILAVERYLKQ 38

RESULT 16
US-10-351-641-507
Sequence 507, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Metucka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641

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; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-10-351-641-507

Query Match          96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 17
; Sequence 604, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-10-351-641-604

Query Match          96.3%; Score 180; DB 14; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 18
; Sequence 165, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
```

```

; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
;
US-10-005-305-165

Query Match          96.3%; Score 180; DB 15; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 19
; Sequence 202, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
;
US-10-005-305-202

Query Match          96.3%; Score 180; DB 15; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 20
; Sequence 203, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
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FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match      96.3%; Score 180; DB 15; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
Db      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 21
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US2004006035A1.
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Biact, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
TITLE OF INVENTION: Interactions
FILE REFERENCE: MBH02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/366,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234
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Query Match      96.3%; Score 180; DB 15; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
Db      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 22
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US20040076637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use In Therapy to Inhibit Transmission of Human
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match      96.3%; Score 180; DB 16; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
Db      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38

RESULT 23
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: peptides, and trimers formed therefrom
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match      96.3%; Score 180; DB 16; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
Db      1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKQ 38
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RESULT 24
US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-682-8

Query Match 96.3%; Score 180; DB 12; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
DB 4 NNLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 41

RESULT 25
US-10-267-748-8
Sequence 8, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.

Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-748-8

Query Match 96.3%; Score 180; DB 12; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
DB 4 NNLRRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 41

RESULT 26
US-10-663-589-30
Sequence 30, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimetris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
PRIOR FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patent In version 3.2
SEQ ID NO 30
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial
FEATURE:

OTHER INFORMATION: synthesized
US-10-663-589-30

Query Match 96.3%; Score 180; DB 12; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
|||||
4 NNLLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 41

RESULT 27
US-10-663-589-33

Sequence 33, Application US/10663589
Publication No. US20040063637A1

GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003

CURRENT APPLICATION NUMBER: US/10/663,589

PRIOR FILING DATE: 2003-09-16

NUMBER OF SEQ ID NOS: 95

SOFTWARE: Patentin version 3.2

SEQ ID NO 33

LENGTH: 41

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: synthesized

US-10-663-589-33

Query Match 96.3%; Score 180; DB 12; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
|||||
4 NNLLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 41

RESULT 28
US-10-663-589-35

Sequence 35, Application US/10663589
Publication No. US20040063637A1

GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003

CURRENT APPLICATION NUMBER: US/10/663,589

PRIOR FILING DATE: 2003-09-16

NUMBER OF SEQ ID NOS: 95

SOFTWARE: Patentin version 3.2

SEQ ID NO 35

LENGTH: 41

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: synthesized

US-10-663-589-35

DB 1 NNLLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 38

RESULT 29
US-10-252-136-8

Sequence 8, Application US/10252136
Publication No. US20030103998A1

GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross

TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER

TITLE OF INVENTION: USING COMBINATORY THERAPY

FILE REFERENCE: 7872-036

CURRENT APPLICATION NUMBER: US/10/252,136

PRIOR FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 82

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 41

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-10-252-136-8

Query Match 96.3%; Score 180; DB 14; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILAVERYLKQ 38
|||||
4 NNLLRAIEAQOHLQLTWGIGIKQLQARILAVERYLKQ 41

RESULT 30
US-10-414-192-3

Sequence 3, Application US/10414192
Publication No. US20030181382A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

Bolognesi, Daniel P.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/414,192

FILING DATE: 15-Apr-2003

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-107-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-414-192-3

Query Match 96.3%; Score 180; DB 14; Length 41;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLATEAQOHLQLTWQIKQLQARIILAVERYLKDQ 38
Db 4 NNLRLATEAQOHLQLTWGIKQLQARIILAVERYLKDQ 41

Search completed: June 2, 2004, 12:29:23
Job time : 36.0054 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 46.3505 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336A-147
Sequence: 1 NNILRAIEAQOHLLQTLWQIKQLQARILAVERYLKD 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : A_Geneseq_29Jun04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	100.0	37	3 AAB14705	Aab14705 HIV-1 iso
2	182	100.0	37	4 AAB54969	Aab54969 Anti-HIV
3	182	100.0	38	2 AAB98408	Aab98408 DP107 cor
4	182	100.0	38	4 AAB54785	Aab54785 HIV anti
5	182	100.0	38	4 AAB55005	Aab55005 Anti-HIV
6	182	100.0	38	4 AAB54970	Aab54970 Anti-HIV
7	182	100.0	38	4 AAB92244	Aab92244 Virus rel
8	182	100.0	38	4 AAU14011	AAU14011 DP107 pep
9	182	100.0	38	5 AA018771	AA018771 HIV gp41
10	176	96.7	36	3 AAB14704	Aab14704 HIV-1 iso
11	176	96.7	36	4 AAB54968	Aab54968 Anti-HIV
12	176	96.7	37	3 AAB14739	Aab14739 HIV-1 iso
13	176	96.7	37	4 AAB55004	Aab55004 Anti-HIV
14	175	96.2	37	3 AAB52751	Aab52751 T21/DP107
15	175	96.2	38	2 AAB55635	Aab55635 DP-139 -
16	175	96.2	38	2 AAB55636	Aab55636 DP-140 -
17	175	96.2	38	2 AAR47216	Aar47216 DP-107 -
18	175	96.2	38	2 AAU27614	AAU27614 Human imm
19	175	96.2	38	3 AAY88666	Aay88666 Core poly
20	175	96.2	38	3 AAY88730	Aay88730 Core poly
21	175	96.2	38	3 AAY88731	Aay88731 Core poly
22	175	96.2	38	3 AAY89145	Aay89145 Core poly
23	175	96.2	38	3 AAY89146	Aay89146 Core poly
24	175	96.2	38	3 AAY89243	Aay89243 Core poly
25	175	96.2	38	3 AAB14530	Aab14530 HIV-1 iso

26	175	96.2	38	3 AAB52824	Aab52824 T21/DP107
27	175	96.2	38	3 AAB52786	Aab52786 T21/DP107
28	175	96.2	38	3 AAB52823	Aab52823 T21/DP107
29	175	96.2	38	4 AAG63858	Aag63858 Amino aci
30	175	96.2	38	4 AAB92349	Aab92349 Virus rel
31	175	96.2	38	4 AAB77021	Aab77021 Core poly
32	175	96.2	38	4 AAB77085	Aab77085 Core poly
33	175	96.2	38	4 AAB77086	Aab77086 Core poly
34	175	96.2	38	4 AAB77596	Aab77596 Core poly
35	175	96.2	38	4 AAB77652	Aab77652 Core poly
36	175	96.2	38	4 AAB77500	Aab77500 Core poly
37	175	96.2	38	4 AAB77624	Aab77624 Core poly
38	175	96.2	38	4 AAU70185	AAU70185 HIV viral
39	175	96.2	38	4 AAU70184	AAU70184 HIV viral
40	175	96.2	38	4 AAB85690	Aab85690 DP107 pep
41	175	96.2	38	4 AAB801489	Abb01489 Viral cor
42	175	96.2	38	4 AAB800505	Abb00505 Viral cor
43	175	96.2	38	4 AAB800090	Abb00090 Viral cor
44	175	96.2	38	4 AAB800657	Abb00657 Viral cor
45	175	96.2	38	4 AAB802077	Abb02077 Viral cor
46	175	96.2	38	4 AAB800025	Abb00025 HIV-1 gp4
47	175	96.2	38	4 AAB800089	Abb00089 Viral cor
48	175	96.2	38	4 AAB800504	Abb00504 Viral cor
49	175	96.2	38	4 AAB800629	Abb00629 Viral cor
50	175	96.2	38	4 AAB800601	Abb00601 RSV Fl pr
51	175	96.2	38	4 AAB801980	Abb01980 Viral cor
52	175	96.2	38	4 AAB802134	Abb02134 Viral cor
53	175	96.2	38	4 AAU12638	AAU12638 DP178-11k
54	175	96.2	38	4 AAU13205	AAU13205 DP178-11k
55	175	96.2	38	4 AAU13053	AAU13053 DP178-11k
56	175	96.2	38	4 AAU13149	AAU13149 DP178-11k
57	175	96.2	38	4 AAU13177	AAU13177 DP178-11k
58	175	96.2	38	4 AAU12574	AAU12574 DP178-11k
59	175	96.2	38	4 AAU12639	AAU12639 DP178-11k
60	175	96.2	38	4 AAB82962	Aab82962 Anti-HIV
61	175	96.2	38	5 AAE22282	Aae22282 gp41 Fusi
62	175	96.2	38	5 ADE02097	Ade02097 Hybrid po
63	175	96.2	38	5 ADE02154	Ade02154 Hybrid po
64	175	96.2	38	5 ADE01509	Ade01509 Hybrid po
65	175	96.2	38	6 AABG75976	Abg75976 HIV-1 gp4
66	175	96.2	38	6 AABU09553	Abu09553 Peptide f
67	175	96.2	38	6 ABO10245	Ab010245 HIV-1 gp
68	175	96.2	38	7 ADC99756	Adc99756 DP-107 an
69	175	96.2	38	7 ADE73011	Ade73011 HIV gp41
70	175	96.2	41	2 AAR52840	Aar52840 DP-125 -
71	175	96.2	41	2 AAR88406	Aar88406 Peptide D
72	175	96.2	41	2 AAU17019	AAU17019 DP-178-11k
73	175	96.2	41	2 AAU27616	AAU27616 Human imm
74	175	96.2	41	2 AAU27622	AAU27622 Human imm
75	175	96.2	41	3 AAY89779	Aay89779 Core poly
76	175	96.2	41	3 AAY89240	Aay89240 Core poly
77	175	96.2	41	3 AAY89134	Aay89134 Core poly
78	175	96.2	41	4 AAB547921	Aab54791 HIV anti
79	175	96.2	41	4 AAB592250	Aab592250 Virus rel
80	175	96.2	41	4 AAB71593	Aab71593 Core poly
81	175	96.2	41	4 AAB78180	Aab78180 Core poly
82	175	96.2	41	4 AAB77489	Aab77489 Core poly
83	175	96.2	41	4 AAB802106	Abb02106 Viral cor
84	175	96.2	41	4 AAB801187	Abb01187 Viral cor
85	175	96.2	41	4 AAB802636	Abb02636 Viral cor
86	175	96.2	41	4 AAB801969	Abb01969 Viral cor
87	175	96.2	41	4 AAG67047	Aag67047 Control P
88	175	96.2	41	4 AAB800493	Abb00493 Viral cor
89	175	96.2	41	4 AAB802074	Abb02074 Viral cor
90	175	96.2	41	4 AAB800598	Abb00598 Viral cor

ALIGNMENTS

RESULT 1
ID AAB14705 standard; peptide; 37 AA.

AC AAB14705;
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 XX HIV-1 isolate LA1 gp41 N-helical domain peptide P-17, fragment #34.
 XX
 XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KM isolate LA1.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX
 PN W0200040616-A1.
 PD
 PD 13-JUL-2000.
 XX
 XX 10-JAN-2000; 2000WO-US000456.
 PF
 XX 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 PR
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 P1 WILD CT, Weiss CD;
 XX
 DR WPI: 2000-465959/40.
 PT
 PT Raising neutralising antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Disclosure: Page 36; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LA1. The invention relates to raising a neutralising antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helix segment), or the gp41 core 6-helix bundle, which is formed by the
 CC intersection of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternatively linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 XX Sequence 37 AA;
 XQ

Db 1 NNLRLRALEAOQHLLQLTWQVQKQCARILLNVERLYKD 37
1 NNLRLRALEAOQHLLQLTWQVQKQCARILLNVERLYKD 37

RESULT 2
ID AAB54969 standard; peptide; 37 AA.
XX AAB54969;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW anti-fusogenic; mobile blood component; measles virus; MeV; HIV; RSV;
KW simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX
XX Disclosure; Page 137; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPiV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 37 AA;
XX

Query Match 100.0%; Score 182; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0

Db 1 NNTLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKD 37

RESULT 3

AA98408 AAR98408 standard; peptide; 38 AA.

AC AAR98408;

DT 16-OCT-2003 (revised)

DT 17-FEB-1997 (first entry)

DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.

KM Antifusogenic activity; antiviral capability; coiled-coil peptide;

KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;

KM Influenza virus; Hepatitis B virus.

OS Human immunodeficiency virus 1.

PN WO9619495-A1.

PD 27-JUN-1996

PF 20-DEC-1995; 95MO-US016733.

PR 20-DEC-1994; 94US-00360107.

PR 06-JUN-1995; 95US-00470896.

PA (UYDU-) UNIV DUKE.

PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;

PI Pecteway SR, Langlois AJ;

DR WPI; 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an

PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence

XX search motif.

XX Disclosure; Page 30; 471pp; English.

PS The sequences given in AAR98398-408 represent peptides which exhibit

CC antifusogenic activity, antiviral capability and/or the ability to

CC modulate intracellular processes involving coiled-coil peptide

CC structures. These peptides are recognised by the ALLMOTIS, 107x178x4 and

CC PLZIP search motifs. These peptides may be used to inhibit the

CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B

CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 38 AA;

XX Query Match 100.0%; Score 182; DB 2; Length 38;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-16;

XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKD 37

Db 1 NNTLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKD 37

RESULT 4

AA98408 AAR98408 standard; peptide; 38 AA.

AC AAR98408;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;

KM antifusogenic; mobile blood component; measles virus; MeV; HIV;

KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

XX human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.

PN WO200069902-A1.

PD 23-NOV-2000.

PR 17-MAY-2000; 2000MO-US013651.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PA (CONU-) CONUICHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

PI WPI; 2001-007496/01.

DR A modified peptide and a reactive group which is reactive with amino

PT groups, hydroxyl groups, or thiol groups on blood components to form

PT stable covalent bonds useful for treatment of viral infections, e.g.

XX human immunodeficiency virus.

XX Claim 6; Page 173; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)

CC comprising a peptide that exhibits anti-viral activity and a reactive

CC group which is reactive with amino groups, hydroxyl groups, or thiol

CC groups on blood components to form stable covalent bonds (II) has anti-

CC viral and anti-fusogenic activities. (I) inhibits viral infection of

CC cells by inhibiting cell-cell fusion or free virus infection or to reduce

CC the level of membrane fusion events between two or more entities, e.g.,

CC virus-cell or cell-cell, relative to the level of membrane fusion that

CC occurs in the absence of the peptide. (II) is useful in the treatment of

CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,

CC MeV, and HIV. (I) may be administered prophylactically to previously

CC uninfected individuals. This is useful in cases where an individual has

CC been subjected to a high risk of exposure to a virus. By bonding of long-

CC lived components of the blood, such as immunoglobulin, serum albumin, red

CC blood cells and platelets the activity is extended for days to weeks.

CC This is due to improved stability in vivo and a reduced susceptibility to

CC peptidase or protease degradation. This minimises the need for more

CC frequent, or even continual, administration of the peptides. AAB54784 to

CC AAB5431 represent peptides used in the exemplification of the present

XX invention. (Updated on 11-SEP-2003 to standardise OS field)

RESULT 5

AA98408 AAR98408 standard; peptide; 38 AA.

AC AAB55005;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 amino truncation peptide #35.

XX Query Match 100.0%; Score 182; DB 4; Length 38;

KM Best Local Similarity 100.0%; Pred. No. 1.4e-16;

KM Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKD 37

Db 1 NNTLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKD 37

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
KW ssmian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
DR A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 139; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 182; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
XX
RESULT 6
AAB54970
ID AAB54970 standard; peptide; 38 AA.
XX
AC AAB54970;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DPl07 carboxy truncation peptide #35.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;

KW anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
KM ssmian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
DR A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 182; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
XX
RESULT 7
AAB92244
ID AAB92244 standard; peptide; 38 AA.
XX
AC AAB92244;
XX
DT 22-JUN-2001 (first entry)
DT 05-MAR-2001 (first entry)
XX
XX Virus related peptide SEQ ID NO:1420.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimide group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000WO-US013576.
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K,
 XX
 DR WPI; 2001-112059/12.
 XX
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 662; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/ethyl groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 182; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 Db 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 RESULT 8
 AAU14011
 ID AAU14011 standard; peptide; 38 AA.
 XX
 AC AAU14011;
 XX
 DT 11-SEP-2003 (revised)
 DT 21-NOV-2001 (first entry)
 XX
 DE DP107 peptide from HIV-1 transmembrane protein gp41.
 XX
 XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KM antifusogenic; antiviral; HIV transmission.
 XX
 XX Human immunodeficiency virus 1; isolate IAI.
 OS
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 1..35
 FT /note= "Amino acids 1-35 can be optionally and serially

FT deleted from the N-terminus"
 FT Misc-difference 4..38
 FT /note= "Amino acids 4-38 can be optionally and serially
 FT deleted from the C-terminus"
 XX
 XX WO200151673-A2.
 XX
 PD 19-JUL-2001.
 XX
 XX 05-JUL-2000; 2000WO-US035727.
 PF
 XX 09-JUL-1999; 99US-00350841.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 PI Jeffe P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 XX
 DR WPI; 2001-442157/47.
 XX
 XX
 PT Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 XX Disclosure; Page 33; 259pp; English.
 PS
 XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents the DP107 peptide. (updated on 11-SEP-2003 to standardise OS
 CC field)
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 182; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 Db 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 RESULT 9
 AA018771
 ID AA018771 standard; peptide; 38 AA.
 XX
 AC AA018771;
 XX
 DT 29-OCT-2002 (first entry)
 DT
 XX
 DE HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
 XX
 XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
 KM gp41.
 XX
 XX Human immunodeficiency virus.
 OS
 XX
 XX WO200256902-A2.
 PN
 XX
 PD 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.
XX
XX 19-DEC-2000; 2000US-0256657P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Baroudy BM;
XX WPI; 2002-636513/68.
XX
XX Treatment of HIV infection in an individual involves administration of a
PT combination of chemokine co-receptor five antagonist and a specified HIV
PT envelope polypeptide.
XX
XX Disclosure; Page 34; 52pp; English.
XX
XX The present invention relates to a method of treating an HIV infection in
CC an individual, which involves administering in combination a chemokine co-
CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
CC derivative. Other viral infections can also be treated using the method.
CC The present sequence is a peptide derived from HIV and useful in the
CC method of the invention
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 182; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
Db
RESULT 10
AAB14704
ID AAB14704 standard; peptide; 36 AA.
XX
XX AAB14704;
AC
XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #33.
DE
XX HIV-1, gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200040616-A1.
PN
XX 13-JUL-2000.
PD
XX 10-JAN-2000; 2000WO-US000456.
PF
XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
XX WILD CT, Weiss CD;
PI
XX WPI; 2000-465959/40.
DR
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.

XX Disclosure; Page 36; 97pp; English.
PS
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralizing antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond to
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
XX Sequence 36 AA;
SQ
Query Match 96.7%; Score 176; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
Db
RESULT 11
AAB54968
ID AAB54968 standard; peptide; 36 AA.
XX
XX AAB54968;
AC
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #33.
DE
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM anti-fusogenic; mobile blood component; measles virus; MeV; STV;
KM simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200069902-A1.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US013651.
PF
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONC-) CONUCHEM INC.
PA
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI

XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent or even continual, administration of the peptides. AAB54784 to
CC AAB5531 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 36 AA;
XX
Query Match 96.7%; Score 176; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
1 NNLRAIEAOQHLLQLTWQIKQIQAARILAVERYLK 36
1 NNLRAIEAOQHLLQLTWQIKQIQAARILAVERYLK 36
XX
RESULT 12
AAB14739
ID AAB14739 standard; peptide; 37 AA.
XX
AC AAB14739;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
XX core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
XX humoral response; broad spectrum vaccine; anti-HIV;
XX envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
XX isolate LAI.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2000040616-A1.
XX
PD 13-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX

PI Wild CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX Disclosure; Page 38; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralising antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 37 AA;
XX
Query Match 96.7%; Score 176; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
2 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKD 37
1 NLRRAIEAOQHLLQLTWQIKQIQAARILAVERYLKD 36
XX
RESULT 13
AAB55004
ID AAB55004 standard; peptide; 37 AA.
XX
AC AAB55004;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 amino truncation peptide #34.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2000069902-A1.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
PF

XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX (CONU-) CONJUCHEM INC.
PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI WPI; 2001-007496/01.
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
PS Disclosure; Page 139; 211pp; English.
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 37 AA;
SQ
Query Match 96.7%; Score 176; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. NO. 8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLLRAIEAQCHLQLTWQIKQLQARILAVERYLKD 37
Db 1 NLLRAIEAQCHLQLTWQIKQLQARILAVERYLKD 36
RESULT 14
AAB52751
ID AAB52751 standard; peptide; 37 AA.
XX
AC AAB52751;
XX
DT 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
DE T21/DP107 peptide fragment #33.
XX
KM Anticellulose; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200066622-A1.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012371.
XX
PR 05-MAY-1999; 99US-0132686P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
PI WPI; 2000-656493/63.
XX
DR WPI; 2000-656493/63.
XX
PT Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
PS Claim 12; Page 28; 148pp; English.
XX
CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 37 AA;
SQ
Query Match 96.2%; Score 175; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. NO. 1.1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLLRAIEAQCHLQLTWQIKQLQARILAVERYLKD 37
Db 1 NLLRAIEAQCHLQLTWQIKQLQARILAVERYLKD 37
RESULT 15
AAR55635
ID AAR55635 standard; peptide; 38 AA.
XX
AC AAR55635;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
DE DP-139 - DP-107 analogue.
XX
KM Leucine zipper; HIV-1; human immunodeficiency virus;
KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.
XX
OS Synthetic.
XX
PN WO9402505-A1.
XX
PD 03-FEB-1994.
XX
PF 19-JUL-1993; 93WO-US006769.
XX
PR 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Wild CT, Matthews TJ, Bolognesi DP;
XX
DR WPI; 1994-048790/06.
XX
PT New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.
XX
PS Disclosure; Page 25; 38pp; English.
XX
CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable

CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV-induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR5633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 38 AA;

Query Match 96.2%; Score 175; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37

RESULT 16

AAR5636 standard; peptide; 38 AA.

XX AAR5636;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-140 - DP-107 analogue.

XX Leucine zipper; HIV-1; human immunodeficiency virus;

KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

XX antiviral; gp41.

OS Synthetic.

PN WO9402505-A1.

XX 03-FEB-1994.

PF 19-JUL-1993; 93WO-US006769.

XX 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.

XX Disclosure; Page 25; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV-induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR5633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 38 AA;

Query Match 96.2%; Score 175; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37

RESULT 17
 AAR47216 standard; peptide; 38 AA.

XX AAR47216;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (558-595).

XX Leucine zipper; HIV-1; human immunodeficiency virus;

KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;

XX antiviral; gp41.

OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 12 /note= "residue 12 of the sequence in Fig 1 is H; residue
 FT 12 of the sequence in Table 4 is G"

PN WO9402505-A1.

XX 03-FEB-1994.

PF 19-JUL-1993; 93WO-US006769.

XX 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.

XX Claim 1; Page 27; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV-induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR5633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 38 AA;

Query Match 96.2%; Score 175; DB 2; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKQIQLQARIILAVERYLKD 37

RESULT 18
 AAR27614 standard; peptide; 38 AA.

XX AAR27614

XX AAR27614 standard; peptide; 38 AA.

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XX AC AAW27614;
XX PR 25-MAR-2003 (revised)
XX DT 22-DEC-1997 (first entry)
XX DE Human immunodeficiency virus gp41 derived peptide DP-107.
XX KM Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
XX KM inhibition; induction; cell fusion; transmembrane; type 1.
XX OS Human immunodeficiency virus.
XX PN US5656480-A.
XX PD 12-AUG-1997.
XX PF 27-JAN-1995; 95US-00374666.
XX PR 20-JUL-1992; 92US-00916540.
XX PR 07-AUG-1992; 92US-00927532.
XX PR 19-JUL-1993; 93WO-US006769.
XX PA (UYDU-) UNIV DUKE.
XX PI Bolognesi DP, Wild CT, Matthews TJ;
XX DR WPI; 1997-414595/38.
XX PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
XX PT syncytia formation and transmissiion.
XX PS Claim 1; Col 13-14; 18pp; English.
XX CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein
XX CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
XX CC cell fusion in a culture and cell free HIV transmissiion in a culture to a
XX CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
XX CC MAR-2003 to correct PF field.)
XX SQ Sequence 38 AA;

Query Match 96.2%; Score 175; DB 2; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37

RESULT 19
AAV88666
XX ID AAV88666 standard; peptide; 38 AA.
XX AC AAV88666;
XX DT 23-MAY-2000 (first entry)
XX DE Core polypeptide fragment T No. 21.
XX KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX KM anti-fusogenic; differentiation factor; interleukin; interferon;
XX KM colony stimulating factor; hormone; angiogenic factor.
XX OS Unidentified.
XX PN WO959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PR 20-MAY-1999; 99WO-US011219.

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XX PR 20-MAY-1998; 98US-00082279.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX DR WPI; 2000-136792/12.
XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX PT comprises enhancer sequence.
XX PS Disclosure; Page 21; 124pp; English.
XX CC The invention relates to hybrid polypeptides comprising enhancer peptide
XX CC sequence linked to core polypeptides. The enhancer polypeptides are
XX CC derived from various retroviral envelope (gp41) protein sequences,
XX CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX CC pharmacokinetic properties such as increasing the half-life of any core
XX CC polypeptide that they are linked to. The core polypeptides are any
XX CC function as a pharmacologically useful peptide for the treatment or
XX CC prevention of a disease. The core polypeptides are bioactive peptides
XX CC selected from a growth factor, cytokine, differentiation factor,
XX CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX CC factor. The peptides of the invention can be used for inhibiting viral
XX CC infection and can be used in anti-viral and anti-fusogenic treatments.
XX CC Sequences AAV88651-Y90055 represent core polypeptide fragments that can
XX CC be used in the invention. Some sequences among those indicated also
XX CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX SQ Sequence 38 AA;

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37

RESULT 20
AAV88730
XX ID AAV88730 standard; peptide; 38 AA.
XX AC AAV88730;
XX DT 23-MAY-2000 (first entry)
XX DE Core polypeptide fragment T No. 85.
XX KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX KM anti-fusogenic; differentiation factor; interleukin; interferon;
XX KM colony stimulating factor; hormone; angiogenic factor.
XX OS Unidentified.
XX PN WO959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PR 20-MAY-1998; 98US-00082279.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX DR WPI; 2000-136792/12.

```

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
comprises enhancer sequence.
XX
PS Disclosure; Page 22; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
1 NNTLRRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
Db

RESULT 21
AAY88731
ID AAY88731 standard; peptide; 38 AA.
AC AAY88731;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 86.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
DR A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 22; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
1 NNTLRRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
Db

RESULT 22
AAY89145
ID AAY89145 standard; peptide; 38 AA.
AC AAY89145;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 583.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
DR A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 30; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC Sequences AAY88651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA:

Query Match 96.2%; Score 175; DB 3; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 23

AAY89146
 ID AAY89146 standard; peptide; 38 AA.

XX AAY89146;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 583.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 KM colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

PS Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY88651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA:

Query Match 96.2%; Score 175; DB 3; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 24
 AAY89243
 ID AAY89243 standard; peptide; 38 AA.

XX AAY89243;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 681.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 KM colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

PS Disclosure; Page 32; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY88651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA:

Query Match 96.2%; Score 175; DB 3; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
 DB 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 25

AAB14530
 ID AAB14530 standard; peptide; 38 AA.

XX AAB14530;
 AC 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 PI WILD CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Claim 5; Page 56; 97pp; English.
 XX
 CC Sequences AAB14529-B14531 and AAB14537-B14568 represent specifically
 CC claimed peptides derived from the N-helical domain of the gp41 envelope
 CC glycoprotein from a variety of HIV-1 isolates. The invention relates to
 CC raising a neutralizing antibody response to a broad spectrum of HIV
 CC (human immunodeficiency virus) strains and isolates, comprising the
 CC administration of a peptide which corresponds to or mimics highly
 CC conserved portions of gp41 which are important in mediating the process
 CC of viral entry into host cells. Such peptides can correspond to or mimic
 CC the coiled coil solution structure of the N-helical domain (the heptad
 CC repeat region), or can correspond or mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41
 CC core 6-helix bundle, which is formed by the interaction of the N- and C-
 CC helical domains of three gp41 proteins. The peptides can be administered
 CC either singly or as a combination (particularly a combination of N-
 CC helical and C-helical peptides), and can be multimerised. For example, N-
 CC and C-helical domain peptides can be alternately linked together to form
 CC a peptide which mimics the core 6-helix bundle. Administration of the
 CC peptide(s) generates a humoral response, with the production of
 CC antibodies against gp41 structures involved in viral entry. As these
 CC antibodies against gp41 structures involved in viral entry may be effective
 CC against a broad range of HIV strains and isolates. The peptide
 CC compositions may be administered as a prophylactic or therapeutic vaccine
 CC to generate antibodies which reduce or inhibit the ability of HIV to
 CC infect uninfected cells. A composition comprising polyclonal or
 CC monoclonal antibodies can be administered to reduce HIV infection of
 CC uninfected cells. Antibodies raised against entry-relevant gp41
 CC structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 38 AA;

Query Match 96.2%; Score 175; DB 3; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRLAIEAQOHLLQLTWQIKOLQRLAVERLYKD 37
 DB 1 NNLRLAIEAQOHLLQLTWQIKOLQRLAVERLYKD 37
 RESULT 26
 ID AAB52824 standard; peptide; 38 AA.
 XX
 AC AAB52824;
 XX
 DT 12-SEP-2003 (revised)
 DT 23-FEB-2001 (first entry)
 XX
 DE T21/DP107 peptide fragment #101.
 XX
 KM Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
 KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
 KM chemottractant.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200066622-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 05-MAY-2000; 2000MO-US012371.
 XX
 PR 05-MAY-1999; 99US-0132686P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
 PI WPI; 2000-656493/63.
 XX
 DR
 XX
 PT Administration of peptide agents with a sequence corresponding to a
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
 PT is used to modulate inflammation.
 XX
 PS Disclosure; Page 28; 148pp; English.
 XX
 CC The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
 CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
 CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
 CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
 CC interacts with members of the formyl peptide receptor (FPR) family and
 CC thereby up-regulates an inflammatory response, and acts as a potent
 CC chemottractant and activator of human peripheral blood phagocytes (but
 CC not T cells). The present peptide can be used to modulate an inflammatory
 CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 38 AA;

QY 1 NNLRLAIEAQOHLLQLTWQIKOLQRLAVERLYKD 37
 DB 1 NNLRLAIEAQOHLLQLTWQIKOLQRLAVERLYKD 37
 RESULT 27
 ID AAB52786 standard; peptide; 38 AA.
 XX
 AC AAB52786;
 XX
 DT 12-SEP-2003 (revised)
 DT 23-FEB-2001 (first entry)
 XX
 DE T21/DP107 peptide fragment #68.

Query Match 96.2%; Score 175; DB 3; Length 38;
 Best Local Similarity 97.3%; Pred. No. 1,1e-15;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
OS Human immunodeficiency virus 1.
XX WO20006622-A1.
PN 09-NOV-2000.
PD 05-MAY-2000; 2000WO-US012371.
PF 05-MAY-1999; 99US-0132686P.
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
PI WPI; 2000-656493/63.
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
PS Claim 12; Page 29; 148pp; English.
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
RESULT 28
AAB52823
ID AAB52823 standard; peptide; 38 AA.
XX
AC AAB52823;
XX
DT 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
DE T21/DP107 peptide fragment #100.
XX
KM Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
OS Human immunodeficiency virus 1.
XX WO20006622-A1.
PN 09-NOV-2000.
PD 05-MAY-2000; 2000WO-US012371.
PF 05-MAY-1999; 99US-0132686P.
PR
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
PI WPI; 2000-656493/63.
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
PS Claim 15; Page 42; 148pp; English.
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 38 AA;
Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 1.1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
RESULT 29
AAG63858
ID AAG63858 standard; peptide; 38 AA.
XX
AC AAG63858;
XX
DT 11-SEP-2003 (revised)
DT 29-OCT-2001 (first entry)
XX
DE Amino acid sequence of a HIV-1 gp41 peptide fragment.
XX
KM HIV-1; isolate LAI; gp41; viral entry; envelope protein; glycoprotein;
KM viral infection; antiviral.
XX
OS Human immunodeficiency virus 1.
XX WO200159457-A2.
PN 16-AUG-2001.
PD 09-FEB-2001; 2001WO-US004030.
PF 10-FEB-2000; 2000US-0181543P.
PR 28-SEP-2000; 2000US-0235901P.
XX
PA (PANNA-) PANACOS PHARM INC.
XX
PI Wild CT, Allaway GP;
XX
DR WPI; 2001-522493/57.
XX
PT Screening for inhibitors of viral entry structure formation by
PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.
PS Disclosure; Page 23; 68pp; English.
XX The present sequence represents a fragment of a Human immunodeficiency
CC virus type 1 (HIV-1) isolate LAI gp41 protein. The peptide is used to

CC raise antibodies for use in the method of the invention. The
CC specification describes a method of screening for inhibitors of viral
CC entry structure formation. The method comprises contacting a viral
CC envelope protein or glycoprotein (e.g. gp41) with a triggering agent and
CC a candidate compound to form a mixture, and measuring the effect that the
CC candidate compound has on the formation of conformational intermediates.
CC The effect of the candidate compound can be measured by antibody binding
CC to these conformational intermediates. The compounds identified by the
CC method are useful as inhibitors for inhibiting or preventing viral
CC infection and to treat humans infected with HIV-1 or other viruses. This
CC antiviral compounds can also be used to inactivate viruses in body
CC fluids, e.g. blood or blood compounds used for therapeutic purposes. The
CC assay is also useful for detecting antibodies in virus-infected
CC individuals or virus-infected body fluids or tissues that inhibit entry-
CC relevant conformational changes in one or more viral envelope proteins or
CC glycoproteins. The presence of the antibodies in infected individuals or
CC samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 38 AA;
QY
Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
1 NNLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKD 37
Db
RESULT 30
AAB92349
ID AAB92349 standard; peptide; 38 AA.
XX
AC AAB92349;
XX
DT 22-JUN-2001 (first entry)
XX
DE Virus related peptide SEQ ID NO:1525.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONT-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thihaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 704; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 38 AA;
QY
Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 1,1e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
1 NNLRAIEAQOHLQLTWGIGIKQLQARIILAVERYLKD 37
Db
Search completed: June 2, 2004, 11:41:42
Job time : 47.3505 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 10.0543 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336a-147
Perfect score: 182
Sequence: 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : PIR_78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	96.2	357	2	S21996 envelope protein g
2	175	96.2	851	2	S31985 env polypotein g
3	175	96.2	853	2	S54384 env polypotein g
4	175	96.2	854	2	S13288 env polypotein - huma
5	175	96.2	855	1	VCLJZR env polypotein pr
6	175	96.2	856	1	VCLJH3 env polypotein pr
7	175	96.2	856	1	VCLJVL env polypotein pr
8	175	96.2	861	1	VCLJLV env polypotein pr
9	174	95.6	357	2	S22006 envelope protein g
10	174	95.6	357	2	S21994 envelope protein g
11	174	95.6	357	2	S22004 envelope protein g
12	174	95.6	358	2	S22002 envelope protein g
13	174	95.6	358	2	S22000 envelope protein g
14	174	95.6	358	2	S70417 envelope protein g
15	172	94.5	357	2	S21990 envelope protein g
16	172	94.5	859	1	VCLJMN env polypotein pr
17	171	94.0	443	2	C41621 env polypotein pr
18	171	94.0	445	2	A41621 env polypotein pr
19	171	94.0	454	2	B41621 env polypotein pr
20	171	94.0	729	1	VCLJXK env polypotein pr
21	171	94.0	843	1	H44001 env polypotein pr
22	171	94.0	846	1	VCLJND env polypotein pr
23	171	94.0	852	2	T12016 envelope glycoprot
24	171	94.0	855	2	VCLJAJ env polypotein pr
25	171	94.0	856	1	VCLJW env polypotein pr
26	171	94.0	856	1	A44963 env polypotein pr
27	171	94.0	861	1	VCLJXB env polypotein pr
28	171	94.0	861	1	VCLJSC env polypotein pr
29	171	94.0	868	1	VCLJH4 env polypotein pr

30	170	93.4	859	2	T01672 envelope polypote
31	167	91.8	357	2	S21998 envelope protein g
32	166	91.2	358	2	S21992 envelope protein g
33	163	89.6	852	1	VCLJBR env polypotein -
34	160	87.9	854	1	VCLJST env polypotein pr
35	157	86.3	847	2	T09448 envelope glycoprot
36	157	86.3	847	2	S13289 env polypotein - huma
37	122	67.0	104	2	S52930 GP41 ENV protein -
38	120	65.9	864	1	VCLJG4 env polypotein -
39	120	65.9	877	2	C46356 env polypotein -
40	119	65.4	877	2	S49197 envelope protein p
41	115	63.2	732	2	S46352 env polypotein -
42	111	61.0	863	2	A53034 env polypotein -
43	110	60.4	366	2	B41565 env polypotein pr
44	108	59.3	712	1	VCLJG4 env polypotein pr
45	108	59.3	851	2	S12159 env polypotein - huma
46	108	59.3	852	1	VCLJG4 env polypotein pr
47	108	59.3	859	1	VCLJST env polypotein pr
48	108	59.3	859	2	S53098 env polypotein pr
49	107	58.8	859	1	VCLJCT Env transmembrane
50	106	58.2	855	2	A45713 env polypotein pr
51	106	58.2	858	1	VCLJG2 env polypotein pr
52	106	58.2	881	2	S03068 env polypotein - huma
53	106	58.2	885	2	S04322 env polypotein -
54	106	58.2	886	2	T11555 env polypotein - sti
55	105	57.7	881	1	VCLJG3 env polypotein -
56	104	57.1	859	2	S24571 env polypotein - huma
57	104	57.1	869	2	A47665 env polypotein gp120 (
58	103	56.6	880	1	VCLJG2 env polypotein pr
59	102	56.0	151	2	S30458 env polypotein - huma
60	102	56.0	786	2	S28084 env polypotein -
61	102	56.0	889	1	VCLJG5 env polypotein -
62	101	55.5	887	2	T11566 envelope glycoprot
63	100	54.9	151	2	S30448 env polypotein - huma
64	100	54.9	151	2	S30453 env polypotein - huma
65	100	54.9	151	2	S30452 env polypotein - huma
66	100	54.9	151	2	S30450 env polypotein - huma
67	100	54.9	151	2	S30451 env polypotein - huma
68	98	53.8	151	2	S30459 env polypotein - huma
69	98	53.8	151	2	S30457 env polypotein - huma
70	98	53.8	151	2	S30456 env polypotein - huma
71	98	53.8	151	2	S30455 env polypotein - huma
72	98	53.8	151	2	S30454 env polypotein - huma
73	97	53.3	68	2	S60695 env polypotein -
74	97	53.3	68	2	S60696 env polypotein -
75	97	53.3	68	2	S60705 env polypotein -
76	97	53.3	68	2	S60707 env polypotein -
77	97	53.3	68	2	S60694 env polypotein -
78	97	53.3	68	2	S60706 env polypotein -
79	92	50.5	68	2	S60693 env polypotein -
80	92	50.5	68	2	S60687 env polypotein -
81	90	49.5	68	2	S60692 env polypotein -
82	89	48.9	68	2	S60688 env polypotein -
83	86	47.3	69	2	S60690 env polypotein -
84	86	47.3	69	2	S60689 env polypotein -
85	86	47.3	69	2	S60691 env polypotein -
86	82	45.1	294	2	S60525 envelope polypote
87	82	45.1	297	2	S60538 envelope polypote
88	87	41.2	372	2	S46344 env polypotein -
89	75	41.2	375	2	S46345 env polypotein -
90	73	40.1	294	2	S60545 envelope polypote

ALIGNMENTS

RESULT 1
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27),
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422, S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A:Reference number: S70417; MUID:92144209; PMID:11736940

A:Accession: S70422

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:g1067129

A:Experimental source: patient 27L

A>Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 96.2%; Score 175; DB 2; Length 357;

Best Local Similarity 97.3%; Pred. No. 6.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 37

Db 54 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 90

RESULT 2

S33985

env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:g60199

C:Superfamily: type E retrovirus env polyprotein

Query Match 96.2%; Score 175; DB 2; Length 851;

Best Local Similarity 97.3%; Pred. No. 1.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 37

Db 548 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 584

RESULT 3

S54384

envelope polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-853 <THR>

A:Cross-references: EMBL:M26639; NID:9329377; PIDN:AAA45370.1; PID:g329385

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: polyprotein

Query Match 96.2%; Score 175; DB 2; Length 853;

Best Local Similarity 97.3%; Pred. No. 1.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 37

Db 550 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 586

RESULT 4

S13288

env protease - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namashe, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match 96.2%; Score 175; DB 2; Length 854;

Best Local Similarity 97.3%; Pred. No. 1.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 37

Db 551 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 587

RESULT 5

VCL42R

env polyprotein precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus Zr-6

C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C:Accession: D26192

R:Strinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic

A:Reference number: A26192; MUID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: GB:X03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-855/Product: env polyprotein #status predicted <MAT>

F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>

F:501-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 96.2%; Score 175; DB 1; Length 855;

Best Local Similarity 97.3%; Pred. No. 1.8e-15;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 37

Db 552 NNLRAIEAQOHLQLTWGKIKOLQARILAVERYLKD 588

RESULT 6

VCL42R

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorai

herberger, J.A.; Papas, T.S.; Ghayab, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; MUID:85111123; PMID:2578615

A:Accession: A03973

A:Molecule type: DNA

A;Residues: 1-856 <RAT>
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326363; PIDN:AAA442
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.2%; Score 175; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 1 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 37
Db 553 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 589
RESULT 7
VCLUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03974
R;Huesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A;Reference number: A93355; MUID:5511157; PMID:2982104
A;Accession: A03974
A;Molecule type: DNA
A;Residues: 1-856 <MBE>
A;Cross-references: GB:K02083; NID:g555008; PIDN:AA59873.1; PID:g328559
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.2%; Score 175; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 1 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 37
Db 553 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 589
RESULT 8
VCLUTL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Main-Hobson, S.; Sonigo, P.; Damos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <MAI>
A;Cross-references: GB:K02013; NID:g326417; PIDN:AA59751.1; PID:g326424
C;Genetics:

A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 96.2%; Score 175; DB 1; Length 861;
Best Local Similarity 97.3%; Pred. No. 1.8e-15;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 1 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 37
Db 558 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 594
RESULT 9
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S70420; S22006
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <STE1>
A;Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A;Experimental source: Patient L
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type B retrovirus env polyprotein
Query Match 95.6%; Score 174; DB 2; Length 357;
Best Local Similarity 94.6%; Pred. No. 9.3e-16;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Query 1 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 37
Db 54 NNTLRATIAEQHLLQTLTWGKIKOLQARILAVERYLKD 90
RESULT 10
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 27B
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C;Accession: S21994; S70421
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A;Reference number: S21990
A;Accession: S21994
A;Molecule type: DNA
A;Residues: 1-357 <STE1>
A;Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A;Cross-references: EMBL:X61355; NID:g60179
C;Superfamily: type B retrovirus env polyprotein
Query Match 95.6%; Score 174; DB 2; Length 357;

Best Local Similarity 94.6%; Pred. No. 9.3e-16;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 54 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYLKD 90

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1

S22004

C/Species: human immunodeficiency virus type 1, HIV-1

A/Variety: isolate 48

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C/Accession: S22004; S70419

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990

A/Accession: S22004

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-357 <STE1>

A/Cross-references: EMBL:X61353; NID:g60186; PIDN:CAA43618.1; PID:g60189

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A/Reference number: S70417; PMID:92144209; PMID:1736940

A/Accession: S70419

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-292, 'X', 294-357 <STE2>

A/Cross-references: EMBL:X61353; NID:g60188

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.6%; Score 174; DB 2; Length 357;

Best Local Similarity 94.6%; Pred. No. 9.3e-16;

Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 54 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYLKD 90

RESULT 12
envelope protein gp120/gp41 - human immunodeficiency virus type 1

S22002

C/Species: human immunodeficiency virus type 1, HIV-1

A/Variety: isolate 3L

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C/Accession: S22002; S70418

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990

A/Accession: S22002

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-358 <STE1>

A/Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A/Reference number: S70417; PMID:92144209; PMID:1736940

A/Accession: S70418

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-333, 'X', 335-358 <STE2>

A/Cross-references: EMBL:X61352; NID:g60186

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.6%; Score 174; DB 2; Length 358;

Best Local Similarity 94.6%; Pred. No. 9.3e-16;

Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYLKD 91

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1

S22000

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

C/Accession: S22000

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990

A/Accession: S22000

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-358 <STE>

A/Cross-references: EMBL:X61351

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.6%; Score 174; DB 2; Length 358;

Best Local Similarity 94.6%; Pred. No. 9.3e-16;

Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYLKD 91

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)

S70417

C/Species: human immunodeficiency virus type 1, HIV-1

A/Variety: patient 3B

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

C/Accession: S70417

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A/Reference number: S70417; PMID:92144209; PMID:1736940

A/Accession: S70417

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-358 <STE>

A/Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185

C/Superfamily: type E retrovirus env polypeptide

Query Match 95.6%; Score 174; DB 2; Length 358;

Best Local Similarity 94.6%; Pred. No. 9.3e-16;

Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 55 NNLRAIEAQOHLQLTWQIKOLQARVLAVERYLKD 91

RESULT 15
envelope protein gp120/gp41 - human immunodeficiency virus type 1

S21990

C/Species: human immunodeficiency virus type 1, HIV-1

A/Variety: isolate 20

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C/Accession: S21990; S70423

R/Seuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A/Reference number: S21990

A/Accession: S21990

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-357 <STE1>

A/Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A;Reference number: S70417; MUID:92144209; PMID:11736940
A;Accession: S70423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332, 'X', 334-357 <STE2>
A;Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
C;Superfamily: type E retrovirus env polyprotein

Query Match 94.5%; Score 172; DB 2; Length 357;
Best Local Similarity 91.9%; Pred. No. 1,7e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLKD 37
Db 54 NNILRAIEAQOHMLQLTWGIKOLQARVLAVERYLKD 90

RESULT 16

VCLJMN
env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: A28922
R;Gurgio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A>Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3365091
A;Accession: A28922
A;Molecule type: DNA
A;Residues: 1-859 <GUR>
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-253/Product: signal sequence #status predicted <SIG>
F;30-859/Product: env polyprotein #status predicted <EPF>
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 94.5%; Score 172; DB 1; Length 859;
Best Local Similarity 91.9%; Pred. No. 4.5e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLKD 37
Db 557 NNILRAIEAQOHMLQLTWGIKOLQARVLAVERYLKD 593

RESULT 17

C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: C41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: C41621
A;Molecule type: DNA
A;Residues: 1-443 <BUR>
A;Cross-references: GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:G555015
A;Note: this virus was isolated from the mother's sexual partner
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;424-443/Domain: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 94.0%; Score 171; DB 2; Length 443;
Best Local Similarity 91.9%; Pred. No. 3e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLKD 37
Db 293 NNILRAIEAQOHMLQLTWGIKOLQARVLAVERYLKD 329

RESULT 18

A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: A41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: A41621
A;Molecule type: DNA
A;Residues: 1-445 <BUR>
A;Cross-references: GB:M77228; NID:G328627; PIDN:AAB03790.1; PID:G555013
A;Note: this virus was isolated from the mother
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/Domain: transmembrane #status predicted <TMN>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 94.0%; Score 171; DB 2; Length 445;
Best Local Similarity 91.9%; Pred. No. 3e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLKD 37
Db 295 NNILRAIEAQOHMLQLTWGIKOLQARVLAVERYLKD 331

RESULT 19

B41621
env polyprotein D - human immunodeficiency virus type 1 (fragment)
N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
C;Accession: B41621
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:11763038
A;Accession: B41621
A;Molecule type: DNA
A;Residues: 1-454 <BUR>
A;Cross-references: GB:M77279
A;Note: this virus was isolated from the daughter
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F:1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:263-554/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:435-454/Domin: transmembrane #status predicted <TM>
F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo

Query Match 94.0%; Score 171; DB 2; Length 454;
Best Local Similarity 91.9%; Pred. No. 3.1e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 304 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 340

RESULT 20
VCLJXK
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp32

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992

A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587

A:Accession: B42995
A:Molecule type: mRNA

A:Residues: 1-729 <SH1>
A:Cross-references: GB:S41266; GB:D01206

C:Genetics:
A:Gene: env

C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domin: extracellular #status predicted <EXT>
F:1-33/Domin: signal sequence #status predicted <SIG>

F:17-33/Region: hydrophobic #status predicted <CP1>
F:34-517/Product: coat protein gp120 #status predicted <CP2>

F:514-517/Region: cleavage processing #status predicted <CP2>
F:518-729/Product: coat protein gp32 #status predicted <CP2>

F:538-534/Region: hydrophobic #status predicted <TM1>
F:690-711/Domin: transmembrane #status predicted <INT>
F:712-729/Domin: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,308,338,345,361,367,397,403,408,414

Query Match 94.0%; Score 171; DB 1; Length 729;
Best Local Similarity 91.9%; Pred. No. 5.1e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 37
Db 559 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 595

RESULT 21
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)

N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C:Accession: H44001

R:Li, Y.; Hu, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605

A:Accession: H44001
A:Molecule type: DNA

A:Residues: 1-843 <LTY>
A:Cross-references: GB:M93258

C:Genetics:

A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-29/Domin: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic

F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-493/Product: coat protein gp41 #status predicted <GP2>

F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domin: transmembrane #status predicted <TM>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,

Query Match 94.0%; Score 171; DB 1; Length 843;
Best Local Similarity 91.9%; Pred. No. 6e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 37
Db 540 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 576

RESULT 22
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00066

R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunoc
A:Reference number: J00065; MUID:90034200; PMID:2806917

A:Accession: J00066
A:Molecule type: DNA

A:Residues: 1-846 <SE1>
A:Cross-references: GB:M2723; NID:G328154; PIDN:AAA44873.1; PID:G328162

A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env

C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-29/Domin: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>

F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domin: transmembrane #status predicted <TM1>

F:574-692/Domin: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606,

Query Match 94.0%; Score 171; DB 1; Length 846;
Best Local Similarity 91.9%; Pred. No. 6e-15;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 37
Db 543 NNTLRATIAOQHLLQTLTWGKIQOLQARVLAVERLYKD 579

RESULT 23
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: Z17379; MUID:9818716; PMID:9519894

A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DDDU

A:Molecule type: DNA
A:Residues: 1-852 <MCC>

A/Cross-references: EMBL:U90934; NID:92351783; PIDN:AAC59271.1; PID:92351784
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

Query Match 94.0%; Score 171; DB 2; Length 852;
 Best Local Similarity 91.9%; Pred. No. 6.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 549 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 585

RESULT 24
 VCLJAZ
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1
 A/Note: host Homo sapiens (man)
 C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C/Accession: A03976
 R/Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-SH
 Science 227, 484-492, 1985
 A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
 A/Reference number: A04003; MUID:85090453; PMID:2578227

A/Accession: A03976

A/Molecule type: DNA

A/Residues: 1-855 <SAN>

A/Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F/1-30/Domain: signal sequence #status predicted <SIG>

F/1-509/Product: extrinsic membrane glycoprotein #status predicted <EXT>

F/510-855/Product: transmembrane glycoprotein #status predicted <TM>

F/87,129,140,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,458

F/610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.0%; Score 171; DB 1; Length 855;
 Best Local Similarity 91.9%; Pred. No. 6.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 552 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 588

RESULT 25
 VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMU1)

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

C/Accession: A24774

R/Starchich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986

A/Title: Identification and characterization of conserved and variable regions in the en

A/Reference number: A24774; MUID:86218077; PMID:2423250

A/Accession: A24774

A/Molecule type: DNA

A/Residues: 1-856 <SRA>

A/Cross-references: GB:K03455; GB:M38432; NID:g1906382

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-501/Product: coat protein gp120 #status predicted <GP1>

F/502-847/Product: coat protein gp41 #status predicted <GP2>

F/87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,458

Query Match 94.0%; Score 171; DB 1; Length 856;
 Best Local Similarity 91.9%; Pred. No. 6.1e-15;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 553 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 589

RESULT 26

A44963

env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999

C/Accession: A44963

R/Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989

A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc

A/Reference number: A44963; MUID:89228766; PMID:2713163

A/Accession: A44963

A/Molecule type: DNA

A/Residues: 1-856 <SRI>

A/Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-520/Product: coat protein gp120 #status predicted <CP1>

F/521-856/Product: coat protein gp41 #status predicted <CP2>

F/684-705/Domain: transmembrane #status predicted <TM>

F/87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 94.0%; Score 171; DB 1; Length 856;
 Best Local Similarity 94.6%; Pred. No. 6.1e-15;
 Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 553 NNTLRATEAOQHLLQTLTWQIKOLQARILAVERYLKD 589

RESULT 27
 VCLJKB
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N/Alternate names: coat polyprotein

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992

A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t

A/Reference number: A42995; MUID:92351552; PMID:1322587

A/Accession: A42995

A/Molecule type: mRNA

A/Residues: 1-861 <SHI>

A/Cross-references: GB:S41266; GB:D01206

C/Genetics:

A/Gene: env

C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F/1-689/Domain: extracellular #status predicted <EXT>

F/1-33/Region: signal sequence #status predicted <SIG>

F/34-517/Product: coat protein gp120 #status predicted <CP1>

F/514-517/Region: cleavage processing #status predicted <CP2>

F/518-861/Product: coat protein gp41 #status predicted <CP2>

F/518-534/Region: hydrophobic #status predicted

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 6.03261 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-147
Perfect score: 182
Sequence: 1 NMLRAIEAQHLLQLTWQIKQLQARIILAVERYLKD 37

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	96.2	853	ENV_HV1EL	P04581 human immun
2	175	96.2	853	ENV_HV1MP	P19551 human immun
3	175	96.2	853	ENV_HV122	P12487 human immun
4	175	96.2	855	ENV_HV126	P04580 human immun
5	175	96.2	856	ENV_HV1B1	P03375 human immun
6	175	96.2	856	ENV_HV1H2	P04578 human immun
7	175	96.2	856	ENV_HV1H3	P04624 human immun
8	175	96.2	856	ENV_HV1LM	Q70626 human immun
9	175	96.2	856	ENV_HV1PV	P03376 human immun
10	175	96.2	861	ENV_HV1BR	P03377 human immun
11	174	95.6	847	ENV_HV1S1	P19550 human immun
12	174	95.6	855	ENV_HV1OY	P20887 human immun
13	172	94.5	848	ENV_HV1UR	P20887 human immun
14	172	94.5	856	ENV_HV1MN	P05877 human immun
15	171	94.0	843	ENV_HV1Y2	P35961 human immun
16	171	94.0	846	ENV_HV1ND	P18799 human immun
17	171	94.0	851	ENV_HV1B8	P04582 human immun
18	171	94.0	852	ENV_HV1S3	P19549 human immun
19	171	94.0	855	ENV_HV1A2	P03378 human immun
20	171	94.0	856	ENV_HV1SC	P05878 human immun
21	171	94.0	856	ENV_HV1W1	P31872 human immun
22	171	94.0	856	ENV_HV1ZH	P05881 human immun
23	171	94.0	861	ENV_HV1KH	P31819 human immun
24	171	94.0	865	ENV_HV1RH	P04579 human immun
25	171	94.0	867	ENV_HV1C3	P12489 human immun
26	171	94.0	868	ENV_HV1C4	P05879 human immun
27	170	93.4	859	ENV_HV1MA	P04583 human immun
28	168	92.3	847	ENV_HV1W2	P05880 human immun
29	166	91.2	863	ENV_HV1Z8	P05882 human immun
30	163	89.6	852	ENV_HV1BN	P12488 human immun
31	160	87.9	854	ENV_SIVCZ	P17281 chimpanzee
32	120	65.9	865	ENV_SIVAT	P05886 simian immu
33	120	65.9	877	ENV_SIVAG	P27977 simian immu

34	117	64.3	854	1	ENV_SIVAI	O02837 simian immu
35	111	61.0	768	1	ENV_SIVAI	P27757 simian immu
36	108	59.3	712	1	ENV_HV2S2	P32536 human immun
37	108	59.3	851	1	ENV_HV2D1	P17755 human immun
38	108	59.3	851	1	ENV_HV2G1	P18040 human immun
39	108	59.3	856	1	ENV_HV2NZ	P05883 human immun
40	108	59.3	859	1	ENV_HV2ST	P20872 human immun
41	107	58.8	859	1	ENV_HV2CA	P24105 human immun
42	106	58.2	380	1	ENV_SIVM2	P08810 simian immu
43	106	58.2	858	1	ENV_HV2RO	P04577 human immun
44	106	58.2	885	1	ENV_SIVS4	P12492 simian immu
45	106	58.2	889	1	ENV_SIVSP	P19503 simian immu
46	105	57.7	882	1	ENV_SIVM1	P05885 simian immu
47	104	57.1	859	1	ENV_HV2D2	P15831 human immun
48	103	56.6	880	1	ENV_SIVM	P11267 simian immu
49	102	56.0	821	1	ENV_SIVGB	P22360 simian immu
50	102	56.0	846	1	ENV_HV2SB	P12449 human immun
51	102	56.0	860	1	ENV_HV2BE	P18094 human immun
52	102	56.0	881	1	ENV_SIVWK	P05884 simian immu
53	101	55.5	857	1	ENV_HV2KR	Q74126 human immun
54	53	29.1	2564	1	SPCQ_HUMAN	Q9h254 homo sapien
55	52	28.6	1379	1	M3K5_MOUSE	Q35099 mus musculu
56	52	28.0	1938	1	MYH4_MOUSE	Q28641 oryctolagus
57	51	28.0	1411	1	BEA1_HUMAN	Q15075 homo sapien
58	50	27.5	1374	1	M3K5_HUMAN	Q99663 homo sapien
59	50	27.5	1938	1	MYH4_HUMAN	P24723 aequipecten
60	50	27.5	1939	1	MYH4_AEQIR	Q9y623 homo sapien
61	49.5	27.2	445	1	EX7L_STRAM	Q99KX0 staphylococ
62	49.5	27.2	581	1	FRIZ_DROME	P18537 drosophila
63	49.5	27.2	583	1	FRIZ_DROVI	Q24760 drosophila
64	49	26.9	236	1	GT6_SCHNA	P46435 schistosoma
65	49	26.9	1756	1	PEPL_HUMAN	O60437 homo sapien
66	49	26.9	4349	1	DYHC_FUSO	P78736 fusarium so
67	49	26.9	8797	1	SNE1_HUMAN	O8nf91 homo sapien
68	48.5	26.6	790	1	BEA1_MOUSE	O8b166 mus musculu
69	48	26.4	551	1	YD25_YEAST	Q07657 saccharomyc
70	48	26.4	702	1	AT11_VARI	P34011 variola vir
71	48	26.4	906	1	CTN1_HUMAN	P35221 homo sapien
72	48	26.4	906	1	CTN1_MOUSE	P26231 mus musculu
73	48	26.4	1935	1	MYSS_CYPCA	Q90339 cyprinus ca
74	47.5	26.1	74	1	CYSH_VIRCH	O9KX22 vibrio chol
75	47.5	26.1	303	1	ALB3_MAIZE	P10593 zea mays (m
76	47.5	26.1	467	1	EUTE_ECOLI	P77445 escherichia
77	47.5	26.1	467	1	EUTE_SALTY	P41793 salmonella
78	47.5	26.1	924	1	HXK3_RAT	P27996 rattus norv
79	47.5	26.1	962	1	ARVC_HUMAN	O00132 homo sapien
80	47.5	26.1	969	1	ARVC_MOUSE	P98293 mus musculu
81	47.5	26.1	1319	1	SOS1_MOUSE	Q62245 mus musculu
82	47.5	26.1	1333	1	SOS1_HUMAN	Q07889 homo sapien
83	47.5	26.1	1955	1	PUMA_PARUN	O61308 parascaris
84	47	25.8	376	1	O43A_DROME	P11917 drosophila
85	47	25.8	418	1	DAD1_RHILIO	Q98F08 rhizobium 1
86	47	25.8	684	1	RPOC_MARPO	P06273 marchantia
87	47	25.8	1941	1	MYH2_HUMAN	Q9UKK2 homo sapien
88	46.5	25.5	132	1	RSB_CLOAB	Q97632 clostridium
89	46.5	25.5	1093	1	AF17_HUMAN	P51198 homo sapien
90	46.5	25.5	1583	1	GCC2_HUMAN	Q9liw2 homo sapien

ALIGNMENTS

RESULT 1
ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DB glycoprotein (GP120); Transmembrane glycoprotein (GP41).
GN ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).

CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 CC NCBI_TaxID=11689;
 CC [1]
 CC MEDLINE=66245056; PubMed=2424612;
 CC Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 CC "Genetic variability of the AIDS virus: nucleotide sequence analysis
 CC of two isolates from African patients";
 CC Cell 46:63-74(1986).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K03454; AAA44329.1; -;
 CC EMBL; A07108; CA00616.1; -;
 CC HIV; K03454; ENVSELI.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam; PF00516; GP120; 1.
 CC Pfam; PF00517; GP41; 1.
 CC DR
 CC AIDS; Coat protein; Glycoprotein; Transmembrane;
 CC Signal.
 CC
 CC FT SIGNAL 1 31 BY SIMILARITY.
 CC CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 CC FT 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 CC FT DISULFID 53 73 BY SIMILARITY.
 CC FT DISULFID 118 206 BY SIMILARITY.
 CC FT DISULFID 125 197 BY SIMILARITY.
 CC FT DISULFID 130 154 BY SIMILARITY.
 CC FT DISULFID 219 248 BY SIMILARITY.
 CC FT DISULFID 229 240 BY SIMILARITY.
 CC FT DISULFID 297 330 BY SIMILARITY.
 CC FT DISULFID 376 442 BY SIMILARITY.
 CC FT DISULFID 383 416 BY SIMILARITY.
 CC FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 129 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 853 AA; 96721 MW; PSCD864DAAD0707A5 CMC64;
 CC Query Match 96.2%; Score 175; DB 1; Length 853;

Best Local Similarity 97.3%; Pred. No. 1.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NMLRAIEAQHLLQTLTWQIKQLQARILAVERYLD 37
 Db 550 NMLRAIEAQHLLQTLTWQIKQLQARILAVERYLD 586
 RESULT 2
 ENV_HVLMF ID ENV_HVLMF STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 CC NCBI_TaxID=11704;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=90317877; PubMed=1695254;
 CC Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
 CC Wasiak A.;
 CC "Cloning and characterization of human immunodeficiency virus type 1
 CC variants diminished in the ability to induce syncytium-independent
 CC cytolysis";
 CC J. Virol. 64:3792-3803 (1990).
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M33943; AAA44850.1; -;
 CC PDB; 1A1K; 16-JUN-97.
 CC HIV; M33943; ENVSMFA.
 CC InterPro: IPR000328; Env GP41.
 CC InterPro: IPR000777; GP120.
 CC Pfam; PF00516; GP120; 1.
 CC Pfam; PF00517; GP41; 1.
 CC DR
 CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 CC 3D-structure.
 CC
 CC FT SIGNAL 1 30
 CC CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 CC FT 510 853 TRANSMEMBRANE GLYCOPROTEIN.
 CC FT DISULFID 54 74 BY SIMILARITY.
 CC FT DISULFID 119 203 BY SIMILARITY.
 CC FT DISULFID 126 194 BY SIMILARITY.
 CC FT DISULFID 131 157 BY SIMILARITY.
 CC FT DISULFID 216 245 BY SIMILARITY.
 CC FT DISULFID 226 237 BY SIMILARITY.
 CC FT DISULFID 294 329 BY SIMILARITY.
 CC FT DISULFID 376 443 BY SIMILARITY.
 CC FT DISULFID 383 416 BY SIMILARITY.
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 CC FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 CC FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22A8A CRC64;

Query Match 96.2%; Score 175; DB 1; Length 853;
 Best Local Similarity 97.3%; Pred. No. 1.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
 DB 551 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 587

RESULT 3
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RA Submitted (NOV-1988) to the HIV data bank.

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 CC -----
 DR EMBL; M22639; AAA45370.1; -.
 DR PIR; S54384; S54384.
 DR HIV; M22639; ENV52226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT CHAIN 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.

FT DISULFID 383 415 BY SIMILARITY.
 FT CARBOHYD . 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 97043 MW; 849B08CBAFF7008 CRC64;

Query Match 96.2%; Score 175; DB 1; Length 853;
 Best Local Similarity 97.3%; Pred. No. 1.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
 DB 550 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 586

RESULT 4
 ID ENV_HV126 STANDARD; PRT; 855 AA.
 AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-JUL-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87248097; PubMed=3036660;
 RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
 RA Schuchman G., Curran J., Kalyanaraman V.S., Luthi P.A.,
 RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
 RT Gene 52:71-82 (1987).
 RL Gene 52:71-82 (1987).
 CC -----
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 CC -----

[illegible][illegible]

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FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931B327 CRC64;

Query Match 96.2%; Score 175; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 1,8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLLRAIEAQQHLLQLTWGKIKQLARILAVERYLKD 37
553 NNLLRAIEAQQHLLQLTWGKIKQLARILAVERYLKD 589

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; O09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; Pubmed=3040055;
RA Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN REVISIONS.
RA Rattner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF038199; AAC82596.1; -
DR PDB; 1DF4; 2C-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DLB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.

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DR Pfam; PF00516; GP120, 1.
DR Pfam; PF00517; GP41, 1.
KM AIDS; Goat protein; Polypeptide; Transmembrane; Signal; 3D-structure.
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FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
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FT DISULFID 385 418
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FT CARBOHYD 230 230
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FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match 96.2%; Score 175; DB 1; Length 856;
Best Local Similarity 97.3%; Pred. No. 1,8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 NNLLRAIEAQQHLLQLTWGKIKQLARILAVERYLKD 37
553 NNLLRAIEAQQHLLQLTWGKIKQLARILAVERYLKD 589

RESULT 7
ENV_HV1H3 STANDARD; PRT; 856 AA.
ID ENV_HV1H3
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=85228248; PubMed=2988795;
 RA Crowl R., Ganguly R., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-III env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients";
 RL Cell 41:979-986(1985).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M14100; AAA4679.1; -;
 DR PDB; 1JAV; 17-OCT-01.
 DR HIV; M14100; ENV\$HXB3.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
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 Query March 96.2%; Score 175; DB 1; Length 856;
 Best Local Similarity 97.3%; Pred. No. 1.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 553 NLLRAIEAOQHLLQTLTWQIKOLQARILAVERYLKD 589
 RESULT 8
 ENV_HV1LM STANDARD; PRT; 856 AA.
 ID ENV_HV1LM
 AC Q70626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U12055; AAA7690.1; -;
 DR PDB; 1IF3; 02-MAY-01.
 DR GlycoSiteDB; Q70626; -;
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 512 856
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 FT DISULFID 126 196
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FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRLAEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 553 NNLRLAEAOQHLLQTLTWQIKOLQARILAVERYLKD 589
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 ENV_HVLPV STANDARD; PRT; 856 AA.
 ID _ENV_HVLPV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NC NCB1_Taxid=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=8511157; Pubmed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laasy L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
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 CC -----
 CC EMBL: K02083; AAB59873.1; -;
 DR EMBL: X01762; CA25903.1; ALT_SEQ.
 DR PTR: A03974; VCLJVL.
 DR HIV: K02083; ENV:PV22.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 30
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 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
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 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.
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 FT DISULFID 378 445 BY SIMILARITY.
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 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCBD1DC3C1209B3 CRC64;
 Query Match 96.2%; Score 175; DB 1; Length 856;
 Best Local Similarity 97.3%; Pred. No. 1.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRLAEAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 Db 553 NNLRLAEAOQHLLQTLTWQIKOLQARILAVERYLKD 589
 RESULT 10
 ENV_HVLPV STANDARD; PRT; 861 AA.
 ID _ENV_HVLPV
 AC P03377;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NC NCB1_Taxid=11686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=8509333; Pubmed=2981635;
 RA Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV.";
 RL Cell 40:9-17(1985).
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 CC -----

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CC -----
DR EMBL; K02013; AAB59751.1; -.
DR EMBL; A04321; CA000352.1; -.
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV$BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL 1 30
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Query Match 96.2%; Score 175; DB 1; Length 861;
Best Local Similarity 97.3%; Pred. No. 1.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRLRAEAOOHLLQLTVMQIKQALRIAVERYLKD 37
Db 558 NNLRLRAEAOOHLLQLTVMQIKQALRIAVERYLKD 594

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP150 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN Env.
OS Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RT J. Virol. 64:4390-4398(1990).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M65024; AAA45072.1; -.
DR PDB; IOBE; 15-MAY-97.
DR HIV; M38428; ENV$SF162.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT CARBOHYD 503 847
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
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SQ SEQUENCE 847 AA; 96135 MW; 0A901317ED7FE2AB CRC64;

Query Match 95.6%; Score 174; DB 1; Length 847;
Best Local Similarity 94.6%; Pred. No. 2.4e-16;

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FT	CARBOHYD	399	399	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	610	610	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .)	(POTENTIAL).
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FT	CARBOHYD	636	636	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. . .)	(POTENTIAL).
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Db	Matches 35;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
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552	NNLLRLALEAOOHLLOLTFWQIKQLOARVLAVERYLKD	588			
RESULT 13					
ID	ENV_HV1JR	STANDARD;	PRT;	848 AA.	
AC	P20871;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.				
OX	NCBI_TaxID=11688;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Koyanagi S., Chen I.S.Y.;				
RL	Submitted (DEC-1988) to the HIV data bank.				
CC	-----				
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CC	-----				
DR	EMBL; M38429; AAB03749.1; -.				
DR	PDB; 1CE4; 18-MAR-99.				
DR	HIV; M38429; ENVJRCSF.				
DR	InterPro; IPR000328; Env GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal; 3D-structure.				
FT	SIGNAL	1	32		
FT	CHAIN	33	503		
FT	CHAIN	504	848		
FT	DISULFID	53	73		
FT	DISULFID	118	203		
FT	DISULFID	125	194		
FT	DISULFID	130	154		
FT	DISULFID	216	245		
FT	DISULFID	226	237		
FT	DISULFID	294	328		
FT	DISULFID	374	437		
FT	DISULFID	381	410		
FT	CARBOHYD	87	87		
FT	CARBOHYD	134	134		
FT	CARBOHYD	137	137		

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 848 AA; 96475 MW; 20767F5127EC3F9 CRC64;

Query Match 94.5%; Score 172; DB 1; Length 848;
 Best Local Similarity 91.9%; Pred. No. 4.6e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37
 Db 545 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 581

RESULT 14
 ENV_HV1MN STANDARD; PRT; 856 AA.

AC P05877;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11696;

RP SEQUENCE FROM N.A.
 RX MEDLINE=88219542; PubMed=3369091;
 RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal P., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS PATIENT IN 1984.

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CC EMBL; M17449; AAA44857.1; -
 DR PDB; 1ACJ; 31-JUL-94.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1N12; 25-FEB-03.
 DR PDB; 1NU0; 25-FEB-03.
 DR HIV; M17449; ENVSMN.

DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure; 1
 FT SIGNAL 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 445
 FT DISULFID 388 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 141 141
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT CARBOHYD 202 202
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 336 336
 FT CARBOHYD 343 343
 FT CARBOHYD 359 359
 FT CARBOHYD 365 365
 FT CARBOHYD 395 395
 FT CARBOHYD 401 401
 FT CARBOHYD 405 405
 FT CARBOHYD 413 413
 FT CARBOHYD 448 448
 FT CARBOHYD 465 465
 FT CARBOHYD 612 612
 FT CARBOHYD 617 617
 FT CARBOHYD 626 626
 FT CARBOHYD 638 638
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match 94.5%; Score 172; DB 1; Length 856;
 Best Local Similarity 91.9%; Pred. No. 4.6e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37
 Db 554 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 590

RESULT 15
 ENV_HV1Y2 STANDARD; PRT; 843 AA.

AC P35961;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;

Query Match	Similarity	Score	DB	Length
Best	94.0%	171	DB 1	843
Local	91.9%	6.3e-16		
Matches	34	Conservative	2	Mismatches
			1	Indels
			0	Gaps
			0	

oy	1	NNLRAIEAOQHLLQLTWNGIKLOARITLAVEREYKLD	37
Dd	540	NNLRAIEAOQHLLQLTWNGIKLOARIVAVERTLRD	576


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RESULT_16
ID ENV_HVIND STANDARD; PRT;      846 AA.
AC p18799;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Vitruvius; Retroviridae; Lentivirus.
OX NCBI_Taxid=11695;
RN [1]
RX SEQUENCE FROM N.A. MEDLINE=90034200; PubMed=2806917;
RA Spire B.; Site J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
RA Hampe A.; Chermann J.C.;
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the
RL human immunodeficiency virus." ;
Gene 81:275-284(1989).
CC CC
CC -1. MISCELLANEOUS: NDK. ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
-----
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or send an email to license@isb-sib.ch).
CC CC
DR EMBL/M27323; AAA44873.1; -.
DR PIR/J00066; VLCJND.
DR HIV/M27323; ENVSNDK.
DR InterPro/IPR000328; Env_GP41.
DR InterPro/IPRO00777; GP120.
DR Pfam/PF00516; GP120; 1.
DR Pfam/PFO0517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycopoltein; Transmembrane;
Signal.
KW Signal.
FT FT          1        29
FT CHAIN       30     501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN       502     846 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID    53         73 BY SIMILARITY.
FT DISULFID   118        200 BY SIMILARITY.
FT DISULFID   125        191 BY SIMILARITY.
FT DISULFID   130        152 BY SIMILARITY.
FT DISULFID   213        242 BY SIMILARITY.
FT DISULFID   223        234 BY SIMILARITY.
FT DISULFID   291        328 BY SIMILARITY.
FT DISULFID   374        435 BY SIMILARITY.
FT DISULFID    381        408 BY SIMILARITY.
FT CARBOHYD    87         87 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   129        129 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   151        151 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   179        179 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   182        182 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   229        229 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   236        236 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   257        257 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   271        271 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   284        284 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   290        290 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   351        351 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   382        382 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD   388        388 N-LINKED (GLCNAC. . ) (POTENTIAL).
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2B83 CRC64;
 Query Match 94.0%; Score 171; DB 1; Length 846;
 Best Local Similarity 91.9%; Pred. No. 6.3e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQTLTWQIKQARILAVERYLKD 37
 DB 543 NNLRAIEAQOHLQTLTWQIKQARILAVERYLKD 579
 RESULT 17
 ID ENV_HV1B8 STANDARD; PRT; 851 AA.
 AC P04582;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11684;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Chirayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III." Nature 313:277-284(1985).
 RL Nature 313:277-284(1985).
 CC -----
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 CC -----
 CC EMBL; K02011; AAA4461.1; -.
 DR PDB; 1DDH; 13-JAN-99.
 DR PDB; 1HHG; 31-OCT-93.
 DR PDB; 1QO3; 02-JAN-00.
 DR PDB; 1S2T; 24-DEC-97.
 DR HIV; K02011; ENVSBB8.
 DR Glycosylated; P04582; -.
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 1 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.

FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 231 BY SIMILARITY.
 FT DISULFID 296 339 BY SIMILARITY.
 FT DISULFID 378 440 BY SIMILARITY.
 FT DISULFID 385 413 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
 Query Match 94.0%; Score 171; DB 1; Length 851;
 Best Local Similarity 94.6%; Pred. No. 6.3e-16;
 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQTLTWQIKQARILAVERYLKD 37
 DB 548 NNLRAIEAQOHLQTLTWQIKQARILAVERYLKD 584
 RESULT 18
 ID ENV_HV1S3 STANDARD; PRT; 852 AA.
 AC P15549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317906; PubMed=2370688;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RA "Human immunodeficiency virus type 1 cellular host range," replication, and cytopathicity are linked to the envelope region of the viral genome." J. Virol. 64:4016-4020(1990).
 RL J. Virol. 64:4016-4020(1990).
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 CC -----

SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
 Query Match 94.0%; Score 171; DB 1; Length 855;
 Best Local Similarity 91.9%; Pred. No. 6,4e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLTLTWQIKOLQARVLAVERYLKD 37
 DB 552 NNILRAIEAQOHLTLTWQIKOLQARVLAVERYLKD 588

RESULT 20
 ENV_HV1SC STANDARD; PRT; 856 AA.
 ID ENV_HV1SC
 AC P05878;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88219542; PubMed=3369091;
 RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Rietz M.S., Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN 1984 IN SOUTHERN CALIFORNIA.
 CC -----
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 CC -----
 CC EMBL, M17450; -; NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 30 510 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 511 856 IN-FRAME TERMINATION CODON.
 FT SITE 760 760
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 SQ SEQUENCE 856 AA; 97055 MW; DAF4DA60EBA7A08 CRC64;

Query Match 94.0%; Score 171; DB 1; Length 856;
 Best Local Similarity 91.9%; Pred. No. 6,4e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLTLTWQIKOLQARVLAVERYLKD 37
 DB 553 NNILRAIEAQOHLTLTWQIKOLQARVLAVERYLKD 589

RESULT 21
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 ID ENV_HV1M1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MMU1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86218077; PubMed=2423250;
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."
 RT AIDS. 45:637-648(1986).
 RL Cell 45:637-648(1986).
 CC -1- MISCELLANEOUS: ISOLATES MMU1, MMU2, AND MMU3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
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 CC PIR: A24774; VCLJ3W.
 DR PDB; 1LBO; 04-DEC-02.
 DR PDB; 1LCK; 04-DEC-02.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 KM SIGNAL.
 FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 30 510 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.


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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
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SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C0404DE5 CRC64;

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Query Match 94.0%; Score 171; DB 1; Length 856;
Best Local Similarity 91.9%; Pred. No. 6,4e-16;
Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 553 NNTLRATEAOOHLTLTWQIKOLQARITLAVERYLKD 37
1 NNTLRATEAOOHLTLTWQIKOLQARITLAVERYLKD 589
ENV_HV1ZH STANDARD; PRT: 856 AA.
AC P05881;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H3231 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11692;
RN SEQUENCE FROM N.A.
RP MEDLINE=69228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D., Jannoun-Naser R., Getchell J.,
McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
RT generation of hybrid HIV.";
RL AIDS Res. Hum. Retroviruses 5:121-129 (1989).

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DR EMBL; M15896; AAB53948.1; -
DR PIR; A44963; A44963.
DR HIV; M15896; ENV52321.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 511
FT CHAIN 512 856
FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 153
FT DISULFID 219 248
FT DISULFID 229 240
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FT DISULFID 379 445
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FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 856 AA; 96909 MW; 8396B3F8BBD174E CRC64;

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Query Match 94.0%; Score 171; DB 1; Length 856;
Best Local Similarity 94.6%; Pred. No. 6,4e-16;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 553 NNTLRATEAOOHLTLTWQIKOLQARITLAVERYLKD 37
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ENV_HV1KB STANDARD; PRT: 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (XB-1 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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NCBI_TaxID=36375;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=9231552; PubMed=1322587;
 Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
 Kitanura T.,
 "Analysis of a human immunodeficiency virus type 1 isolate carrying a
 truncated transmembrane glycoprotein."
 Virology 189:534-546(1992).
 -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
 THE CODONS FOR 729-ALA AND 730-ARG.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; D12582; BAA02124.1; ALT_SEQ.
 PIR; A42995; VCLJKB.
 InterPro; IPR000328; Env GP41.
 InterPro; IPR000777; GP120.
 Pfam; PF00516; GP120; 1.
 Pfam; PF00517; GP41; 1.
 AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 signal.
 KW
 FT SIGNAL 1 35 POTENTIAL.
 FT CHAIN 36 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 518 861 TRANSMEMBRANE GLYCOPROTEIN.
 FT TRANSMEM 690 711 POTENTIAL.
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 FT DISULFID 136 160 BY SIMILARITY.
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Query Match 94.0%; Score 171; DB 1; Length 861;
 Best Local Similarity 91.9%; Pred. No. 6, 4e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQQHLLQTLTWQIQKOLARILAVERYLD 37
 DB 559 NNLRAIDAOQHLLQTLTWQIQKOLARILAVERYLD 595
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 AC P04579;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP120 precursor (Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66218077; PubMed=2423250;
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.,
 "Identification and characterization of conserved and variable
 regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 AIDS."
 RT Cell 45:637-648(1986).
 RL
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 EMBL; M17451; AAA5057.1; -.
 DR HIV; M17451; ENV\$RF.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 signal.
 KW
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 FT CHAIN 30 519 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 520 865 TRANSMEMBRANE GLYCOPROTEIN.
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 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCA6 CRC64;

Query Match 94.0%; Score 171; DB 1; Length 865;
 Best Local Similarity 91.9%; Pred. No. 6,4e-16;
 Matches 34; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLVWQIKOLQARILAVERYLKD 37
 Db 562 NNLRAIEAQOHLQTLVWQIKOLQARILAVERYLKD 598

ENV_HV1J3 STANDARD; PRT; 867 AA.

AC P12489; 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 ON NCBI_Taxid=11694;
 RX MEDLINE=69352108; PubMed=2669897;
 RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria."
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
 CC -----
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 CC -----
 CC EMBL; M21138; AB03526.1; -
 DR HIV; M21138; ENVJ3.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP41; 1.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM AIDS; Signal.
 FT SIGNAL. 1 30
 FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 217 BY SIMILARITY.
 FT DISULFID 125 208 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 230 259 BY SIMILARITY.
 FT DISULFID 240 251 BY SIMILARITY.
 FT DISULFID 308 342 BY SIMILARITY.
 FT DISULFID 388 457 BY SIMILARITY.
 FT DISULFID 395 430 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8B8680 CRC64;

Query Match 94.0%; Score 171; DB 1; Length 867;
 Best Local Similarity 94.6%; Pred. No. 6.5e-16;
 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQTLVWQIKOLQARILAVERYLKD 37
 Db 564 NNLRAIEAQOHLQTLVWQIKOLQARILAVERYLKD 600

ENV_HV1C4 STANDARD; PRT; 868 AA.

AC P05879; 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 ON NCBI_Taxid=11687;
 RX MEDLINE=87041461; PubMed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
 RA Andersen P.R., Devare S.G.;
 RT "Molecular cloning and primary nucleotide sequence analysis of a RT distinct human immunodeficiency virus isolate reveal significant RT divergence in its genomic sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RP SEQUENCE OF 34-43.

Query Match	Similarity	Score	DB	Length
Best Local	91.9%	Pred. 8.8e-16;		
Matches	34;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

DB	Sequence	Score	DB	Length
555	NNLRLATEAQOHLQLTWYQKCOLARLTAERYRYLKD 37	93.4%	DB 1;	Length 859;
	NNLRLATEAQOHLQLTWYQKCOLARLTAERYRYLKD 591			

Result	ID	ENV	ENV	STD	PRT	847	AA
ENV_HV1W2	ENV_HV1W2	STANDARD	PRT	847	AA		
AC	P05880						
DT	01-NOV-1988	(Rel. 09, Created)					
DT	01-NOV-1988	(Rel. 09, Last sequence update)					
DT	15-JUL-1999	(Rel. 38, Last annotation update)					
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120), Transmembrane glycoprotein (GP41)].						
GN	ENV.						
OS	Human immunodeficiency virus type 1 (WM2 isolate) (HIV-1).						
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.						
OX	NCBI_TaxID=11705;						
RA	Medline=86235450; PubMed=3012778;						
RA	Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;						
RT	"Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS."						
RL	Science 232:1548-1553(1986).						
CC	-1- MISCELLANEOUS: ISOLATES WM01, WM02, AND WM03 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						
CC	-----						
DR	EMBL, M12507; AAB12990.1; -.						
DR	HIV, M12507; ENVSMWJ2.						
DR	InterPro: IPR000328; Env GP41.						
DR	InterPro: IPR000777; GP120.						
DR	Pfam: PF00517; GP120.1.						
KW	AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; Signal.						
KW	SIGNAL.						
FT	CHAIN	1	29				
FT	CHAIN	30	501				
FT	CHAIN	502	847				
FT	DISULFID	53	73				
FT	DISULFID	118	202				
FT	DISULFID	125	193				
FT	DISULFID	130	152				
FT	DISULFID	215	244				
FT	DISULFID	225	236				

FT	CARBOHYD	364	364	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>368</td> <td>388</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	368	388	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>394</td> <td>394</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	394	394	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>406</td> <td>406</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>448</td> <td>448</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	448	448	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>460</td> <td>460</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	460	460	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>467</td> <td>467</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	467	467	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>613</td> <td>613</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	613	613	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>618</td> <td>618</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	618	618	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>627</td> <td>627</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	627	627	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>639</td> <td>639</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	639	639	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT <td>CARBOHYD</td> <td>819</td> <td>819</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	CARBOHYD	819	819	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	859	97109	MM; DBCF9AA5E3ABF29	CRC64;

Query Match	Best Local Similarity	Score 168; DB 1;	Length 847;
Matches 33;	Conservative 3;	Mismatches 1;	Indels 0; Gaps 0;
SO	SEQUENCE	847 AA; 96466 MW; CD133D73AA5BCAF CRC64;	
FT	DISULFID	293 326	BY SIMILARITY.
FT	DISULFID	372 435	BY SIMILARITY.
FT	DISULFID	379 408	BY SIMILARITY.
FT	CARBOHYD	87 87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	134 134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140 140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151 151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155 155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183 183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184 184	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	194 194	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	231 231	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	238 238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	259 259	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	273 273	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	286 286	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292 292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	327 327	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	334 334	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	350 350	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	356 356	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	380 380	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	386 386	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390 390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	602 602	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	607 607	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	616 616	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	628 628	N-LINKED (GLCNAC. . .) (POTENTIAL).
OY	1 NNTLRATEAOQHLLQLTWVOIKQLQALILAVERTLKD 37		
DB	544 NNTLRATAIDAOHLLQLTWVGIKQLQALILAVERTLKD 580		
ENV_HV128	STANDARD;	PRT;	863 AA.
AC	P05882;		
DT	01-NOV-1988 (Rel. 09, Created)		
DT	01-NOV-1988 (Rel. 09, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11681;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86281278; PubMed=3395517;		
RA	Younou J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F., Gallo R.C.;		
RT	"Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."		
RL	AIDS Res. Hum. Retroviruses 4:165-173(1988).		
CC	-1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.		
CC	-----		
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CC	or send an email to license@ebi.ac.uk .		

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CC -----
DR EMBL; J03653; AAA44684.1; -.
DR HIV; J03653; ENV5J1.
DR Interpro: IPR000328; Env GP41.
DR Interpro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL. 1 29
FT CHAIN 30 518 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 519 863 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 452 BY SIMILARITY.
FT DISULFID 388 442 BY SIMILARITY.
FT DISULFID 395 425 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FAD1641 CRC64;

Query Match 91.2%; Score 166; DB 1; Length 863;
Best Local Similarity 89.2%; Pred. No. 3.2e-15;
Matches 33; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2789516;
RA Anand R., Thayer R., Srinivasan A., Nayar S., Gardner M., Luciw P.,
RA Dandekar S.,
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia.";
RT Virology 168:79-89(1989).
RU -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
RU HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M21098; AAA44221.1; -.
DR PIR; A3167; VCLJBR.
DR PDB; 1IM7; 23-OCT-02.
DR HIV; M21098; ENV5BRVA.
DR Interpro: IPR000328; Env GP41.
DR Interpro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL. 1 30
FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 155 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 439 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match 89.6%; Score 163; DB 1; Length 852;
Best Local Similarity 86.5%; Pred. No. 8.2e-15;
Matches 32; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHHLLQLTWQIKQLQARILAVERYLKD 37
|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 549 NNILMAIEAQOHHMLTVMGIIKQLQARVLAVERYLKD 585

Search completed: June 2, 2004, 11:42:54
Job time : 6.03261 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 ; Search time 31.0679 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-147
Perfect score: 182
Sequence: 1 NMLRAIEAQHLLQLTWQIKQLQARIILAVERYLKD 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

SPTRMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	96.2	132	15	090052 human immun
2	175	96.2	132	15	078122 human immun
3	175	96.2	143	15	07SM06 human immun
4	175	96.2	144	15	07ZCD7 human immun
5	175	96.2	144	15	07ZCD6 human immun
6	175	96.2	153	15	07SM03 human immun
7	175	96.2	357	15	078119 human immun
8	175	96.2	588	15	0993A8 human immun
9	175	96.2	588	15	0993A7 human immun
10	175	96.2	589	15	0993B1 human immun
11	175	96.2	590	15	0993A9 human immun
12	175	96.2	616	15	0993B0 human immun
13	175	96.2	618	15	0993B2 human immun
14	175	96.2	727	15	09Q723 human immun
15	175	96.2	747	15	070607 human immun
16	175	96.2	748	15	070606 human immun

17	175	96.2	752	15	070604 human immun
18	175	96.2	752	15	070605 human immun
19	175	96.2	752	15	070608 human immun
20	175	96.2	757	15	09Q722 human immun
21	175	96.2	811	15	09DVL6 human immun
22	175	96.2	842	15	073341 human immun
23	175	96.2	842	15	070895 human immun
24	175	96.2	842	15	073340 human immun
25	175	96.2	847	15	069996 human immun
26	175	96.2	851	15	078243 human immun
27	175	96.2	854	15	056566 human immun
28	175	96.2	854	15	085582 human immun
29	175	96.2	854	15	072502 human immun
30	175	96.2	854	15	090178 human immun
31	175	96.2	854	15	078705 human immun
32	175	96.2	855	15	08A0V7 human immun
33	175	96.2	855	15	08ADT7 human immun
34	175	96.2	856	15	074090 human immun
35	175	96.2	856	15	092877 human immun
36	175	96.2	856	15	074599 human immun
37	175	96.2	856	15	041772 human immun
38	175	96.2	857	15	092822 human immun
39	175	96.2	857	15	071013 human immun
40	175	96.2	857	15	089654 human immun
41	175	96.2	854	15	091P39 human immun
42	175	96.2	864	15	07ZJC8 human immun
43	174	95.6	125	15	091WP9 human immun
44	174	95.6	132	15	091W05 human immun
45	174	95.6	133	15	090020 human immun
46	174	95.6	137	15	09DQ04 human immun
47	174	95.6	142	15	091W07 human immun
48	174	95.6	142	15	070207 human immun
49	174	95.6	144	15	07ZCC6 human immun
50	174	95.6	144	15	07ZCC5 human immun
51	174	95.6	144	15	07ZCC2 human immun
52	174	95.6	144	15	07ZCB1 human immun
53	174	95.6	144	15	07ZCB0 human immun
54	174	95.6	144	15	07ZC96 human immun
55	174	95.6	144	15	07ZC95 human immun
56	174	95.6	144	15	07ZC89 human immun
57	174	95.6	144	15	07ZC88 human immun
58	174	95.6	144	15	07ZC71 human immun
59	174	95.6	144	15	07ZC70 human immun
60	174	95.6	145	15	07ZC57 human immun
61	174	95.6	145	15	07ZC40 human immun
62	174	95.6	145	15	07ZC35 human immun
63	174	95.6	145	15	07ZC31 human immun
64	174	95.6	146	15	07SM37 human immun
65	174	95.6	155	15	0803P2 human immun
66	174	95.6	155	15	0803Q3 human immun
67	174	95.6	155	15	0803Q1 human immun
68	174	95.6	156	15	08JAL7 human immun
69	174	95.6	174	15	08JEO8 human immun
70	174	95.6	192	15	08JAL2 human immun
71	174	95.6	219	15	080AJ4 human immun
72	174	95.6	225	15	0991C1 human immun
73	174	95.6	225	15	0991B9 human immun
74	174	95.6	225	15	0991C5 human immun
75	174	95.6	225	15	0991C0 human immun
76	174	95.6	357	15	078118 human immun
77	174	95.6	357	15	078156 human immun
78	174	95.6	357	15	078155 human immun
79	174	95.6	358	15	078140 human immun
80	174	95.6	358	15	078141 human immun
81	174	95.6	380	15	080DX2 human immun
82	174	95.6	392	15	080511 human immun
83	174	95.6	398	15	072603 human immun
84	174	95.6	421	15	08J514 human immun
85	174	95.6	606	15	09Q6V8 human immun
86	174	95.6	679	15	091K02 human immun
87	174	95.6	797	15	003808 human immun
88	174	95.6	797	15	003810 human immun
89	174	95.6	799	15	003807 human immun

90 174 95.6 801 15 Q03809 Q03809 human immun
ALIGNMENTS

RESULT 1

Q90052 ID Q90052 PRELIMINARY; PRT; 132 AA.
AC Q90052;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-M01496;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855 (2001).
DR EMBL: AF31089; AK92300.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR00328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15708 MW; 51D9DBAED574FAB CRC64;
Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 132;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
Db 10 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 46
RESULT 2
Q7SLZ2 ID Q7SLZ2 PRELIMINARY; PRT; 132 AA.
AC Q7SLZ2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT970;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF330024; AAP87755.1; -
DR Envelope protein.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;
Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 132;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
Db 11 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 47

RESULT 3

Q7SM06 ID Q7SM06 PRELIMINARY; PRT; 143 AA.
AC Q7SM06;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF330010; AAP87741.1; -
KM Envelope protein.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738F76BB0 CRC64;
Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 143;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
Db 11 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 47

RESULT 4

Q7ZCD7 ID Q7ZCD7 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Straub T., Boulevarde R., Ayraud V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY185383; AA065658.1; -
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR00328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318BE CRC64;
Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 144;

Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQQHLLQTLTWQIKOLQARIILAVERYLKD 37
DB 24 NNLRAIEAQQHLLQTLTWGIGIKOLQARIILAVERYLKD 60

RESULT 5

Q7ZCD6 PRELIMINARY; PRT; 144 AA.

AC Q7ZCD6; (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 1.25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRU53-2;
RA Roman F., Gonzalez D., Lambert C., Derco S., Fischer A., Baurith T.,
Staub T., Boume R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185384; AAC65659.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EEB CRC64;

Query Match 96.2%; Score 175; DB 15; Length 144;

Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQQHLLQTLTWQIKOLQARIILAVERYLKD 37
DB 24 NNLRAIEAQQHLLQTLTWGIGIKOLQARIILAVERYLKD 60

RESULT 6

Q7SM03 PRELIMINARY; PRT; 153 AA.

AC Q7SM03; (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 1.25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 1.25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT598;
RA Gonzalez Perez M.P., Garcia Saiz A.,
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530013; AAP87744.1; -
KW Envelope protein.
FT NON_TER 1 153
SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1FFEC035 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 153;
Best Local Similarity 97.3%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQQHLLQTLTWQIKOLQARIILAVERYLKD 37
DB 11 NNLRAIEAQQHLLQTLTWGIGIKOLQARIILAVERYLKD 47

RESULT 7

Q78119 PRELIMINARY; PRT; 357 AA.

AC Q78119; (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92144209; PubMed=1736940;
RX Steuler H., Storch-Hagenlocher B., Wildemann B.,
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61356; CAA43624.1; -
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 357 AA; 41118 MW; FE4CA7E122A8B6 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 357;

Best Local Similarity 97.3%; Pred. No. 2.e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQQHLLQTLTWQIKOLQARIILAVERYLKD 37
DB 54 NNLRAIEAQQHLLQTLTWGIGIKOLQARIILAVERYLKD 90

RESULT 8

Q993A8 PRELIMINARY; PRT; 588 AA.

AC Q993A8; (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 1.17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 1.17, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Dosta S.S., Hurwitz J.L.,
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221147; AAK20295.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240A8 CRC64;

Query Match
Best Local Similarity 97.3%; Score 175; DB 15; Length 588;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 496 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 532

RESULT 9
QY 0993A7 PRELIMINARY; PRT; 588 AA.
ID ID
AC 0993A7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt1;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF221148; AAK20296.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match
Best Local Similarity 97.3%; Score 175; DB 15; Length 588;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 496 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 532

RESULT 10
QY 0993B1 PRELIMINARY; PRT; 589 AA.
ID ID
AC 0993B1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=1F8;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF221144; AAK20292.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 589 589
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match
Best Local Similarity 97.3%; Score 175; DB 15; Length 589;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 496 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 532

RESULT 11
QY 0993A9 PRELIMINARY; PRT; 590 AA.
ID ID
AC 0993A9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA Dcosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF221146; AAK20294.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polyporein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 590 590
SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;

Query Match
Best Local Similarity 97.3%; Score 175; DB 15; Length 590;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 497 NNILRAIEAQOHLQLTWQIKQLQARILAVERYLKD 533

RESULT 12
QY 0993B0 PRELIMINARY; PRT; 616 AA.
ID ID
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AC Q993B0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF21145; AAK20293.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 616 AA; 69189 MW; 57ABE20F9A5E0AAE CRC64;

Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 616;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAEQHLLQTLTWQIKOLQARIILAVERYLKD 37
Db 497 NNTLRATIAEQHLLQTLTWGIKOLQARIILAVERYLKD 533

RESULT 13
Q993B2 PRELIMINARY; PRT; 618 AA.
AC Q993B2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF21143; AAK20291.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;

Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 618;
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Best Local Similarity 97.3%; Pred. No. 4.7e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAEQHLLQTLTWQIKOLQARIILAVERYLKD 37
Db 499 NNTLRATIAEQHLLQTLTWGIKOLQARIILAVERYLKD 535

RESULT 14
Q90723 PRELIMINARY; PRT; 727 AA.
AC Q90723;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RX MEDLINE=9272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189158; AAF25627.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD62ED26B9566 CRC64;

Query Match
Best Local Similarity 96.2%; Score 175; DB 15; Length 727;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATIAEQHLLQTLTWQIKOLQARIILAVERYLKD 37
Db 548 NNTLRATIAEQHLLQTLTWGIKOLQARIILAVERYLKD 564

RESULT 15
Q70607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12034; AAA76669.1; -
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 747 747
 SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;
 Query Match 96.2%; Score 175; DB 15; Length 747;
 Best Local Similarity 97.3%; Pred. No. 5.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 Db 548 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 584
 RESULT 16
 Q70606 PRELIMINARY; PRT; 748 AA.
 ID 070606
 AC 070606
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 CX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12032; AAA76668.1; -
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 748 748
 SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C6794B CRC64;
 Query Match 96.2%; Score 175; DB 15; Length 748;
 Best Local Similarity 97.3%; Pred. No. 5.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 Db 549 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 585
 RESULT 17
 Q70604 PRELIMINARY; PRT; 752 AA.
 ID 070604
 AC 070604
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 CX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12030; AAA76665.1; -
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 752 752
 SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
 Query Match 96.2%; Score 175; DB 15; Length 752;
 Best Local Similarity 97.3%; Pred. No. 5.8e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
 Db 553 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 589
 RESULT 18
 Q70605 PRELIMINARY; PRT; 752 AA.
 ID 070605
 AC 070605
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AAA76667.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW NON TER 752 AA; 84894 MW; 8830AB894013B45A CRC64;
SQ SEQUENCE 752 AA; 84894 MW; 8830AB894013B45A CRC64;

Query Match 96.2%; Score 175; DB 15; Length 752;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 37
Db 553 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 589

RESULT 19
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AAA76670.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 752;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 37
Db 553 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 589

RESULT 20
Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.,
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.,
RT "Determinants of CD4 independence for a human immunodeficiency virus
type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -
DR PIR: A53591; A53591.
DR GO: GO:0042025; C: host cell nucleus; IEA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR GO: GO:0003700; F: transcription factor activity; IEA.
DR GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR InterPro: IPR00625; REV protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BD2E CRC64;

Query Match 96.2%; Score 175; DB 15; Length 757;
Best Local Similarity 97.3%; Pred. No. 5.8e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 37
Db 548 NNTLRATIAEQOHLQLTWVGKIQKQARILAVERYLKD 584

RESULT 21

Q9DVL6
ID Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D_97DC.KCD4;
RX MEDLINE=20499072; PubMed=11044094;
RA Viland N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa."
RL J. Virol. 74:10498-10507(2000).
DR EMBL: AJ301037; CAC15045.1; -
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 811
FT NON_TER 1 811
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;
Query Match 96.2%; Score 175; DB 15; Length 811;
Best Local Similarity 97.3%; Pred. No. 6.3e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 37
Db 557 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 593
RESULT 22
Q73341
ID Q73341 PRELIMINARY; PRT; 842 AA.
AC Q73341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR/93/29;
RX MEDLINE=96305593; PubMed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization".
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL: U39236; AAB37173.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1B9F1 CRC64;
Query Match 96.2%; Score 175; DB 15; Length 842;
Best Local Similarity 97.3%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 37
Db 539 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 575
RESULT 23
Q70895
ID Q70895 PRELIMINARY; PRT; 842 AA.
AC Q70895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RX MEDLINE=98285725; PubMed=9621027;
RA Gao F., Robertson D.L., Carnuthers C.D., Morrison S.G., Jian B.,
RT "A comprehensive panel of near-full-length clones and reference
RT sequences for non-subtype B isolates of human immunodeficiency virus
RT type 1.";
RL J. Virol. 72:5680-5698(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Gao F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005495; AAD03179.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 842 AA; 94810 MW; F82041B1D932DCAD CRC64;
Query Match 96.2%; Score 175; DB 15; Length 842;
Best Local Similarity 97.3%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 37
Db 539 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLKD 575
RESULT 24
Q73340
ID Q73340 PRELIMINARY; PRT; 842 AA.
AC Q73340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DR Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585;
 RA Penny M.A., Thomas S.D., Douglas N.W., Ranjbar S., Holmes H.,
 RA Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
 RT D, E, and F obtained from the World Health Organization Network for
 RT HIV Isolation and Characterization."; 741-747(1996).
 RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL; U39235; AAB37172.1; -
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00517; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 607BAF2A47B791B8 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 842;
 Best Local Similarity 97.3%; Pred. No. 6.5e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 DB 539 NNTLRATIAOQHLLQTLTWQIKOLQARILAVERYLKD 575

RESULT 25
 Q69996 PRELIMINARY; PRT; 847 AA.
 AC Q69996;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.J., Craig S.,
 RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
 RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Han B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1657(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA NIAID/NIH DAIDS Variation Program;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA McEvilly M.M.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U08445; AAB04071.1; -

DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00517; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 847 AA; 95602 MW; FCBCBA7AF446FB20 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 847;
 Best Local Similarity 97.3%; Pred. No. 6.6e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRATIAOQHLLQTLTWQIKOLQARILAVERYLKD 37
 DB 544 NNTLRATIAOQHLLQTLTWQIKOLQARILAVERYLKD 580

RESULT 26
 Q78243 PRELIMINARY; PRT; 851 AA.
 AC Q78243;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Env polypotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carlini F., Federici M., Equestre M., Ricci S., Ratti G., Zibai Q.,
 RA Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer
 RT chronically infected HUT-78 cellular clone.";
 RL J. Viral Diseases 1:40-55(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352106; PubMed=2765297;
 RA Federici M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Macchi B., Mangano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non
 RT producer clones from HUT-78 infected with a patient HIV isolate.";
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Titti F., Federici M., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Borsetti A., Saggio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not
 RT productive clone.";
 RL Int. J. Immunopharmacol. 3:17-23(1990).
 DR EMBL; J11530; CAA77628.1; -
 DR PIR; A53591; A53591.
 DR PIR; S13288; S13288.
 DR PIR; S13288; S13288.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00517; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A376B9B7E98027 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 851;
 Best Local Similarity 97.3%; Pred. No. 6.6e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
 DB 548 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 584

RESULT 27

056566 PRELIMINARY; PRT; 854 AA.
 AC 056566;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PIH309;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Ataman-Onal Y., Colifler C., Girud A., Babic-Erces A., Biron F.,
 RA Verrier B.;
 RT "Comparison of complete env gene sequences from individuals with
 RT symptomatic primary HIV type 1 infection."
 RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL: AF041132; ACC02523.1; -
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97062 MW; 58B012C83A0C3DA2 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 854;
 Best Local Similarity 97.3%; Pred. No. 6.6e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
 DB 551 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 587

RESULT 28
 085582 PRELIMINARY; PRT; 854 AA.
 AC 085582;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope polypeptide.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folke T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone."
 RL J. Virol. 59:284-291(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.,
 RA Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RA Buckler C.E.;
 RL Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92219406; PubMed=1373204;
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T
 RT lymphocytes."
 RL J. Virol. 66:3151-3154(1992).
 DR EMBL: M19921; AAA4992.1; -
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97124 MW; ABA0A1B36D5555A CRC64;

Query Match 96.2%; Score 175; DB 15; Length 854;
 Best Local Similarity 97.3%; Pred. No. 6.6e-16;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
 DB 551 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKD 587

RESULT 29
 072502 PRELIMINARY; PRT; 854 AA.
 ID 072502;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE ENV polypeptide.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NL4-3;
 RX MEDLINE=96036482; PubMed=7483282;
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
 RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
 RT from primary virus cultures using the polymerase chain reaction."
 RL Virology 213:80-86(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NL4-3;
 RX MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folke T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone."
 RL J. Virol. 59:284-291(1986).
 DR EMBL: U26942; AAB60578.1; -
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT CONFLICT 214 214 H -> L (IN REF. 2).
FT CONFLICT 530 530 A -> S (IN REF. 2).
FT CONFLICT 739 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF264B3841D1220 CRC64;

Query Match 96.2%; Score 175; DB 15; Length 854;
Best Local Similarity 97.3%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLTLTWQIKQLQARI LAVERYIKD 37
DB 551 NNLRAIEAQOHLTLTWQIKQLQARI LAVERYIKD 587

RESULT 30

090178 PRELIMINARY; PRT; 854 AA.
ID 090178;
AC 090178;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells.";
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070521; AAC28452.1; -
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 96.2%; Score 175; DB 15; Length 854;
Best Local Similarity 97.3%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLTLTWQIKQLQARI LAVERYIKD 37
DB 551 NNLRAIEAQOHLTLTWQIKQLQARI LAVERYIKD 587

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Job time : 31.0679 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 13.6739 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-147
Perfect score: 182
Sequence: 1 NMLRAIEAQHLLQLTWQIKQLQARILAVERYLKD 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents AA:*
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3: /cgn2_6/ptodata/2/1aa/6A COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	175	96.2	38	3	US-08-486-099-89
5	175	96.2	38	3	US-08-360-107A-99
6	175	96.2	38	3	US-08-360-107A-132
7	175	96.2	38	3	US-08-484-223B-89
8	175	96.2	38	3	US-08-919-597-89
9	175	96.2	38	3	US-08-475-668A-89
10	175	96.2	38	3	US-08-485-551A-89
11	175	96.2	38	3	US-08-471-913A-89
12	175	96.2	38	3	US-08-485-264A-89
13	175	96.2	38	3	US-09-082-279B-16
14	175	96.2	38	3	US-09-082-279B-507
15	175	96.2	38	3	US-09-082-279B-604
16	175	96.2	38	3	US-09-082-279B-661
17	175	96.2	38	4	US-08-474-349A-89
18	175	96.2	38	4	US-08-474-349A-441
19	175	96.2	38	4	US-09-315-304B-16
20	175	96.2	38	4	US-09-315-304B-507
21	175	96.2	38	4	US-09-315-304B-604
22	175	96.2	38	4	US-09-315-304B-661
23	175	96.2	38	4	US-08-255-208A-25
24	175	96.2	38	4	US-08-470-896-89
25	175	96.2	38	4	US-08-485-546A-89
26	175	96.2	38	4	US-09-796-202-11
27	175	96.2	38	4	US-09-834-784-16

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31	175	96.2	38	4	US-08-464-003-1	Sequence 1, Appli
32	175	96.2	38	4	US-09-779-451-2	Sequence 2, Appli
33	175	96.2	38	4	US-09-515-965A-16	Sequence 16, Appli
34	175	96.2	38	4	US-09-515-965A-507	Sequence 507, App
35	175	96.2	38	4	US-09-515-965A-604	Sequence 604, App
36	175	96.2	38	4	US-09-515-965A-661	Sequence 661, App
37	175	96.2	38	4	US-09-350-641C-16	Sequence 16, Appli
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40	175	96.2	38	4	US-09-350-641C-661	Sequence 661, App
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44	175	96.2	41	3	US-08-486-099-8	Sequence 8, Appli
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48	175	96.2	41	3	US-08-484-223B-243	Sequence 243, App
49	175	96.2	41	3	US-08-919-597-8	Sequence 8, Appli
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51	175	96.2	41	3	US-08-485-551A-8	Sequence 8, Appli
52	175	96.2	41	3	US-08-471-913A-8	Sequence 8, Appli
53	175	96.2	41	3	US-08-554-616-8	Sequence 8, Appli
54	175	96.2	41	3	US-08-485-264A-8	Sequence 8, Appli
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56	175	96.2	41	3	US-09-082-279B-601	Sequence 601, App
57	175	96.2	41	3	US-09-082-279B-633	Sequence 633, App
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59	175	96.2	41	4	US-08-474-349A-8	Sequence 8, Appli
60	175	96.2	41	4	US-09-315-304B-496	Sequence 496, App
61	175	96.2	41	4	US-09-315-304B-601	Sequence 601, App
62	175	96.2	41	4	US-09-315-304B-633	Sequence 633, App
63	175	96.2	41	4	US-09-315-304B-1163	Sequence 1163, App
64	175	96.2	41	4	US-08-255-208A-8	Sequence 8, Appli
65	175	96.2	41	4	US-08-973-952-8	Sequence 8, Appli
66	175	96.2	41	4	US-08-470-896-8	Sequence 8, Appli
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68	175	96.2	41	4	US-09-834-784-496	Sequence 496, App
69	175	96.2	41	4	US-09-834-784-601	Sequence 601, App
70	175	96.2	41	4	US-09-834-784-633	Sequence 633, App
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72	175	96.2	41	4	US-08-464-003-3	Sequence 3, Appli
73	175	96.2	41	4	US-08-464-003-9	Sequence 9, Appli
74	175	96.2	41	4	US-09-515-965A-496	Sequence 496, App
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76	175	96.2	41	4	US-09-515-965A-633	Sequence 633, App
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80	175	96.2	41	4	US-09-350-641C-633	Sequence 633, App
81	175	96.2	41	4	US-09-350-641C-1163	Sequence 1163, App
82	175	96.2	44	1	US-08-374-666-10	Sequence 10, Appli
83	175	96.2	44	1	US-08-464-003-10	Sequence 10, Appli
84	175	96.2	45	3	US-09-082-279B-1164	Sequence 1164, App
85	175	96.2	45	4	US-09-315-304B-1164	Sequence 1164, App
86	175	96.2	45	4	US-09-834-784-1164	Sequence 1164, App
87	175	96.2	45	4	US-09-779-451-9	Sequence 9, Appli
88	175	96.2	45	4	US-09-515-965A-1164	Sequence 1164, App
89	175	96.2	45	4	US-09-350-641C-1164	Sequence 1164, App
90	175	96.2	49	4	US-09-796-202-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-973-952-82
Sequence 82, Application US/08973952A
Patent No. 6475491
GENERAL INFORMATION:

```

; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORIAL THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/08/973,952A
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/481,957
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match      100.0%; Score 182; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37
DB      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37

RESULT 2
US-09-515-965A-1722
; Sequence 1722, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1722
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1722

Query Match      96.2%; Score 175; DB 4; Length 37;
Best Local Similarity 97.3%; Pred. No. 3.2e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37
DB      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37

RESULT 3
US-08-374-666-1
; Sequence 1, Application US/08374666
; Patent No. 5656480
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Bolognesi, Dani P.
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
```

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,666
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-374-666-1

Query Match      96.2%; Score 175; DB 1; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37
DB      1  NNLLRAIEAQOHLQLTWQIKQARILAVERYLKD 37

RESULT 4
US-08-486-099-89
; Sequence 89, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
```

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37

RESULT 5
US-08-360-107A-99

Sequence 99, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-360-107A-99

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37

RESULT 6
US-08-360-107A-132

Sequence 132, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-132

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37
DB 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37

RESULT 7
US-08-484-223B-89

Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRATEAOQHLLQLTVMQIKOLQARIILAVERYLKD 37
Db 1 NNLRATEAOQHLLQLTVMQIKOLQARIILAVERYLKD 37

RESULT 8
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRATEAOQHLLQLTVMQIKOLQARIILAVERYLKD 37
Db 1 NNLRATEAOQHLLQLTVMQIKOLQARIILAVERYLKD 37

RESULT 9
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 606065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37

RESULT 10
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37

RESULT 11
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARIILAVERYLKD 37

RESULT 12
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:

```

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-264A-89

Query Match          96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37

RESULT 13
US-09-082-279B-16
; Sequence 16, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match          96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37

RESULT 14
US-09-082-279B-507
; Sequence 507, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match          96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYLKD 37

RESULT 15
US-09-082-279B-604
; Sequence 604, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-604
```

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37

RESULT 16

US-09-082-279B-661
Sequence 661, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merucka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-661

Query Match 96.2%; Score 175; DB 3; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
DB 2 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 38

RESULT 17

US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKD 37

RESULT 18

US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 19

US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 20

US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Core polypeptide
US-09-315-304B-507

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 21

US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIKOLQARIILAVERYLKD 37

RESULT 22

US-09-315-304B-661
Sequence 661, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-661

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 37
Db 2 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 38

RESULT 23

US-08-255-208A-25
Sequence 25, Application US/08255208A
Patent No. 6440656

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway Jr., Stephen R.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-010

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-255-208A-25

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 37
Db 1 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 37

RESULT 24

US-08-470-896-89

Sequence 89, Application US/08470896
Patent No. 6479055

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,896

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-470-896-89

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 37
Db 1 NNILRAIEAOQHLLQTLTWGIKQIQAARILAVERYIKD 37

RESULT 25

US-08-485-546A-89

Sequence 89, Application US/08485546A
Patent No. 6518013

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 214

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARI LAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARI LAVERYLKD 37

RESULT 26
US-09-796-202-11
Sequence 11, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARI LAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARI LAVERYLKD 37

RESULT 27
US-09-834-784-16
Sequence 16, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:

APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Metutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARI LAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARI LAVERYLKD 37

RESULT 28
US-09-834-784-507
Sequence 507, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Metutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-507

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARI LAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIGIKQLQARI LAVERYLKD 37

RESULT 29
US-09-834-784-604
Sequence 604, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-604

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37

RESULT 30
US-09-834-784-661
Sequence 661, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-661

Query Match 96.2%; Score 175; DB 4; Length 38;
Best Local Similarity 97.3%; Pred. No. 3.3e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 37
Db 2 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLKD 38

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Job time: 13.6739 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:48:34 ; Search time 34.0842 Seconds
(without alignments)
305.406 Million cell updates/sec

Title: US-09-657-336a-147
Perfect score: 182
Sequence: 1 NMLRAIEAQHLLQTLVWQIKQLQARILLAVERYLKD 37

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 90 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	100.0	38	14	US-10-252-136-82
2	175	96.2	37	15	US-10-005-305-130
3	175	96.2	38	9	US-09-796-202-11
4	175	96.2	38	9	US-09-779-451-2
5	175	96.2	38	10	US-09-493-346-2
6	175	96.2	38	12	US-10-267-682-89
7	175	96.2	38	12	US-10-267-748-89
8	175	96.2	38	12	US-09-809-060-6
9	175	96.2	38	12	US-10-663-589-3
10	175	96.2	38	12	US-10-681-879-2
11	175	96.2	38	12	US-09-828-615-2
12	175	96.2	38	14	US-10-116-797-2
13	175	96.2	38	14	US-10-323-314-11
14	175	96.2	38	14	US-10-414-192-1
15	175	96.2	38	14	US-10-414-192-1

16	175	96.2	38	14	US-10-351-641-16	Sequence 16, Appl
17	175	96.2	38	14	US-10-351-641-507	Sequence 507, App
18	175	96.2	38	14	US-10-351-641-604	Sequence 604, App
19	175	96.2	38	14	US-10-351-641-661	Sequence 661, App
20	175	96.2	38	15	US-10-005-305-165	Sequence 165, App
21	175	96.2	38	15	US-10-005-305-202	Sequence 202, App
22	175	96.2	38	15	US-10-005-305-203	Sequence 203, App
23	175	96.2	38	15	US-10-420-194-1234	Sequence 1234, App
24	175	96.2	38	16	US-10-664-021-2	Sequence 2, Appl
25	175	96.2	38	16	US-10-671-316-2	Sequence 2, Appl
26	175	96.2	41	12	US-10-267-682-8	Sequence 8, Appl
27	175	96.2	41	12	US-10-267-748-8	Sequence 8, Appl
28	175	96.2	41	12	US-10-663-589-30	Sequence 30, Appl
29	175	96.2	41	12	US-10-663-589-33	Sequence 33, Appl
30	175	96.2	41	12	US-10-663-589-35	Sequence 35, Appl
31	175	96.2	41	14	US-10-252-136-8	Sequence 8, Appl
32	175	96.2	41	14	US-10-414-192-3	Sequence 3, Appl
33	175	96.2	41	14	US-10-414-192-9	Sequence 9, Appl
34	175	96.2	41	14	US-10-351-641-436	Sequence 436, App
35	175	96.2	41	14	US-10-351-641-601	Sequence 601, App
36	175	96.2	41	14	US-10-351-641-633	Sequence 633, App
37	175	96.2	41	14	US-10-351-641-1163	Sequence 1163, App
38	175	96.2	41	16	US-10-664-021-27	Sequence 27, Appl
39	175	96.2	41	16	US-10-671-316-27	Sequence 27, Appl
40	175	96.2	44	12	US-10-663-589-36	Sequence 36, Appl
41	175	96.2	44	14	US-10-414-192-10	Sequence 10, Appl
42	175	96.2	45	9	US-09-779-451-9	Sequence 9, Appl
43	175	96.2	45	12	US-09-809-060-50	Sequence 50, Appl
44	175	96.2	45	12	US-10-663-589-29	Sequence 29, Appl
45	175	96.2	45	14	US-10-351-641-1164	Sequence 1164, App
46	175	96.2	45	16	US-10-664-021-26	Sequence 26, Appl
47	175	96.2	45	16	US-10-671-316-26	Sequence 26, Appl
48	175	96.2	49	9	US-09-796-202-3	Sequence 3, Appl
49	175	96.2	49	14	US-10-323-316-3	Sequence 3, Appl
50	175	96.2	51	12	US-10-663-589-27	Sequence 27, Appl
51	175	96.2	51	14	US-10-351-641-745	Sequence 745, App
52	175	96.2	51	16	US-10-664-021-24	Sequence 24, Appl
53	175	96.2	51	16	US-10-671-316-24	Sequence 24, Appl
54	175	96.2	52	14	US-10-351-641-1119	Sequence 1119, App
55	175	96.2	53	14	US-10-351-641-955	Sequence 955, App
56	175	96.2	53	14	US-10-351-641-1062	Sequence 1062, App
57	175	96.2	55	9	US-09-779-451-1	Sequence 1, Appl
58	175	96.2	55	12	US-09-809-060-14	Sequence 14, Appl
59	175	96.2	57	15	US-10-438-691-1	Sequence 1, Appl
60	175	96.2	59	16	US-10-664-021-1	Sequence 1, Appl
61	175	96.2	59	16	US-10-671-316-1	Sequence 1, Appl
62	175	96.2	60	12	US-10-663-589-1	Sequence 1, Appl
63	175	96.2	63	12	US-10-267-682-201	Sequence 201, App
64	175	96.2	63	12	US-10-267-748-201	Sequence 201, App
65	175	96.2	63	14	US-10-252-136-54	Sequence 29, Appl
66	175	96.2	103	14	US-10-263-103-29	Sequence 29, Appl
67	175	96.2	103	15	US-10-438-691-3	Sequence 3, Appl
68	175	96.2	105	14	US-10-263-103-28	Sequence 28, Appl
69	175	96.2	105	14	US-10-263-103-30	Sequence 30, Appl
70	175	96.2	113	15	US-10-438-691-4	Sequence 4, Appl
71	175	96.2	177	14	US-10-040-349B-2	Sequence 2, Appl
72	175	96.2	188	9	US-09-854-816-88	Sequence 88, Appl
73	175	96.2	188	9	US-09-854-816-89	Sequence 89, Appl
74	175	96.2	200	14	US-10-263-103-25	Sequence 25, Appl
75	175	96.2	200	15	US-10-438-691-8	Sequence 8, Appl
76	175	96.2	232	14	US-10-059-271-81	Sequence 81, Appl
77	175	96.2	254	14	US-10-059-271-82	Sequence 82, Appl
78	175	96.2	256	14	US-10-059-271-97	Sequence 97, Appl
79	175	96.2	258	9	US-09-854-816-15	Sequence 16, Appl
80	175	96.2	258	9	US-09-854-816-17	Sequence 17, Appl
81	175	96.2	258	9	US-09-854-816-18	Sequence 18, Appl
82	175	96.2	258	9	US-09-854-816-19	Sequence 19, Appl
83	175	96.2	259	9	US-09-854-816-43	Sequence 43, Appl
84	175	96.2	338	12	US-10-267-682-90	Sequence 90, Appl
85	175	96.2	344	14	US-10-267-748-90	Sequence 90, Appl
86	175	96.2	344	14	US-10-040-349B-1	Sequence 1, Appl
87	175	96.2	345	9	US-09-779-451-8	Sequence 8, Appl
88	175	96.2	345	14	US-10-026-741-49	Sequence 49, Appl

89 175 96.2 359 14 US-10-214-670-58
90 175 96.2 391 14 US-10-059-271-93

ALIGNMENTS

RESULT 1

US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 182; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.8e-18;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37

RESULT 2

US-10-005-305-130
; Sequence 130, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DPI78 AND T21/DPI07 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PRAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-130

Query Match 96.2%; Score 175; DB 15; Length 37;
Best Local Similarity 97.3%; Pred. No. 5.2e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37

RESULT 3

US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DPI07
US-09-796-202-11

Query Match 96.2%; Score 175; DB 9; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37

RESULT 4

US-09-779-451-2
; Sequence 2, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 96.2%; Score 175; DB 9; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGIKOLQARILAVERYLKD 37

RESULT 5

US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J

TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
FILE OF INVENTION: Infection
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/09/493,346
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-09-493-346-2

Query Match 96.2%; Score 175; DB 10; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37

RESULT 6
US-10-267-682-89
Sequence 89, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Petteaway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37

RESULT 7
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Petteaway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-748-89

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37
Db 1 NNLLRAIEAQOHLQLTWQIKOLQARILAVERYLKD 37

RESULT 8
US-09-809-060-6
; Sequence 6, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37

RESULT 9
US-09-809-060-7
; Sequence 7, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37

RESULT 10
US-10-663-589-3
; Sequence 3, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Timmeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV

; TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37

RESULT 11
US-10-681-879-2
; Sequence 2, Application US/10681879
; Publication No. US20040062767A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; TITLE OF INVENTION: Infection
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/10/681,879
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/493,346
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLKD 37

RESULT 12
US-09-828-615-2
; Sequence 2, Application US/09828615
; Publication No. US20020146415A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672
; CURRENT APPLICATION NUMBER: US/09/828,615
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 38

TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 96.2%; Score 175; DB 12; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37

RESULT 13
US-10-116-797-2

Sequence 2, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37

RESULT 14
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37

RESULT 15
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
Matthews, Thomas J.
Bolognesi, Dani P.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-414-192-1

Query Match 96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYLKD 37

RESULT 16
US-10-351-641-16

Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Mertuka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641

CURRENT FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/315,304

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match          96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37

RESULT 17
US-10-351-641-507
; Sequence 507, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthe, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match          96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37

RESULT 18
US-10-351-641-604
; Sequence 604, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthe, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
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; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match          96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37

RESULT 19
US-10-351-641-661
; Sequence 661, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthe, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 661
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-661

Query Match          96.2%; Score 175; DB 14; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 37
Db 2 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLKD 38

RESULT 20
US-10-005-305-165
; Sequence 165, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
```

APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 165
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 96.2%; Score 175; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37

RESULT 21
US-10-005-305-202
Sequence 202, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match 96.2%; Score 175; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37

RESULT 22
US-10-005-305-203
Sequence 203, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services

TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match 96.2%; Score 175; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 5,4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37
Db 1 NNLRAIEAQOHLQLTWGKIQLOARILAVERYLKD 37

RESULT 23
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US2004006035A1
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: MCSwigen, Jim
APPLICANT: Blatt, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
TITLE OF INVENTION: Interactions
FILE REFERENCE: MHB02-305-A (400/011)
CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences

NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match 96.2%; Score 175; DB 15; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37

RESULT 24
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US20040076637A1
GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
TITLE OF INVENTION: Immunodeficiency Virus
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match 96.2%; Score 175; DB 16; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37

RESULT 25
US-10-671-316-2
Sequence 2, Application US/1067316
Publication No. US20040091855A1
GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: peptides, and trimers formed therefrom
FILE REFERENCE: TRM-002
CURRENT APPLICATION NUMBER: US/10/671,316
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,515
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-316-2

Query Match 96.2%; Score 175; DB 16; Length 38;
Best Local Similarity 97.3%; Pred. No. 5.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37
DB 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37

RESULT 26
US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petreway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-267-682-8

Query Match 96.2%; Score 175; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 5.8e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 37
DB 4 NNLRAIEAQOHLQLTWGKIQOLARILAVERYLKD 40

RESULT 27
US-10-267-748-8
Sequence 8, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.

Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petreway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-748-8

Query Match 96.2%; Score 175; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 5.8e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 37
DB 4 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 40

RESULT 28
US-10-663-589-30
Sequence 30, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
PRIOR FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patent In version 3.2
SEQ ID NO 30
LENGTH: 41

TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-30

Query Match 96.2%; Score 175; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 5.8e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 37
DB 4 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 40

RESULT 29
US-10-663-589-33
Sequence 33, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
PRIOR FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patent In version 3.2
SEQ ID NO 33
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-33

Query Match 96.2%; Score 175; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 5.8e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 37
DB 4 NNLLRAIEAQOHLQLTWQIKQLQARILLAVERYLKD 40

RESULT 30
US-10-663-589-35
Sequence 35, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
PRIOR FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patent In version 3.2
SEQ ID NO 35
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-35

Query Match 96.2%; Score 175; DB 12; Length 41;
Best Local Similarity 97.3%; Pred. No. 5.8e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAQOQHLLQLTWQIKQLOARILAVERYLKD 37
| | | | | | | | | | | | | | | | | | | | | |
Db 1 NNLRAIEAQOQHLLQLTWQIKQLOARILAVERYLKD 37
| | | | | | | | | | | | | | | | | | | | | |

Search completed: June 2, 2004, 12:29:24
Job time : 35.0842 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 45.0978 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336A-148
Perfect score: 176
Sequence: 1 NNLLRAIEAQHLLQLTWQIKQARILAVERYLK 36

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : A_Geneseq_29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	176	100.0	36 3 AAB14704	Aab14704 HIV-1 iso
2	176	100.0	36 4 AAB54968	Aab54968 Anti-HIV
3	176	100.0	37 3 AAB14705	Aab14705 HIV-1 iso
4	176	100.0	37 4 AAB54969	Aab54969 Anti-HIV
5	176	100.0	38 2 AAB98408	Aab98408 DP107 cor
6	176	100.0	38 4 AAB54785	Aab54785 HIV antiiv
7	176	100.0	38 4 AAB55005	Aab55005 Anti-HIV
8	176	100.0	38 4 AAB54970	Aab54970 Anti-HIV
9	176	100.0	38 4 AAB92244	Aab92244 Virus rel
10	176	100.0	38 4 AAU14011	AAU14011 DP107 pep
11	176	100.0	38 5 AA018771	AA018771 HIV gp41
12	171	97.2	35 3 AAB14703	Aab14703 HIV-1 iso
13	171	97.2	35 4 AAB54967	Aab54967 Anti-HIV
14	170	96.6	37 3 AAB14739	Aab14739 HIV-1 iso
15	170	96.6	37 4 AAB55004	Aab55004 Anti-HIV
16	169	96.0	36 3 AAB52750	Aab52750 T21/DP107
17	169	96.0	37 3 AAB52751	Aab52751 T21/DP107
18	169	96.0	38 2 AAB55635	Aab55635 DP-139 -
19	169	96.0	38 2 AAB55636	Aab55636 DP-140 -
20	169	96.0	38 2 AAB47216	Aab47216 DP-107 -
21	169	96.0	38 2 AAB27614	Aab27614 Human imm
22	169	96.0	38 3 AAB88666	Aab88666 Core poly
23	169	96.0	38 3 AAB88730	Aab88730 Core poly
24	169	96.0	38 3 AAB88731	Aab88731 Core poly
25	169	96.0	38 3 AAB89145	Aab89145 Core poly

25	169	96.0	38 3 AAB89146	Aab89146 Core poly
27	169	96.0	38 3 AAB99243	Aab99243 Core poly
28	169	96.0	38 3 AAB14530	Aab14530 HIV-1 iso
29	169	96.0	38 3 AAB52824	Aab52824 T21/DP107
30	169	96.0	38 3 AAB52786	Aab52786 T21/DP107
31	169	96.0	38 3 AAB52823	Aab52823 T21/DP107
32	169	96.0	38 4 AAG63858	Aag63858 Amino acil
33	169	96.0	38 4 AAB92349	Aab92349 Virus rel
34	169	96.0	38 4 AAB77021	Aab77021 Core poly
35	169	96.0	38 4 AAB77653	Aab77653 Core poly
36	169	96.0	38 4 AAB77085	Aab77085 Core poly
37	169	96.0	38 4 AAB77596	Aab77596 Core poly
38	169	96.0	38 4 AAB77652	Aab77652 Core poly
39	169	96.0	38 4 AAB77500	Aab77500 Core poly
40	169	96.0	38 4 AAB77624	Aab77624 Core poly
41	169	96.0	38 4 AAU70185	AAU70185 HIV viral
42	169	96.0	38 4 AAU70184	AAU70184 HIV viral
43	169	96.0	38 4 AAB85680	Aab85680 DP107 pep
44	169	96.0	38 4 AAB01489	Aab01489 Viral cor
45	169	96.0	38 4 AAB00505	Aab00505 Viral DP1
46	169	96.0	38 4 AAB00090	Aab00090 Viral DP1
47	169	96.0	38 4 AAB00657	Aab00657 Viral DP1
48	169	96.0	38 4 AAB02077	Aab02077 Viral cor
49	169	96.0	38 4 ABB00025	Abb00025 HIV-1 gp4
50	169	96.0	38 4 ABB00089	Abb00089 Viral DP1
51	169	96.0	38 4 ABB00504	Abb00504 Viral DP1
52	169	96.0	38 4 ABB00658	Abb00658 Viral DP1
53	169	96.0	38 4 ABB00629	Abb00629 Viral DP1
54	169	96.0	38 4 ABB00601	Abb00601 RSV Fl pr
55	169	96.0	38 4 ABB01980	Abb01980 Viral cor
56	169	96.0	38 4 ABB02134	Abb02134 Viral cor
57	169	96.0	38 4 AAU12638	AAU12638 DP178-11k
58	169	96.0	38 4 AAU13205	AAU13205 DP178-11k
59	169	96.0	38 4 AAU13053	AAU13053 DP178-11k
60	169	96.0	38 4 AAU13177	AAU13177 DP178-11k
61	169	96.0	38 4 AAU13149	AAU13149 DP178-11k
62	169	96.0	38 4 AAU12574	AAU12574 DP178-11k
63	169	96.0	38 4 AAU13206	AAU13206 DP178-11k
64	169	96.0	38 4 AAU12639	AAU12639 DP178-11k
65	169	96.0	38 4 AAB82962	Aab82962 Anti-HIV
66	169	96.0	38 5 AAE22297	AAE22297 gp41 fusi
67	169	96.0	38 5 AAE22292	AAE22292 gp41 fusi
68	169	96.0	38 5 ADE02097	AdE02097 Hybrid po
69	169	96.0	38 5 ADE02154	AdE02154 Hybrid po
70	169	96.0	38 5 ADE02155	AdE02155 Hybrid po
71	169	96.0	38 5 ADE01509	AdE01509 Hybrid po
72	169	96.0	38 6 ABO10245	AbO10245 Peptide f
73	169	96.0	38 7 ADC99756	AdC99756 DP-107 an
74	169	96.0	38 7 ADE37011	AdE37011 HIV gp41
75	169	96.0	41 2 AAB52840	Aab52840 DP-125 -
76	169	96.0	41 2 AAB98406	Aab98406 Peptide D
77	169	96.0	41 2 AAU17019	AAU17019 DP-178-11
78	169	96.0	41 2 AAU27616	AAU27616 Human imm
79	169	96.0	41 2 AAU27622	AAU27622 Human imm
80	169	96.0	41 3 AAB89779	Aab89779 Core poly
81	169	96.0	41 3 AAB89240	Aab89240 Core poly
82	169	96.0	41 3 AAB89134	Aab89134 Core poly
83	169	96.0	41 4 AAB54791	Aab54791 HIV antiiv
84	169	96.0	41 4 AAB92250	Aab92250 Virus rel
85	169	96.0	41 4 AAB77593	Aab77593 Core poly
86	169	96.0	41 4 AAB78180	Aab78180 Core poly

ALIGNMENTS

RESULT 1
AAB14704
ID AAB14704 standard; peptide; 36 AA.

XX AAB14704;
AC
XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #33.
DE
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibitor; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
KW isolate LAI.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000MO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
XX 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
XX (WEIS/) WEISS C D.
XX
XX WILD CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX Disclosure; Page 36; 97pp; English.
XX
XX Sequences AAB14672-B1473 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralizing antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
XX
XX Sequence 36 AA;
SQ

Query Match 100.0%; Score 176; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNILRAIEAQOHLLQITWQIKOLQARIILAVERYLK 36
Db 1 NNILRAIEAQOHLLQITWQIKOLQARIILAVERYLK 36
RESULT 2
ID AAB54968 standard; peptide; 36 AA.
XX
XX AAB54968;
AC
XX 11-SEP-2003 (revised)
DT 03-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #33.
DE
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antitumor; mobile blood component; measles virus; MeV; SiV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000MO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX
XX (CONF-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjelab N, Robitaille M, Milner PG;
PI
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (II) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SiV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB54783 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
XX Sequence 36 AA;
SQ

Query Match 100.0%; Score 176; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NNILRAIEAQOHLLQITWQIKOLQARIILAVERYLK 36

DB 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 3
AAB14705
ID AAB14705 standard; peptide; 37 AA.
XX AAB14705;
AC
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
DE
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000456.
PF
XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
XX Wild CT, Weiss CD;
PI
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX Disclosure; Page 36; 97pp; English.

Sequences AAB14672-B1473 represent peptides derived from the N-helical domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B, isolate LAI. The invention relates to raising a neutralizing antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of gp41 which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond or mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-helical segment), or the gp41 core 6-helix bundle, which is formed by the interaction of the N- and C-helical domains of three gp41 proteins. The peptides can be administered either singly or as a combination (particularly a combination of N-helical and C-helical peptides), and can be multimerised. For example, N- and C-helical domain peptides can be alternately linked together to form a peptide which mimics the core 6-helix bundle. Administration of the peptide(s) generates a humoral response, with the production of antibodies against gp41 structures involved in viral entry. As these portions of gp41 are well conserved, such antibodies may be effective against a broad range of HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 37 AA;
XX
XX Query Match 100.0%; Score 176; DB 3; Length 37;
XX Best Local Similarity 100.0%; Pred. No. 2,5e-16;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
DB 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 4
AAB54969
ID AAB54969 standard; peptide; 37 AA.
XX
XX AAB54969;
AC
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Anti-HIV peptide DP107 carboxy truncation peptide #34.
DE
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antitumorigenic; mobile blood component; measles virus; MeV; SiV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200069902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
PF
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
PI
XX WPI; 2001-007496/01.
DR
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX Disclosure; Page 137; 211pp; English.

The present invention describes a modified anti-viral peptide (I) comprising a peptide that exhibits anti-viral activity and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds. (I) has anti-viral and anti-fusogenic activities. (I) inhibits viral infection of cells by inhibiting cell-cell fusion or free virus infection or to reduce the level of membrane fusion events between two or more entities, e.g., virus-cell or cell-cell, relative to the level of membrane fusion that occurs in the absence of the peptide. (I) is useful in the treatment of patients who are suffering from viral infection, e.g., HIV, RSV, HPIV, MeV, and SiV. (I) may be administered prophylactically to previously uninfected individuals. This is useful in cases where an individual has been subjected to a high risk of exposure to a virus. By bonding of long-lived components of the blood, such as immunoglobulin, serum albumin, red blood cells and platelets the activity is extended for days to weeks. This is due to improved stability in vivo and a reduced susceptibility to peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 to AAB55431 represent peptides used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 37 AA:

Query Match 100.0%; Score 176; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36
 DB 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36

RESULT 5

AAR984408
 ID AAR984408 standard; peptide; 38 AA.

AC AAR984408;

DT 16-OCT-2003 (revised)
 DT 17-FEB-1997 (first entry)

DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX MO9619495-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95MO-US016733.

XX 20-DEC-1994; 94US-00360107.

XX 06-JUN-1995; 95US-00470896.

XX (UYDU-) UNIV DUKE.

XX (TRIM-) TRIMERIS INC.

PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;

PI Petteway SR, Langlois AJ;

XX WPI; 1996-309517/31.

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP sequence
 PT search motif.

XX Disclosure; Page 30; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit
 CC antifusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALLMOTIS, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 38 AA:

Query Match 100.0%; Score 176; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36
 DB 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36

RESULT 6

AAB54785
 ID AAB54785 standard; peptide; 38 AA.

XX AAB54785;
 AC AAB54785;

DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)

DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifusogenic; mobile blood component; measles virus; MeV; SiV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus 1.

XX MO200069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000MO-US013651.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 XX human immunodeficiency virus.

PS Claim 6; Page 173; 211pp; English.

CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SiV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 38 AA:

Query Match 100.0%; Score 176; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36
 DB 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYLK 36

RESULT 7

AAB55005
 ID AAB55005 standard; peptide; 38 AA.

AC AAB55005;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 amino truncation peptide #35.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONT-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007496/01.
 XX
 PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 38 AA;
 XX
 QY Query Match 100.0%; Score 176; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 DB 1 NNLIRATEAQOHLTLTWQIKOLQARIILAVERYLK 36
 1 NNLIRATEAQOHLTLTWQIKOLQARIILAVERYLK 36
 XX
 RESULT 8
 AAB54970
 ID AAB54970 standard; peptide; 38 AA.
 XX
 AC AAB54970;
 XX

XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #35.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONT-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007496/01.
 XX
 PT A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 137; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 38 AA;
 XX
 QY Query Match 100.0%; Score 176; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 DB 1 NNLIRATEAQOHLTLTWQIKOLQARIILAVERYLK 36
 1 NNLIRATEAQOHLTLTWQIKOLQARIILAVERYLK 36
 XX
 RESULT 9
 AAB92244
 ID AAB92244 standard; peptide; 38 AA.
 XX
 AC AAB92244;
 XX

DT 22-JUN-2001 (first entry)
XX Virtue related peptide SEQ ID NO:1420.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimide; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000MO-US013576.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX 15-OCT-1999; 99US-0159783P.
XX
XX (CONU-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX
XX Disclosure; Page 662; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stable therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent inventions which can be used in the
CC exemplification of the present invention
XX
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 176; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No.2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NNLRAIEAOQHLLQTLTWQIKQLQARILAVERYLK 36
DB 1 NNLRAIEAOQHLLQTLTWQIKQLQARILAVERYLK 36
RESULT 10
AAU14011
ID AAU14011 standard; peptide; 38 AA.
XX
XX AAU14011;
XX
XX 11-SEP-2003 (revised)
DT 21-NOV-2001 (first entry)
XX
XX
XX DP107 peptide from HIV-1 transmembrane protein gp41.
XX
XX Anti-retroviral; DP178-1like; DP107-1like; transmembrane protein gp41;

KM antifusogenic; antiviral; HIV transmission.
XX
XX Human immunodeficiency virus 1; isolate IAI.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..35 can be optionally and serially
FT /notes "amino acids 1-35 can be optionally and serially
FT deleted from the N-terminus"
FT Misc-difference 4..38
FT /notes "amino acids 4-38 can be optionally and serially
FT deleted from the C-terminus"
XX
XX
XX WO200151673-A2.
XX
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000MO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX
XX Jeffe P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX
XX
XX Disclosure; Page 33; 259pp; English.
XX
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-1like and DP107-1like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-1like/DP107-1like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 176; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No.2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NNLRAIEAOQHLLQTLTWQIKQLQARILAVERYLK 36
DB 1 NNLRAIEAOQHLLQTLTWQIKQLQARILAVERYLK 36
RESULT 11
AAO18771
ID AAO18771 standard; peptide; 38 AA.
XX
XX AAO18771;
XX
XX 29-OCT-2002 (first entry)
DT
XX
XX HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
XX
XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;

KM GP41.
 XX Human immunodeficiency virus.
 XX
 XX WO200256902-A2.
 XX
 XX 25-JUL-2002.
 PD
 XX 17-DEC-2001; 2001WO-US048802.
 PF
 XX 19-DEC-2000; 2000US-0256657P.
 PR
 XX (SCHE) SCHERING CORP.
 XX
 XX Baroudy BM;
 PI
 XX WPI; 2002-636513/68.
 DR
 XX Treatment of HIV infection in an individual involves administration of a
 PT combination of chemokine co-receptor five antagonist and a specified HIV
 PT envelope polypeptide.
 XX
 PS Disclosure; Page 34; 52pp; English.
 CC The present invention relates to a method of treating an HIV infection in
 CC an individual, which involves administering in combination a chemokine co-
 CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
 CC derivative. Other viral infections can also be treated using the method.
 CC The present sequence is a peptide derived from HIV and useful in the
 CC method of the invention
 CC
 XX Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 176; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
 Db 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
 RESULT 12
 AAB14703
 ID AAB14703 standard; peptide; 35 AA.
 XX
 AC AAB14703;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #32.
 XX
 XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
 KW isolate LAI.
 KM
 XX Human immunodeficiency virus 1.
 OS
 XX WO200040616-A1.
 PN
 XX 13-JUL-2000.
 PD
 XX 10-JAN-2000; 2000WO-US000456.
 PF
 XX 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 XX (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX

PI Wild CT, Weiss CD;
 XX
 XX WPI; 2000-465959/40.
 DR
 XX Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 PT
 XX Disclosure; Page 36; 97pp; English.
 PS
 XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralizing antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX Sequence 35 AA;
 SQ
 Query Match 97.2%; Score 171; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 35
 Db 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 35
 RESULT 13
 AAB54967
 ID AAB54967 standard; peptide; 35 AA.
 XX
 AC AAB54967;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #32.
 XX
 XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KW antitumorigenic; mobile blood component; measles virus; MeV; SiV;
 KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
 KM
 XX Human immunodeficiency virus 1.
 OS
 XX WO200069902-A1.
 PN
 XX 23-NOV-2000.
 PD
 XX 17-MAY-2000; 2000WO-US013651.
 PF

XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG,
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX
XX Disclosure; Page 137; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,
CC MEV, and SIV. (I) may be administered prophylactically to individually
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC proteolysis or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB5531 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 35 AA;
Query Match 97.2%; Score 171; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e-15; Mismatches 0; Gaps 0;
Matches 35; Conservative 0; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
DB 1 NNLRAIEAQOHLQLTVMQIKQARILAVERYL 35
RESULT 14
AAB14739 standard; peptide; 37 AA.
XX
AC AAB14739;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
XX Human immunodeficiency virus 1.
XX
XX MO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000MO-US000456.
PF

XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C.T.
PA (WEIS/) WEIS C.D.
XX
XX WILD CT, Weiss CD;
XX
XX WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX
XX Disclosure; Page 38; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate LAI. The invention relates to raising a neutralising antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond to
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
CC
XX
SQ Sequence 37 AA;
Query Match 96.6%; Score 170; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e-15; Mismatches 35;
Matches 35; Conservative 0; Indels 0; Gaps 0;
QY 2 NLRRAIEAQOHLQLTVMQIKQARILAVERYLK 36
DB 1 NLRRAIEAQOHLQLTVMQIKQARILAVERYLK 35
RESULT 15
AAB55004 standard; peptide; 37 AA.
XX
AC AAB55004;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE Anti-HIV peptide DP107 amino truncation peptide #34.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antifusogenic; mobile blood component; measles virus; MEV; SIV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX

OS Human immunodeficiency virus 1.
XX WO200069902-A1.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US013651.
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX (CONJ-) CONJUCHEM INC.
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 139; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC Mev, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 37 AA;
Query Match 96.6%; Score 170; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
DB 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 35
RESULT 16
AAB52750
ID AAB52750 standard; peptide; 36 AA.
XX
XX AAB52750;
XX
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #32.
DE
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
XX Human immunodeficiency virus 1.
OS
XX

PN WO20006622-A1.
XX
XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Claim 12; Page 28; 148pp; English.
PS
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 36 AA;
Query Match 96.0%; Score 169; DB 3; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.1e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
DB 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
RESULT 17
AAB52751
ID AAB52751 standard; peptide; 37 AA.
XX
XX AAB52751;
XX
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #33.
DE
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO20006622-A1.
XX
XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT

PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Claim 12; Page 28; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 37 AA;
SQ
Query Match 96.0%; Score 169; DB 3; Length 37;
Best Local Similarity 97.2%; Pred. No. 2.1e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
RESULT 18
AAR55635
ID AAR55635 standard; peptide; 38 AA.
XX
XX AAR55635;
AC
XX 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
XX DP-139 - DP-107 analogue.
DE
XX Leucine zipper; HIV-1; human immunodeficiency virus;
KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.
XX
XX Synthetic.
OS
XX WO9402505-A1.
PN
XX 03-FEB-1994.
PD
XX 19-JUL-1993; 93WO-US006769.
PF
XX 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
XX
XX (UYDU-) UNIV DUKE.
PA
XX Wild CT, Matthews TJ, Bolognesi DP;
PI WPI; 1994-048790/06.
DR
XX New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.
XX
XX Disclosure; Page 25; 38pp; English.
XX
XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 38 AA;
SQ
Query Match 96.0%; Score 169; DB 2; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
RESULT 19
AAR55636
ID AAR55636 standard; peptide; 38 AA.
XX
XX AAR55636;
AC
XX 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
XX DP-140 - DP-107 analogue.
DE
XX Leucine zipper; HIV-1; human immunodeficiency virus;
KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.
XX
XX Synthetic.
OS
XX WO9402505-A1.
PN
XX 03-FEB-1994.
PD
XX 19-JUL-1993; 93WO-US006769.
PF
XX 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
XX
XX (UYDU-) UNIV DUKE.
PA
XX Wild CT, Matthews TJ, Bolognesi DP;
PI WPI; 1994-048790/06.
DR
XX New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.
XX
XX Disclosure; Page 25; 38pp; English.
XX
XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 38 AA;
SQ
Query Match 96.0%; Score 169; DB 2; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36
RESULT 20
AAR47216

ID AAR47216 standard; peptide; 38 AA.
 AC AAR47216;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX
 DE DP-107 - HIV-1 TM protein (558-595).
 XX
 XX Leucine zipper; HIV-1; human immunodeficiency virus;
 KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KM antiviral; gp41.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 12 /note= "residue 12 of the sequence in Fig 1 is H; residue
 FT 12 of the sequence in Table 4 is G"
 XX
 PN MO9402505-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006769.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Wild CT, Matthews TJ, Bolognesi DP;
 XX
 DR WPI; 1994-048790/06.
 XX
 PT New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Claim 1; Page 27; 38pp; English.
 XX
 CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fuscogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR5633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 SQ Sequence 38 AA;
 XX
 QY Query Match 96.0%; Score 169; DB 2; Length 38;
 DB Best Local Similarity 97.2%; Pred. No. 2.2e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
 RESULT 21
 ID AAR27614 standard; peptide; 38 AA.
 AC AAR27614;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-DEC-1997 (first entry)
 XX
 DE Human immunodeficiency virus gp41 derived peptide DP-107.
 XX

KM Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
 KW inhibition; induction; cell fusion; transmembrane; type 1.
 OS Human immunodeficiency virus.
 XX
 PN US5656480-A.
 XX
 PD 12-AUG-1997.
 XX
 PF 27-JAN-1995; 95US-00374666.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 PR 19-JUL-1993; 93WO-US006769.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Bolognesi DP, Wild CT, Matthews TJ;
 XX
 DR WPI; 1997-414595/38.
 XX
 PT Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
 PT syncytia formation and transmembrane.
 XX
 PS Claim 1; Col 13-14; 18pp; English.
 XX
 CC The present human immunodeficiency virus (HIV) transmembrane glycoprotein
 CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
 CC cell fusion in a culture and cell free HIV transmembrane in a culture to a
 CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX
 SQ Sequence 38 AA;
 XX
 QY Query Match 96.0%; Score 169; DB 2; Length 38;
 DB Best Local Similarity 97.2%; Pred. No. 2.2e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
 1 NNLRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
 RESULT 22
 ID AAY8666 standard; peptide; 38 AA.
 AC AAY8666;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Core polypeptide fragment T No. 21.
 XX
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN WO9959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US011219.
 XX
 PR 20-MAY-1998; 98US-00082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Mernutka G, Anwer MK, Lambert DM;
 XX
 DR WPI; 2000-136792/12.
 XX

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
XX Disclosure; Page 21; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLLRAIEAQOHLQLTWGKIQQLQARILLAVERYLK 36
1 NNLLRAIEAQOHLQLTWGKIQQLQARILLAVERYLK 36
DB
RESULT 23
ID AAY86730 standard; peptide; 38 AA.
AC AAY86730;
XX
XX 23-MAY-2000 (first entry)
DE Core polypeptide fragment T No. 85.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLLRAIEAQOHLQLTWGKIQQLQARILLAVERYLK 36
1 NNLLRAIEAQOHLQLTWGKIQQLQARILLAVERYLK 36
DB
RESULT 24
ID AAY86731 standard; peptide; 38 AA.
AC AAY86731;
XX
XX 23-MAY-2000 (first entry)
DE Core polypeptide fragment T No. 86.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral

CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8851-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
DB

RESULT 25

AAV89145
ID AAV89145 standard; peptide; 38 AA.

AC AAV89145;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 583.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

PS Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8851-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
DB

RESULT 26
AAV89146
ID AAV89146 standard; peptide; 38 AA.

AC AAV89146;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 583.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

PS Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8851-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX

SO Sequence 38 AA;

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
1 NNILRAIEAQOHLQLTWGIKQLQARIILAVERYLK 36
DB

RESULT 27
AAV89243

ID AAY89243 standard; peptide; 38 AA.
 AC AAY89243;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Core polypeptide fragment T No. 681.
 XX
 XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 KM colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN MO959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99MO-US011219.
 XX
 PR 20-MAY-1998; 98US-00082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 DR WPI; 2000-136792/12.
 XX
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.
 XX
 PS Disclosure; Page 32; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 SO Sequence 38 AA;
 QY
 Db 1 NNLRAIEAQOHLTLTWGKIQOLARILAVERYLK 36
 1 NNLRAIEAQOHLTLTWGKIQOLARILAVERYLK 36
 RESULT 28
 AAB14530
 ID AAB14530 standard; peptide; 38 AA.
 AC AAB14530;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).
 XX

KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN W0200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 PI Wild CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Claim 5; Page 56; 97pp; English.
 XX
 CC Sequences AAB14529-B14531 and AAB14537-B14568 represent specifically
 CC claimed peptides derived from the N-helical domain of the gp41 envelope
 CC glycoprotein from a variety of HIV-1 isolates. The invention relates to
 CC raising a neutralizing antibody response to a broad spectrum of HIV
 CC (human immunodeficiency virus) strains and isolates, comprising the
 CC administration of a peptide which corresponds to or mimics highly
 CC conserved portions of gp41 which are important in mediating the process
 CC of viral entry into host cells. Such peptides can correspond to or mimic
 CC the coiled coil solution structure of the N-helical domain (the heptad
 CC repeat region), or can correspond or mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41
 CC core 6-helix bundle, which is formed by the interaction of the N- and C-
 CC helical domains of three gp41 proteins. The peptides can be administered
 CC either singly or as a combination (particularly a combination of N-
 CC helical and C-helical peptides), and can be multimerised. For example, N-
 CC and C-helical domain peptides can be alternately linked together to form
 CC a peptide which mimics the core 6-helix bundle. Administration of the
 CC peptide(s) generates a humoral response, with the production of
 CC antibodies against gp41 structures involved in viral entry. As these
 CC portions of gp41 are well conserved, such antibodies may be effective
 CC against a broad range of HIV strains and isolates. The peptide
 CC compositions may be administered as a prophylactic or therapeutic vaccine
 CC to generate antibodies which reduce or inhibit the ability of HIV to
 CC infect uninfected cells. A composition comprising polyclonal or
 CC monoclonal antibodies can be administered to reduce HIV infection of
 CC uninfected cells. Antibodies raised against entry-relevant gp41
 CC structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 SO Sequence 38 AA;
 QY
 Db 1 NNLRAIEAQOHLTLTWGKIQOLARILAVERYLK 36
 1 NNLRAIEAQOHLTLTWGKIQOLARILAVERYLK 36
 RESULT 29
 AAB52824
 ID AAB52824 standard; peptide; 38 AA.


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XX AAB52824;
AC
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #101.
DE
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemoattractant.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200066622-A1.
XX
XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Disclosure; Page 28; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemoattractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 38 AA;

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

RESULT 30
AAB52786
ID AAB52786 standard; peptide; 38 AA.
XX
XX AAB52786;
AC
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #68.
DE
XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemoattractant.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200066622-A1.
XX

```

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XX 09-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012371.
XX
XX 05-MAY-1999; 99US-0132686P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Claim 12; Page 29; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemoattractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 38 AA;

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

```

Search completed: June 2, 2004, 11:41:43
Job time : 46.0978 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:58 ; Search time 9.78261 Seconds
(without alignments)
353.985 Million cell updates/sec

Title: US-09-657-336A-148
Perfect score: 176
Sequence: 1 NNILRAIEAQHLLQLTWQIKQLQARILLAVERYLK 36

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	96.0	357	2 S21996	envelope protein g
2	169	96.0	851	2 S33985	env polypotein -
3	169	96.0	853	2 S54384	envelope polypote
4	169	96.0	854	2 S13288	env protein - huma
5	169	96.0	855	1 VCLJZR	env polypotein pr
6	169	96.0	856	1 VCLJH3	env polypotein pr
7	169	96.0	856	1 VCLJVL	env polypotein pr
8	169	96.0	861	1 VCLJIV	env polypotein pr
9	168	95.5	357	2 S22006	envelope protein g
10	168	95.5	357	2 S21994	envelope protein g
11	168	95.5	357	2 S22004	envelope protein g
12	168	95.5	358	2 S22002	envelope protein g
13	168	95.5	358	2 S22000	envelope protein g
14	168	95.5	358	2 S70417	envelope protein g
15	168	94.3	357	2 S21990	envelope protein g
16	166	94.3	859	1 VCLJMN	env polypotein pr
17	166	93.8	443	2 C41621	env polypotein pr
18	165	93.8	445	2 A41621	env polypotein pr
19	165	93.8	454	2 B41621	env polypotein pr
20	165	93.8	729	1 VCLJTK	env polypotein pr
21	165	93.8	843	1 H44001	env polypotein pr
22	165	93.8	846	1 VCLJND	env polypotein pr
23	165	93.8	852	2 T12016	envelope glycoprot
24	165	93.8	855	1 VCLJJA	env polypotein pr
25	165	93.8	856	1 VCLJW	env polypotein pr
26	165	93.8	856	1 A44963	env polypotein pr
27	165	93.8	861	1 VCLJXB	env polypotein pr
28	165	93.8	861	1 VCLJSC	env polypotein pr
29	165	93.8	868	1 VCLJH4	env polypotein -

30	164	93.2	859	2 T01672	envelope polypote
31	161	91.5	358	2 S21998	envelope protein g
32	160	90.9	357	2 S21992	envelope protein g
33	157	89.2	852	1 VCLJBR	env polypotein -
34	154	87.5	854	1 VCLJST	env polypotein pr
35	153	86.9	847	2 T09448	envelope glycoprot
36	153	86.9	847	2 S13289	env protein - huma
37	121	68.8	104	2 S52930	GP41 ENV protein -
38	118	67.0	877	2 S49197	envelope protein p
39	114	64.8	864	1 VCLJG4	env polypotein -
40	114	64.8	877	2 C46356	env polypotein -
41	110	62.5	863	2 A53034	gag polypotein -
42	109	61.9	732	2 S46352	env polypotein -
43	104	59.1	366	2 B41665	env polypotein -
44	102	58.0	712	1 VCLJSA	env polypotein pr
45	102	58.0	851	2 S12159	env protein - huma
46	102	58.0	852	1 VCLJSG	env polypotein pr
47	102	58.0	859	1 VCLJST	env polypotein pr
48	102	58.0	869	2 S53098	envelope polypote
49	101	57.4	859	1 VCLJCT	env polypotein pr
50	100	56.8	855	2 A45713	Env transmembrane
51	100	56.8	858	1 VCLJG2	env polypotein pr
52	100	56.8	881	2 S03068	env protein - huma
53	100	56.8	885	2 S04322	env polypotein -
54	100	56.8	886	2 T11555	env protein - stim
55	99	56.2	881	1 VCLJG3	env polypotein -
56	98	55.7	859	2 S24571	env protein - huma
57	98	55.7	869	2 A47665	env protein gp120 (
58	97	55.1	68	2 S60695	env protein - huma
59	97	55.1	68	2 S60696	env protein - huma
60	97	55.1	68	2 S60705	gag protein - huma
61	97	55.1	68	2 S60707	env protein - huma
62	97	55.1	68	2 S60694	env protein - huma
63	97	55.1	68	2 S60706	env protein - huma
64	97	55.1	880	1 VCLJ82	env polypotein pr
65	96	54.5	151	2 S30458	env protein - huma
66	96	54.5	786	2 S28084	env polypotein -
67	96	54.5	889	1 VCLJG5	env polypotein -
68	95	54.0	887	2 T11566	envelope glycoprot
69	94	53.4	151	2 S30448	env protein - huma
70	94	53.4	151	2 S30453	env protein - huma
71	94	53.4	151	2 S30452	env protein - huma
72	94	53.4	151	2 S30450	env protein - huma
73	94	53.4	151	2 S30451	env protein - huma
74	92	52.3	68	2 S60693	env protein - huma
75	92	52.3	68	2 S60687	env protein - huma
76	92	52.3	151	2 S30459	env protein - huma
77	92	52.3	151	2 S30457	env protein - huma
78	92	52.3	151	2 S30456	env protein - huma
79	92	52.3	151	2 S30455	env protein - huma
80	92	52.3	151	2 S30454	env protein - huma
81	90	51.1	68	2 S60692	env protein - huma
82	89	50.6	68	2 S60688	env protein - huma
83	86	48.9	69	2 S60690	env protein - huma
84	86	48.9	69	2 S60689	env protein - huma
85	86	48.9	69	2 S60691	env protein - huma
86	82	46.6	294	2 S60525	envelope polypote
87	82	46.6	297	2 S60538	envelope polypote
88	75	42.6	372	2 S46344	env polypotein -
89	75	42.6	375	2 S46345	env polypotein -
90	73	41.5	294	2 S60545	envelope polypote

ALIGNMENTS

RESULT 1
S21996
C:Species: human immunodeficiency virus type 1 (patient 27L)
C:Date: 20-Feb-1995 #Sequence_Revision 20-Feb-1995 #text_change 26-Aug-1999
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ST2>
A/Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129
A/Experimental source: patient 27L
A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 169; DB 2; Length 357;
Best Local Similarity 97.2%; Pred. No. 2.3e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLK 36
Db 54 NNLRAIEAQOHLLQTLTWGIKOLQARILAVERYLK 89

RESULT 2

S33985
env polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C/Accession: S33985
R/Carlini, F.
Submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33985
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-851 <CAR>
A/Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA7628.1; PID:G60129
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 169; DB 2; Length 851;
Best Local Similarity 97.2%; Pred. No. 5.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLK 36
Db 548 NNLRAIEAQOHLLQTLTWGIKOLQARILAVERYLK 583

RESULT 3

S54384
envelope polyprotein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C/Accession: S54384
R/Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
A/Reference number: S54377
A/Accession: S54384
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-853 <THE>
A/Cross-references: EMBL:M26639; NID:G329377; PIDN:AAA45370.1; PID:G329385
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: polyprotein

Query Match 96.0%; Score 169; DB 2; Length 853;
Best Local Similarity 97.2%; Pred. No. 5.8e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLK 36
Db 550 NNLRAIEAQOHLLQTLTWGIKOLQARILAVERYLK 585

RESULT 4

S13288
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C/Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 346, 69-73, 1990
A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; MUID:91043044; PMID:2172833
A/Accession: S13288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OBR>
C/Superfamily: type E retrovirus env polyprotein

Query Match 96.0%; Score 169; DB 2; Length 854;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLK 36
Db 551 NNLRAIEAQOHLLQTLTWGIKOLQARILAVERYLK 586

RESULT 5

VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus Zr-6
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C/Accession: D26192
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cur
Gene 52, 71-82, 1987
A/Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic
A/Reference number: A26192; MUID:87248097; PMID:3036660
A/Accession: D26192
A/Molecule type: DNA
A/Residues: 1-855 <SRI>
A/Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403
C/Genetics:
A/Genes: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-855/Product: env polyprotein #status predicted <MAT>
F/20-500/Product: exterior membrane glycoprotein #status predicted <TM>
F/501-855/Product: transmembrane glycoprotein #status predicted <TM>
F/87,129,140,145,154,158,186,189,199,236,243,254,278,291,297,333,340,355,386,392,398,404,

Query Match 96.0%; Score 169; DB 1; Length 855;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLLQTLTWQIKOLQARILAVERYLK 36
Db 552 NNLRAIEAQOHLLQTLTWGIKOLQARILAVERYLK 587

RESULT 6

VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HTLV-1
A/Note: host Homo sapiens (man)
C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C/Accession: A03973
R/Reiner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93553; MUID:85111123; PMID:2578615
A/Accession: A03973
A/Molecule type: DNA

A;Residues: 1-856 <RAT>
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326393; PIDN:AAA442
C;Gene: env
A;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

N;Alternate names: coat polyprotein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C;Accession: A03974

R;Muehsing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.

Nature 313, 450-458, 1985

A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov

A;Reference number: A93355; MUID:8511157; PMID:2982104

A;Accession: A03974

A;Molecule type: DNA

A;Residues: 1-856 <MOE>

A;Cross-references: GB:K02083; NID:g555008; PIDN:AA59873.1; PID:g328559

C;Gene: env

C;Superfamily: type B retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F;512-856/Product: transmembrane glycoprotein #status predicted <TM>

F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406

F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A;Gene: env
C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 96.0%; Score 169; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 5.9e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: S70420; S22006

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebri

A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Accession: S70420

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 <STE1>

A;Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191

A;Experimental source: Patient L

A;Note: submitted to the EMBL Data Library, July 1991

C;Superfamily: type B retrovirus env polyprotein

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 36
Db 54 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 89

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 4B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22004; S70419
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22004
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61353; NID:G60188; PIDN:CAA43618.1; PID:G60189
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292, 'X', 294-357 <STE2>
A/Cross-references: EMBL:X61353; NID:G60188
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.5%; Score 168; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 36
Db 54 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 89

RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 3L
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S22002; S70418
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22002
A/Molecule type: DNA
A/Residues: 1-358 <STE1>
A/Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333, 'X', 335-358 <STE2>
A/Cross-references: EMBL:X61352; NID:G60186
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.5%; Score 168; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 36
Db 55 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 90

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C/Accession: S22000
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S22000
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.5%; Score 168; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 36
Db 55 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 90

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A/Reference number: S70417; MUID:92144209; PMID:1736940
A/Accession: S70417
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <STE>
A/Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
C/Superfamily: type E retrovirus env polyprotein

Query Match 95.5%; Score 168; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 3.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 36
Db 55 NNLRRAIEAQOHLLQLTWGIKQLOARVLAVERYLK 90

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 20
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C/Accession: S21990; S70423
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A/Reference number: S21990
A/Accession: S21990
A/Molecule type: DNA
A/Residues: 1-357 <STE1>
A/Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176

F;1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F;263-554/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F;435-454/Domain: transmembrane #status predicted <TMN>
 F;9,23,36,42,48,49,76,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboc

Query Match 93.8%; Score 165; DB 2; Length 454;
 Best Local Similarity 91.7%; Pred. No. 1e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 36
 |||||
 Db 304 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 339

RESULT 20
 VCLJXK
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp32

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996

C;Accession: B42995

R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A;Reference number: A42995; MUID:92351552; PMID:1322587

A;Accession: B42995

A;Molecule type: mRNA

A;Residues: 1-729 <SH1>

A;Cross-references: GB:S41266; GB:D01206

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-689/Domain: extracellular #status predicted <EXT>

F;1-33/Domain: signal sequence #status predicted <SIG>

F;17-33/Region: hydrophobic #status predicted

F;34-517/Product: coat protein gp120 #status predicted <CP1>

F;514-517/Region: cleavage processing #status predicted

F;518-729/Product: coat protein gp32 #status predicted <CP2>

F;518-534/Region: hydrophobic #status predicted

F;690-711/Domain: transmembrane #status predicted <TM1>

F;712-729/Domain: intracellular #status predicted <INT>

F;93,141,145,146,163,191,192,237,241,248,269,283,308,338,345,361,367,397,403,408,414

Query Match 93.8%; Score 165; DB 1; Length 729;
 Best Local Similarity 91.7%; Pred. No. 1.7e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 36
 |||||
 Db 559 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 594

RESULT 21
 H44001
 env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994

C;Accession: H44001

R;Li, Y.; Hui, H.; Burgees, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Accession: H44001

A;Molecule type: DNA

A;Residues: 1-843 <LIV>

A;Cross-references: GB:M93258

C;Genetics:

A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted <SIG>

F;19-35/Region: hydrophobic

F;30-489/Product: coat protein gp120 #status predicted <GP1>

F;490-843/Product: coat protein gp41 #status predicted <GP2>

F;499-515/Region: hydrophobic

F;673-689/Region: hydrophobic

F;738-755/Domain: transmembrane #status predicted <TMN>

F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,

Query Match 93.8%; Score 165; DB 1; Length 843;
 Best Local Similarity 91.7%; Pred. No. 2e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 36
 |||||
 Db 540 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 575

RESULT 22
 VCLJND
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C;Accession: J00066

R;Spire, B.; Sire, U.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.

Gene 81, 275-284, 1989

A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunoc

A;Reference number: J00065; MUID:90034200; PMID:2806917

A;Accession: J00066

A;Molecule type: DNA

A;Residues: 1-846 <SP1>

A;Cross-references: GB:M27323; MUID:9328154; PIDN:AAA44873.1; PID:9328162

A;Note: the authors translated the codon GCG for residue 523 as Arg

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-501/Product: coat protein gp120 #status predicted <CP1>

F;502-846/Product: coat protein gp41 #status predicted <CP2>

F;502-520/Domain: transmembrane #status predicted <TM1>

F;674-682/Domain: transmembrane #status predicted <TM2>

F;87,129,151,179,182,225,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606,

Query Match 93.8%; Score 165; DB 1; Length 846;
 Best Local Similarity 91.7%; Pred. No. 2e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 36
 |||||
 Db 543 NNLRRAIEAOQHLLQLTVMQIKOLQARILAVERYLK 578

RESULT 23

T12016
 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C;Accession: T12016

R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.

AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S

A;Reference number: 217379; MUID:9818716; PMID:9519894

A;Accession: T12016

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-852 <MCC>

A/Cross-references: EMBL:U90934; NID:G2351783; PIDN:AAC59271.1; PID:G2351784
 C/Genetics:
 A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

Query Match 93.8%; Score 165; DB 1; Length 852;
 Best Local Similarity 91.7%; Pred. No. 2e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLK 36
 DB 549 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLR 584

RESULT 24

VCLJAZ
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N/Alternate names: coat polyprotein
 C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C/Accession: A03976

R/Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sch
 Science 227, 484-492, 1985

A/Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A/Reference number: A04003; MUID:85090453; PMID:2578227

A/Accession: A03976

A/Molecule type: DNA

A/Residues: 1-855 <SAN>

A/Cross-references: GB:K02007; NID:G328658; PIDN:AAB59882.1; PID:G328666

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F/1-30/Domain: signal sequence #status predicted <SIG>

F/31-509/Product: exterior membrane glycoprotein #status predicted <EXT>

F/510-855/Product: transmembrane glycoprotein #status predicted <TM>

F/87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
 F/610,624,636,815/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 93.8%; Score 165; DB 1; Length 855;
 Best Local Similarity 91.7%; Pred. No. 2.1e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLK 36
 DB 552 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLR 587

RESULT 25

VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMU1)

N/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

C/Accession: A24774

R/Starchich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986

A/Title: Identification and characterization of conserved and variable regions in the en
 A/Reference number: A24774; MUID:86218077; PMID:2432250

A/Accession: A24774

A/Molecule type: DNA

A/Residues: 1-856 <STB>

A/Cross-references: GB:K03455; GB:M38432; NID:G1906382

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-501/Product: coat protein gp120 #status predicted <GP1>

F/502-847/Product: coat protein gp41 #status predicted <GP2>

F/87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 93.8%; Score 165; DB 1; Length 856;
 Best Local Similarity 91.7%; Pred. No. 2.1e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLK 36
 DB 553 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLR 588

RESULT 26

A44963
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)

N/Alternate names: coat polyprotein

C/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999

C/Accession: A44963

R/Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J
 AIDS Res. Hum. Retroviruses 5, 121-129, 1989

A/Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nuc

A/Reference number: A44963; MUID:89228766; PMID:2713163

A/Accession: A44963

A/Molecule type: DNA

A/Residues: 1-856 <SRI>

A/Cross-references: GB:M15896; NID:G329392; PIDN:AAB5948.1; PID:G329394

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-520/Product: coat protein gp120 #status predicted <CP1>

F/521-856/Product: coat protein gp41 #status predicted <CP2>

F/684-705/Domain: transmembrane #status predicted <TM>

F/87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611,

Query Match 93.8%; Score 165; DB 1; Length 856;
 Best Local Similarity 94.4%; Pred. No. 2.1e-14;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQTLTWQIKOLQARILAVERYLK 36
 DB 553 NNLRAIEAOQHLLQTLTWGIKOLQARILAVERYLR 588

RESULT 27

VCLJKB
 env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N/Alternate names: coat polyprotein

C/Contains: coat protein gp120; coat protein gp41

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C/Accession: A42995

R/Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992

A/Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t

A/Reference number: A42995; MUID:92351552; PMID:1322587

A/Accession: A42995

A/Molecule type: mRNA

A/Residues: 1-861 <SHI>

A/Cross-references: GB:S41266; GB:D01206

C/Genetics:

A/Gene: env
 C/Superfamily: type E retrovirus env polyprotein

C/Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F/1-689/Domain: extracellular #status predicted <EXT>

F/1-33/Domain: signal sequence #status predicted <SIG>

F/17-33/Region: hydrophobic #status predicted

F/34-517/Product: coat protein gp120 #status predicted <CP1>

F/514-517/Region: cleavage processing #status predicted

F/518-861/Product: coat protein gp41 #status predicted <CP2>

F/518-534/Region: hydrophobic #status predicted

F:690-711/Domain: transmembrane #status predicted <TM1>
 F:712-861/Domain: intracellular #status predicted <INT>
 F:756-772/Region: hydrophobic #status predicted
 F:927,141,145,146,163,191,192,227,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.8%; Score 165; DB 1; Length 861;
 Best Local Similarity 91.7%; Pred. No. 2,1e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
 Db 559 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 594

RESULT 28

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C:Accession: B28922

R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
 Virology 164, 531-536, 1988

A:Title: Envelope sequences of two new United States HIV-1 isolates.

A:Reference number: A28922; MUID:86219542; PMID:3369091

A:Accession: B28922

A:Molecule type: DNA

A:Residues: 1-861 <GUR>

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote

F:1.29/Domain: signal sequence #status predicted <SIG>

F:30-861/Product: env polyprotein #status predicted <EBP>

F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 93.8%; Score 165; DB 1; Length 861;
 Best Local Similarity 91.7%; Pred. No. 2,1e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
 Db 558 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 593

RESULT 29

VCLJH4

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C:Accession: C25523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A:Reference number: A94136; MUID:87041461; PMID:3490666

A:Accession: C25523

A:Molecule type: DNA

A:Residues: 1-868 <DESS>

A:Cross-references: GB:ML3137; NID:G326460; PIDN:AAA44311.1; PID:G326467

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote

F:1.521/Product: coat protein gp120 #status predicted <GP1>

F:522-868/Product: coat protein gp41 #status predicted <GP2>

F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,458

Query Match 93.8%; Score 165; DB 1; Length 868;
 Best Local Similarity 94.4%; Pred. No. 2,1e-14;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
 Db 565 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 600

RESULT 30

T01672

env polyprotein precursor - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000

C:Accession: T01672

R:Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A:Reference number: Z14389; MUID:86245056; PMID:2424612

A:Accession: T01672

A>Status: preliminary; translated from GB/EMBL/DDbJ

A:Molecule type: mRNA

A:Residues: 1-859 <ALTI>

C:Cross-references: EMBL:X03456; NID:G60228; PIDN:CA28016.1; PID:G60234

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.2%; Score 164; DB 2; Length 859;
 Best Local Similarity 91.7%; Pred. No. 2,8e-14;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
 Db 555 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 590

Search completed: June 2, 2004, 11:50:09
 Job time : 10.7826 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:57 ; Search time 5.86957 Seconds
(without alignments)
319.364 Million cell updates/sec

Title: US-09-657-336a-148
Perfect score: 176
Sequence: 1 NNILRAIEAQHLLQLTWQIKOLQARIILAVERYLK 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169	96.0	853	1	ENV_HV1EL
2	169	96.0	853	1	ENV_HV1MF
3	169	96.0	853	1	ENV_HV122
4	169	96.0	855	1	ENV_HV126
5	169	96.0	856	1	ENV_HV181
6	169	96.0	856	1	ENV_HV182
7	169	96.0	856	1	ENV_HV183
8	169	96.0	856	1	ENV_HV184
9	169	96.0	856	1	ENV_HV185
10	169	96.0	856	1	ENV_HV186
11	169	96.0	856	1	ENV_HV187
12	168	95.5	855	1	ENV_HV188
13	166	94.3	846	1	ENV_HV189
14	166	94.3	846	1	ENV_HV190
15	165	93.8	843	1	ENV_HV191
16	165	93.8	846	1	ENV_HV192
17	165	93.8	851	1	ENV_HV193
18	165	93.8	852	1	ENV_HV194
19	165	93.8	855	1	ENV_HV195
20	165	93.8	856	1	ENV_HV196
21	165	93.8	856	1	ENV_HV197
22	165	93.8	856	1	ENV_HV198
23	165	93.8	861	1	ENV_HV199
24	165	93.8	865	1	ENV_HV200
25	165	93.8	867	1	ENV_HV201
26	165	93.8	868	1	ENV_HV202
27	164	93.2	859	1	ENV_HV203
28	162	92.0	847	1	ENV_HV204
29	160	90.9	863	1	ENV_HV205
30	157	89.2	852	1	ENV_HV206
31	154	87.5	854	1	ENV_HV207
32	114	64.8	865	1	ENV_HV208
33	114	64.8	877	1	ENV_HV209

34	111	63.1	854	1	ENV_SIVAI	Q02837 simian immu
35	106	60.2	768	1	ENV_SIVAI	P27757 simian immu
36	102	58.0	712	1	ENV_HV2S2	P32536 human immu
37	102	58.0	851	1	ENV_HV2D1	P17755 human immu
38	102	58.0	851	1	ENV_HV2G1	P18040 human immu
39	102	58.0	856	1	ENV_HV2NZ	P05883 human immu
40	102	58.0	859	1	ENV_HV2ST	P20872 human immu
41	102	58.0	860	1	ENV_HV2BE	P18094 human immu
42	101	57.4	859	1	ENV_HV2CA	P24105 human immu
43	100	56.8	380	1	ENV_SIVW2	P08810 simian immu
44	100	56.8	858	1	ENV_HV2RO	P04577 human immu
45	100	56.8	855	1	ENV_SIVS4	P12492 simian immu
46	100	56.8	889	1	ENV_SIVS4	P15053 simian immu
47	99	56.2	882	1	ENV_SIVS4	P05885 simian immu
48	98	55.7	859	1	ENV_HV2D2	P15831 human immu
49	97	55.1	846	1	ENV_HV2SB	P12449 human immu
50	97	55.1	880	1	ENV_SIVWL	P11267 simian immu
51	96	54.5	821	1	ENV_SIVGB	P22380 simian immu
52	96	54.5	881	1	ENV_SIVWK	P05884 human immu
53	95	54.0	857	1	ENV_HV2KR	Q74126 human immu
54	53	30.1	2564	1	SPCQ_HUMAN	O9h254 homo sapien
55	52	29.5	1379	1	M3KS_MOUSE	O35099 mus musculu
56	52	29.0	1938	1	MYH4_MOUSE	Q28641 cryptoleagus
57	50.5	28.7	1411	1	BEAL_MOUSE	Q15075 homo sapien
58	50	28.4	1374	1	M3KS_MOUSE	Q96683 homo sapien
59	50	28.4	1938	1	MYH4_MOUSE	P24733 aequipecten
60	50	28.4	1939	1	MYH4_MOUSE	O96623 homo sapien
61	49.5	28.1	581	1	FRIZ_DROME	P18537 drosophila
62	49.5	28.1	583	1	FRIZ_DROVI	Q24760 drosophila
63	49	27.8	4349	1	DHIC_FUSO	P78716 fusarium so
64	48.5	27.6	445	1	EX7L_STAM	O997X0 staphylococ
65	48.5	27.6	790	1	BEAL_MOUSE	O8b166 mus musculu
66	48	27.3	236	1	GT6_SCHNA	P64435 schistosoma
67	48	27.3	551	1	YD25_YEAST	O07657 saccharomyc
68	48	27.3	906	1	CTN1_HUMAN	P35221 homo sapien
69	48	27.3	906	1	CTN1_MOUSE	P26231 mus musculu
70	48	27.3	1935	1	MYSS_CYPCA	O90339 cyprinus ca
71	48	27.3	8797	1	SNEI_HUMAN	O8nf91 homo sapien
72	47.5	27.0	253	1	CYSH_VIBCH	O9kux2 vibrio chol
73	47.5	27.0	303	1	ALB3_MALZE	P10593 zea mays (m
74	47.5	27.0	467	1	EUTE_ECOLI	P77445 escherichia
75	47.5	27.0	467	1	EUTE_SALTY	P41793 salmonella
76	47.5	27.0	924	1	HXK3_RAT	P27928 rattus norv
77	47.5	27.0	962	1	ARVC_HUMAN	O00192 homo sapien
78	47.5	27.0	969	1	ARVC_MOUSE	P68263 mus musculu
79	47.5	27.0	1319	1	SOS1_MOUSE	O62245 mus musculu
80	47.5	27.0	1333	1	SOS1_HUMAN	Q07889 homo sapien
81	47.5	27.0	1955	1	PUMA_PARKN	P61308 parascaris
82	47	26.7	376	1	O43A_DROME	P81917 drosophila
83	47	26.7	418	1	DADI_RHILLO	O98f08 rhizobium 1
84	47	26.7	684	1	RPOC_MARPO	P06273 marchantia
85	47	26.7	1941	1	MYH2_HUMAN	O9ukx2 homo sapien
86	46.5	26.4	1093	1	AF17_HUMAN	P55128 homo sapien
87	46.5	26.4	1755	1	PEPL_MOUSE	O97268 mus musculu
88	46.5	26.4	2022	1	ANTI_ONCPO	P12149 onchocerca
89	46	26.1	70	1	RL15_BRUPA	P41961 druggia paha
90	46	26.1	286	1	IN35_HUMAN	P80217 homo sapien

ALIGNMENTS

RESULT 1
ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE ENV.
OS Human immunodeficiency virus type 1 (EML isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6245056; PubMed=2424612;
 RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 of two isolates from African patients";
 RL Cell 46:63-74(1986).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K03454; AAA44329.1; -;
 DR EMBL; A07108; CA00616.1; -;
 DR HIV; K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MM; P0CDB64DAA007A5 CMC64;
 Query Match 96.0%; Score 169; DB 1; Length 853;

Best Local Similarity 97.2%; Pred. No. 3 5e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NNLRAIEAQHLLQTLTWQIKQLQARILAVERYLK 36
 Db 550 NNLRAIEAQHLLQTLTWQIKQLQARILAVERYLK 585
 RESULT 2
 ENV HVLMF STANDARD; PRT; 853 AA.
 ID ENV HVLMF AC p19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
 RA Wasik A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1
 RT variants diminished in the ability to induce syncytium-independent
 RT cytolysis";
 RL J. Virol. 64:3792-3803(1990).
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 CC -----
 CC EMBL; M33943; AAA44850.1; -;
 DR PDB; 1A1K; 16-JUN-97.
 DR HIV; M33943; ENVSMFA.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KM 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 203 BY SIMILARITY.
 FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 329 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 337789386P22ABA CRC64;

Query Match 96.0%; Score 169; DB 1; Length 853;
 Best Local Similarity 97.2%; Pred. No. 3.5e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRALAEQOHLTLTWGKIQARILAVERYLK 36
 Db 551 NNTLRALAEQOHLTLTWGKIQARILAVERYLK 586

RESULT 3
 ENV_HV126 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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CC -----
 DR EMBL; M22639; AAA45370.1; .
 DR PIR; S54384; S54384.
 DR HIV; M22639; ENS52226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL.
 FT CHAIN 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.

FT DISULFID 383 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 97043 MW; 849B08BCBAFF7008 CRC64;

Query Match 96.0%; Score 169; DB 1; Length 853;
 Best Local Similarity 97.2%; Pred. No. 3.5e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRALAEQOHLTLTWGKIQARILAVERYLK 36
 Db 550 NNTLRALAEQOHLTLTWGKIQARILAVERYLK 585

RESULT 4
 ENV_HV126 STANDARD; PRT; 855 AA.
 AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87248097; Pubmed=3036660;
 RA Srinivasan A., Anand R., York D., Ranganathan P., Forino P.,
 RA Schoeneman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
 RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
 RT Gene 52:71-82(1987).
 RL

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CC		EMBL; K03458; AAA45380.1; -.	-	
DR	PIR; D26192; VCLJZR.	HIV; K03458; ENV5Z6.	Env GP41.	
DR	InterPro; IPR000328; Env GP41.	InterPro; IPR00777; GP120.	Pfam; PF00516; GP120; 1.	
DR	AIDS; Pf00517; GP41; 1.	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;	Signal.	
KM	SIGNAL.	1	30	
FT	CHAIN	31	510	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	511	855	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	207	BY SIMILARITY.
FT	DISULFID	125	198	BY SIMILARITY.
FT	DISULFID	130	155	BY SIMILARITY.
FT	DISULFID	220	249	BY SIMILARITY.
FT	DISULFID	230	241	BY SIMILARITY.
FT	DISULFID	298	332	BY SIMILARITY.
FT	DISULFID	378	444	BY SIMILARITY.
FT	DISULFID	385	417	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	189	189	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	226	236	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	233	243	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	264	264	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	278	278	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	291	291	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	333	333	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	340	340	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	386	386	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	398	398	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	404	404	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	443	443	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	447	447	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	460	460	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	461	461	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	464	464	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	610	610	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	636	636	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	673	673	N-LINKED (GLCNAC . .) (POTENTIAL).
SO	SEQUENCE	855 AA;	96971 MW;	3BBD3DBE239C3A457 CRC64;
Query Match 96.0%; Score 169; DB 1; Length 855; Best Local Similarity 97.2%; Pred. No. 3.5e-16; Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0,				
OY	1	NNLRAIAAOOHLLOLTWTWQIKOLARILAVERLYK	36	
Db	552	NNLRRAIEAOOHLLOLTWTWGIIKOARIILAVERLYK	587	
RESULT 5 ENV_HVIB1 STANDARD; PRT; 856 AA. AC P03375; DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last annotation update) DT 15-JUN-1999 (Rel. 38, Last sequence update) DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane				

[illegible]

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FT CARBOHYD 386 386 N-LINKED (GLCNAC . . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC . . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC . . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC . . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC . . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC . . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC . . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC . . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC . . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC . . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC . . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC . . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC . . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 3,5e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNLLRAIEAQQHLLQTLTWQIKQLOARILAAVERLYK 36
Db 553 NNLLRAIEAQQHLLQTLTWQIKQLOARILAAVERLYK 588

RESULT 6
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; O09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM: N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; K03455; AAB50262.1; -.
DR EMBL; AF038399; AAB99976.1; -.
DR EMBL; AF038319; AAC82596.1; -.
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DLB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCL; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENV$HXB2.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.

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DR	Pfam; PF00516; GP120; 1.
DR	Pfam; PF00517; GP41; 1.
.KM	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
FT	SIGNAL 1 30
FT	CHAIN 31 511
FT	DISULFID 512 856
FT	DISULFID 54 74
FT	DISULFID 119 205
FT	DISULFID 126 196
FT	DISULFID 131 157
FT	DISULFID 218 247
FT	DISULFID 228 239
FT	DISULFID 296 331
FT	DISULFID 378 445
FT	DISULFID 385 418
FT	CARBOHYD 88
FT	CARBOHYD 136 136
FT	CARBOHYD 141 141
FT	CARBOHYD 156 156
FT	CARBOHYD 160 160
FT	CARBOHYD 186 186
FT	CARBOHYD 197 197
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FT	CARBOHYD 295 295
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FT	CARBOHYD 339 339
FT	CARBOHYD 356 356
FT	CARBOHYD 386 386
FT	CARBOHYD 392 392
FT	CARBOHYD 397 397
FT	CARBOHYD 406 406
FT	CARBOHYD 448 448
FT	CARBOHYD 463 463
FT	CARBOHYD 611 611
FT	CARBOHYD 616 616
FT	CARBOHYD 624 624
FT	CARBOHYD 637 637
FT	CARBOHYD 674 674
FT	CARBOHYD 750 750
FT	CARBOHYD 816 816
SO	SEQUENCE 856 AA; 97212 MW; 6PAB16A8510FE80 CRC64;
Query Match	96.0%; Score 169; DB 1; Length 856;
Best Local Similarity	97.2%; Pred. No. 3.5e-16;
Matches 35; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 NNILRLATEAOQHLLQLTWVQIKQLQAIIIVAVERTLK 36
Dd	553 NNILRLATEAOQHLLQLTWVGKIKQLQAIIIVAVERYLTK 588
RESULT 7	
ID ENV_HV1H3 STANDARD; PRT; 856 AA.	
AC P04624;	
DT 13-AUG-1987 (Rel. 05, Created)	
DT 01-FEB-1996 (Rel. 33, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	
DE gp120	
GN HIV.	
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).	
OC Viruses; Retroviral viruses; Lentiviridae; Lentivirus.	
CC NCBI_Taxid=11707;	
OX [1]	
RP SEQUENCE FROM N.A.	

RX MEDLINE=8528284; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-1 env gene products synthesized in E. coli are recognized by
 RT antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
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 CC -----
 DR EMBL; M14100; AAA44679.1; -.
 DR PDB; 1JAV; 17-OCT-01.
 DR PDB; 1JAV; 17-OCT-01.
 DR HIV; M14100; ENVSHX3.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KM
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 1 511
 FT DISULFID 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT DISULFID 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
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 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
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 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT CARBOHYD 856 AA; 97188 MW; 3373688B84C1AFC CRC64;
 SQ SEQUENCE
 Query Match 96.0%; Score 169; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 3.5e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNTLRALFAOQHLLQITWQIKOLQARILAVERYLK 36
 Db 553 NNTLRALFAOQHLLQITWQIKOLQARILAVERYLK 588
 RESULT 8
 ENV_HVILW STANDARD; PRT; 856 AA.
 ID ENV_HVILW
 AC Q70626;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=82834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.;
 RT "viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type 11B).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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 CC -----
 DR EMBL; U12055; AA76690.1; -.
 DR PDB; 1IP3; 02-MAY-01.
 DR GlycoSuiteDB; Q70626; -.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KM
 FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 1 511
 FT DISULFID 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
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 FT DISULFID 296 331
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 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 FT CARBOHYD 856 AA; 97188 MW; 3373688B84C1AFC CRC64;
 SQ SEQUENCE
 Query Match 96.0%; Score 169; DB 1; Length 856;
 Best Local Similarity 97.2%; Pred. No. 3.5e-16;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E687 CRC64;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKQARILAVERYLK 36
Db 553 NNLRAIEAOQHLLQLTWQIKQARILAVERYLK 588

RESULT 9
ENV_HV1PV STANDARD; PRT; 856 AA.
ID ENV_HV1PV
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RX MEDLINE=8511157; PubMed=2982104;
RA Mesling M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laasy L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
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CC -----
CC EMBL; K02083; AAB59873.1;
DR EMBL; X01762; CA25903.1; ALT_SEQ.
DR PIR; A03974; VCLJVL.
DR HIV; K02083; ENV$PV22.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.

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FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCBBD3C120983 CRC64;

Query Match 96.0%; Score 169; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKQARILAVERYLK 36
Db 553 NNLRAIEAOQHLLQLTWQIKQARILAVERYLK 588

RESULT 10
ENV_HV1BR STANDARD; PRT; 861 AA.
ID ENV_HV1BR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RX MEDLINE=85099333; PubMed=2981635;
RA Main-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
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DR EMBL: K02013; AAB59751.1; -.
DR EMBL: A04321; CA00352.1; -.
DR PIR: A03975; VCLJLV.
DR PDB: 1ERF; 20-FEB-02.
DR HIV: K02013; ENV58BU.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516
FT CARBOHYD 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
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FT DISULFID 383 450
FT DISULFID 390 423
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FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 337 337
FT CARBOHYD 344 344
FT CARBOHYD 361 361
FT CARBOHYD 391 391
FT CARBOHYD 397 397
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 453 453
FT CARBOHYD 468 468
FT CARBOHYD 616 616
FT CARBOHYD 621 621
FT CARBOHYD 630 630
FT CARBOHYD 642 642
FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 96.0%; Score 169; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 3.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNTLRATEAOOHLTLTVMQIKOLARILAVERYLK 36
Db 558 NNTLRATEAOOHLTLTVMQIKOLARILAVERYLK 593

RESULT 11
AC ENV_HV1S1 STANDARD; PRT; 847 AA.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP120 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RX Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.;
RA "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398(1990).
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC EMBL: M65024; AAA45072.1; -.
DR PDB: 1OBE; 15-MAY-97.
DR HIV: M38428; ENV58F162.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 328
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87 87
FT CARBOHYD 135 135
FT CARBOHYD 154 154
FT CARBOHYD 186 186
FT CARBOHYD 195 195
FT CARBOHYD 232 232
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 293 293
FT CARBOHYD 299 299
FT CARBOHYD 329 329
FT CARBOHYD 336 336
FT CARBOHYD 352 352
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 401 401
FT CARBOHYD 438 438
FT CARBOHYD 454 454
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

Query Match 95.5%; Score 168; DB 1; Length 847;
Best Local Similarity 94.4%; Pred. No. 4.8e-16;

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Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLTLTWGKQIQAARVLAVERYLK 36
 DB 544 NNLRRAIEAQOHLTLTWGKQIQAARVLAVERYLK 579

RESULT 12
 ENV_HV10Y STANDARD; PRT; 855 AA.

AC P20688:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Huec T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot."
 RL AIDS 3:707-715(1989).
 CC -!- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
 CC -----
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 CC -----
 CC EMBL: M26727; AAA83397.1; -.
 DR HIV; M26727; ENV50YI.
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 210 BY SIMILARITY.
 FT DISULFID 125 201 BY SIMILARITY.
 FT DISULFID 130 162 BY SIMILARITY.
 FT DISULFID 223 252 BY SIMILARITY.
 FT DISULFID 233 244 BY SIMILARITY.
 FT DISULFID 301 335 BY SIMILARITY.
 FT DISULFID 381 442 BY SIMILARITY.
 FT DISULFID 388 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 95.5%; Score 168; DB 1; Length 855;
 Best Local Similarity 94.4%; Pred. No. 4,9e-16;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLTLTWGKQIQAARVLAVERYLK 36
 DB 552 NNLRRAIEAQOHLTLTWGKQIQAARVLAVERYLK 587

RESULT 13
 ENV_HV10Y STANDARD; PRT; 848 AA.

AC P20671:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11688;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koyanagi S., Chen I.S.Y.;
 RL Submitted (DEC-1988) to the HIV data bank.
 CC -----
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 CC -----
 CC EMBL: M38429; AAB03749.1; -.
 DR PDB: 1CE4; 18-MAR-99.
 DR HIV; M38429; ENV5TRCSF.
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 503 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 504 848 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 203 BY SIMILARITY.
 FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 328 BY SIMILARITY.
 FT DISULFID 374 437 BY SIMILARITY.
 FT DISULFID 381 410 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 848 AA; 96475 MW; 20767F5127EC33 CRC64;

Query Match 94.3%; Score 166; DB 1; Length 848;
 Best Local Similarity 91.7%; Pred. No. 9.4e-16;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
 545 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 580

RESULT 14
 ID ENV_HV1MN STANDARD; PRT; 856 AA.
 AC P05877;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11696;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8219542; PubMed=3369091;
 RA Gargo C., Guo H.-G., Franchini G., Aldovini A., Collalti B.,
 RA Bartell K., Wong-Staal F., Gallo R.C., Reitz M.S.Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates."
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS PATIENT IN 1984.
 CC
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 CC
 CC EMBL; M17449; AAA44857.1; -
 DR PDB; 1ACJ; 31-JUL-94.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1N1Z; 25-FEB-03.
 DR PDB; 1N1O; 25-FEB-03.
 DR HIV; M17449; ENVSMN.

DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 445
 FT DISULFID 388 418
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 141 141
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT CARBOHYD 202 202
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 336 336
 FT CARBOHYD 343 343
 FT CARBOHYD 359 359
 FT CARBOHYD 365 365
 FT CARBOHYD 395 395
 FT CARBOHYD 401 401
 FT CARBOHYD 405 405
 FT CARBOHYD 406 406
 FT CARBOHYD 413 413
 FT CARBOHYD 448 448
 FT CARBOHYD 465 465
 FT CARBOHYD 612 612
 FT CARBOHYD 617 617
 FT CARBOHYD 626 626
 FT CARBOHYD 638 638
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match 94.3%; Score 166; DB 1; Length 856;
 Best Local Similarity 91.7%; Pred. No. 9.5e-16;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
 554 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 589

RESULT 15
 ID ENV_HV1Y2 STANDARD; PRT; 843 AA.
 AC P35961;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=36377;


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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA; 96476 MW; 8A3BD4527DE2E83 CRC64;

Query Match 93.8%; Score 165; DB 1; Length 846;
Best Local Similarity 91.7%; Pred. No. 1,3e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NMLRAEAGQHLQTLTWQIKOLQARILAVERYLK 36
Db 543 NMLRAEAGQHLQTLTWQIKOLQARILAVERYLK 578

RESULT 17
ENV_HY1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (B8 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11694;
RN [1]
RP MEDLINE=9511123; PubMed=2578615;
RX Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalecki J.A., Whitehorn E.A.,
RA Bauteister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Chirgob J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02011; AAA44661.1; -.
DR PDB; 1DH; 13-JAN-99.
DR PDB; 1HH; 31-OCT-93.
DR PDB; 1QO3; 02-JAN-00.
DR PDB; 1S2T; 24-DEC-97.
DR HIV; K02011; ENV588.
DR GlycoSiteDB; P04582; -.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 1 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.

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FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 440 BY SIMILARITY.
FT DISULFID 385 413 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C98057785F1 CRC64;

Query Match 93.8%; Score 165; DB 1; Length 851;
Best Local Similarity 94.4%; Pred. No. 1,3e-15;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 NMLRAEAGQHLQTLTWQIKOLQARILAVERYLK 36
Db 548 NMLRAEAGQHLQTLTWQIKOLQARILAVERYLK 583

RESULT 18
ENV_HY1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11690;
RN [1]
RP MEDLINE=90317906; PubMed=2370688;
RX York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RA "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

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SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
 Query Match 93.8%; Score 165; DB 1; Length 855;
 Best Local Similarity 91.7%; Pred. No. 1,3e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAQOHLQTLTWQIKOLARILAVERYLK 36
 DB 553 NNLRRAIEAQOHLQTLTWQIKOLARILAVERYLK 587

RESULT 20
 ENV_HV1SC STANDARD; PRT; 856 AA.
 AC P05878;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11702;
 RN [1]
 RP MEDLINE=86219542; PubMed=3369091;
 RA Garg C., Guo H.-G., Franchini G., Aldrovini A., Collalti E., Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates";
 RL Virology 164:531-536(1988).
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN 1984 IN SOUTHERN CALIFORNIA.

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CC EMBL, M17450; - NOT_ANNOTATED_CDS.
 DR HIV; M17450; ENV5SC.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;
 Query Match 93.8%; Score 165; DB 1; Length 856;
 Best Local Similarity 91.7%; Pred. No. 1,3e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NNLRRAIEAQOHLQTLTWQIKOLARILAVERYLK 36
 DB 553 NNLRRAIEAQOHLQTLTWQIKOLARILAVERYLK 588

RESULT 21
 ENV_HV1SC STANDARD; PRT; 856 AA.
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MMU1 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=31678;
 RN [1]
 RP MEDLINE=86218077; PubMed=2423250;
 RA Scarlatch B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS";
 RL Cell 45:637-646(1986).
 CC -1- MISCELLANEOUS: ISOLATES MMU1, MMU2, AND MMU3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR; A24774; VCLJ3W.
 DR PDB; 1L80; 04-DEC-02.
 DR PDB; 1LCK; 04-DEC-02.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 205 BY SIMILARITY.
 FT DISULFID 125 196 BY SIMILARITY.


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FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404D95 CRC64;

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Query Match 93.8%; Score 165; DB 1; Length 856;
Best Local Similarity 91.7%; Pred. No. 1.3e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NNLIRATEAOQHLLQTLVWQIKOLQARILAVERYLK 36
553 NNLIRATEAOQHLLQTLVWQIKOLQARILAVERYLK 588

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RESULT 22
ENV_HV1ZH STANDARD; PRT; 856 AA.
AC P05881;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11692;
[1]
SEQUENCE FROM N.A.
MEDLINE=89228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D., Jannoun-Naer R., Getchell J.,
McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of Hybrid HIV-1."
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
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or send an email to license@isb-sib.ch).
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CC -----
DR EMBL; M15896; AAB53948.1; -
DR PIR; A44963; A44963.
DR HIV; M15896; ENV52321.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 511
FT CHAIN 512 856
FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 153
FT DISULFID 219 248
FT DISULFID 229 240
FT DISULFID 297 331
FT DISULFID 379 445
FT DISULFID 386 418
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 839683F8BBD174E CRC64;

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Query Match 93.8%; Score 165; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 1.3e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NNLIRATEAOQHLLQTLVWQIKOLQARILAVERYLK 36
553 NNLIRATEAOQHLLQTLVWQIKOLQARILAVERYLK 588

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RESULT 23
ENV_HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

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CC NCBI_TaxID=36375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92351552; PubMed=1322587;
 RA Shimizu H., Haesebe F., Tsuchie H., Morikawa S., Ushijima H.,
 RA Kitamura T.;
 RT "Analysis of a human immunodeficiency virus type 1 isolate carrying a
 RT truncated transmembrane glycoprotein.";
 RL Virology 189:534-546(1992).
 CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
 CC THE CODONS FOR 729-ALA AND 730-ARG.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D12582; BAA02124.1; ALT_SEQ.
 DR PIR; A42995; VCLJKB.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 35 POTENTIAL.
 FT CHAIN 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 861 TRANSMEMBRANE GLYCOPROTEIN.
 FT TRANSEM 690 711 POTENTIAL.
 FT DISULFID 59 79 BY SIMILARITY.
 FT DISULFID 124 212 BY SIMILARITY.
 FT DISULFID 131 203 BY SIMILARITY.
 FT DISULFID 136 160 BY SIMILARITY.
 FT DISULFID 225 254 BY SIMILARITY.
 FT DISULFID 235 246 BY SIMILARITY.
 FT DISULFID 303 337 BY SIMILARITY.
 FT DISULFID 383 446 BY SIMILARITY.
 FT DISULFID 390 419 BY SIMILARITY.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 861 AA; 98116 MW; 3C06787658F0C9DA CRC64;

Query Match 93.8%; Score 165; DB 1; Length 861;
 Best Local Similarity 91.7%; Pred. No. 1.3e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHILQITWMOIKOLARILLAVEYRK 36
 Db 559 NNLRAIDAOQHILQITWMOIKOLARILLAVEYRK 594
 RESULT 24
 ENV_HVLRH STANDARD; PRT; 865 AA.
 AC P04579;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (RF/HMT isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86218077; PubMed=2423250;
 RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 RT Cell 45:637-648(1986).
 RL
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M17451; AAA45057.1; -.
 DR HIV; M17451; ENV\$RF.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT CHAIN 1 29
 FT CHAIN 519 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 865 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 218 BY SIMILARITY.
 FT DISULFID 125 209 BY SIMILARITY.
 FT DISULFID 130 157 BY SIMILARITY.
 FT DISULFID 231 260 BY SIMILARITY.
 FT DISULFID 241 252 BY SIMILARITY.
 FT DISULFID 309 343 BY SIMILARITY.
 FT DISULFID 389 452 BY SIMILARITY.
 FT DISULFID 396 425 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC314ADCAC CRC64;
 Query Match 93.8%; Score 165; DB 1; Length 865;
 Best Local Similarity 91.7%; Pred. No. 1.3e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 NNLLRAIEAQOHLQLTWQIKOLQARIILAVERYLK 36
 Db 562 NNLLRAIEAQOHLQLTWQIKOLQARIILAVERYLK 597
 RESULT 25
 ENV_HV1J3 STANDARD; PRT; 867 AA.
 AC P12489;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11694;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352108; PubMed=2669897;
 RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
 HIV-1 and their expression in bacteria.";
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; M21138; AAB03526.1; -
 DR HIV; M21138; EMB03526.1; -
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KM signal.
 FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 31 516 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 217 BY SIMILARITY.
 FT DISULFID 125 208 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 230 259 BY SIMILARITY.
 FT DISULFID 240 251 BY SIMILARITY.
 FT DISULFID 308 342 BY SIMILARITY.
 FT DISULFID 388 457 BY SIMILARITY.
 FT DISULFID 395 430 BY SIMILARITY.
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 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8B8680 CRC64;
 Query Match 93.8%; Score 165; DB 1; Length 867;
 Best Local Similarity 94.4%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 NNLLRAIEAQOHLQLTWQIKOLQARIILAVERYLK 36
 Db 564 NNLLRAIEAQOHLQLTWQIKOLQARIILAVERYLK 599
 RESULT 26
 ENV_HV1C4 STANDARD; PRT; 868 AA.
 AC P05879;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041461; PubMed=3490666;
 RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
 RT "Molecular cloning and primary nucleotide sequence analysis of a
 RT distinct human immunodeficiency virus isolate reveal significant
 RT divergence in its genomic sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
 RN [2]
 SQ SEQUENCE OF 34-43.

FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 467 467 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 819 819 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 859 AA; 97109 MW; DBCF9A523ABF29 CRC64;
 Query Match 93.2%; Score 164; DB 1; Length 859;
 Best Local Similarity 91.7%; Pred. No. 1.8e-15;
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIEAQOHLLQTLTWGICQLOARVLAVERYLK 36
 DB 555 NNLLRAIEAQOHLLQTLTWGICQLOARVLAVERYLK 590
 RESULT 28
 ENV_HV1W2 STANDARD; PRT; 847 AA.
 ID ENV_HV1W2
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6235450; PubMed=1012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salanudin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.; "Genetic variation in HIV-1/LAV over time in patients with AIDS or at risk for AIDS."
 RT Science 232:1548-1553(1986).
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
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 CC -----
 CC EMBL; M12507; AAB12990.1; -
 DR HIV; M12507; ENVSWMJ2.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KM SIGNAL. 1 29
 FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.

FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
 FT DISULFID 379 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
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 FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. .) (POTENTIAL).
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 FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73A5BCAE CRC64;
 Query Match 92.0%; Score 162; DB 1; Length 847;
 Best Local Similarity 88.9%; Pred. No. 3.5e-15;
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLLRAIEAQOHLLQTLTWGICQLOARVLAVERYLK 36
 DB 544 NNLLRAIEAQOHLLQTLTWGICQLOARVLAVERYLK 579
 RESULT 29
 ENV_HV1Z8 STANDARD; PRT; 863 AA.
 ID ENV_HV1Z8
 AC P05882;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; PubMed=3395517;
 RA Yorno U., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F., Gallo R.C.; "Nucleotide sequence analysis of the env gene of a new Zairian isolate of HIV-1."
 RT J. Virol. 63:165-173(1989).
 RT AIDS Res. Hum. Retroviruses 4:165-173(1988).
 RL -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIREAN MALE.
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CC -----
DR EMBL; J03653; AAA44684.1; -.
DR HIV; J03653; ENV5JY1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL. 1 29
FT CHAIN 30 518 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 519 863 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 452 BY SIMILARITY.
FT DISULFID 395 425 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729C85A6FAD1641 CRC64;

Query Match 90.9%; Score 160; DB 1; Length 863;
Best Local Similarity 88.9%; Pred. No. 6.8e-15;
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 NNTLRATEAOCHLQTLVWQKQCARLLAVERTLK 36
Db 560 NNTLRATEAOCHLQTLVWQKQCARLLAVERTLK 595

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OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2769516;
RA Mand R., Thayer R., Srinivasan A., Nayar S., Gardner M., Luciw P.,
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia."
RT Virology 168:79-89(1989).
CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC -----
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CC -----
CC EMBL; M21098; AAA44221.1; -.
CC PIR; A3167; VCLJBR.
DR PDB; 1IM7; 23-OCT-02.
DR HIV; M21098; ENV5JY1.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL. 1 30
FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

Wed Jun 2 13:47:03 2004

us-09-657-336a-148.rsp

Page 21

FT	CARBOHYD	812	812	N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ	SEQUENCE	852 AA;	97203 MW;	2BB86345DEC915F CRC64;

Query Match	89.2%	Score 157;	DB 1;	Length 852;
Best Local Similarity	86.1%;	Pred. No. 1.8e-14;		
Matches 31;	Conservative	3;	Mismatches 2;	Indels 0;
				Gaps 0;

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QY      1 NNLLRALEAQOQHLLQLTWQKQKQLQARILAVERYLK 36
        ||||| ||||| : ||||| ||||| : |||||
Db      549 NNLLMALEAQOQHMLLETWVGIKQLQARVLAVERYLK 584
```

Search completed: June 2, 2004, 11:42:55
Job time : 6.86957 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 11:32:18 / Search time 30.2283 Seconds
(without alignments)
375.763 Million cell updates/sec

Title: US-09-657-336a-148
Sequence: 1 NNLRAIEAQHLLQTLTWQIKQLQARIILAVERYLK 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :
1: SPTEMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	96.0	132	15	090052 human immun
2	169	96.0	132	15	07SLI22 human immun
3	169	96.0	143	15	07SM06 human immun
4	169	96.0	144	15	07ZCD7 human immun
5	169	96.0	144	15	07ZCD6 human immun
6	169	96.0	153	15	07SM03 human immun
7	169	96.0	357	15	078119 human immun
8	169	96.0	588	15	0993A8 human immun
9	169	96.0	588	15	0993A7 human immun
10	169	96.0	589	15	0993B1 human immun
11	169	96.0	590	15	0993A9 human immun
12	169	96.0	616	15	0993B0 human immun
13	169	96.0	618	15	0993B2 human immun
14	169	96.0	727	15	09Q723 human immun
15	169	96.0	747	15	070607 human immun
16	169	96.0	748	15	070606 human immun

17	169	96.0	752	15	070604 human immun
18	169	96.0	752	15	070605 human immun
19	169	96.0	752	15	070608 human immun
20	169	96.0	757	15	09Q722 human immun
21	169	96.0	811	15	09DVL6 human immun
22	169	96.0	842	15	073341 human immun
23	169	96.0	842	15	070895 human immun
24	169	96.0	842	15	073340 human immun
25	169	96.0	847	15	069996 human immun
26	169	96.0	851	15	078243 human immun
27	169	96.0	854	15	055566 human immun
28	169	96.0	854	15	085582 human immun
29	169	96.0	854	15	072502 human immun
30	169	96.0	854	15	090178 human immun
31	169	96.0	854	15	078705 human immun
32	169	96.0	855	15	08A0V7 human immun
33	169	96.0	855	15	08ADT7 human immun
34	169	96.0	856	15	074090 human immun
35	169	96.0	856	15	092877 human immun
36	169	96.0	856	15	074599 human immun
37	169	96.0	856	15	041772 human immun
38	169	96.0	857	15	092822 human immun
39	169	96.0	857	15	071013 human immun
40	169	96.0	857	15	089654 human immun
41	169	96.0	854	15	09YP39 human immun
42	169	96.0	864	15	07ZJC8 human immun
43	169	95.5	125	15	091WP9 human immun
44	169	95.5	132	15	091W05 human immun
45	169	95.5	133	15	090020 human immun
46	169	95.5	137	15	09DQ04 human immun
47	169	95.5	142	15	091W07 human immun
48	169	95.5	144	15	070207 human immun
49	169	95.5	144	15	07ZC06 human immun
50	169	95.5	144	15	07ZC05 human immun
51	169	95.5	144	15	07ZC02 human immun
52	169	95.5	144	15	07ZCB1 human immun
53	169	95.5	144	15	07ZCB0 human immun
54	169	95.5	144	15	07ZC96 human immun
55	169	95.5	144	15	07ZC95 human immun
56	169	95.5	144	15	07ZC89 human immun
57	169	95.5	144	15	07ZC88 human immun
58	169	95.5	144	15	07ZC71 human immun
59	169	95.5	144	15	07ZC70 human immun
60	169	95.5	145	15	07ZC57 human immun
61	169	95.5	145	15	07ZC40 human immun
62	169	95.5	145	15	07ZC35 human immun
63	169	95.5	145	15	07ZC31 human immun
64	169	95.5	146	15	07SM37 human immun
65	169	95.5	155	15	0803P2 human immun
66	169	95.5	155	15	0803Q3 human immun
67	169	95.5	155	15	0803Q1 human immun
68	169	95.5	156	15	0803A7 human immun
69	169	95.5	174	15	0803B8 human immun
70	169	95.5	192	15	080AL2 human immun
71	169	95.5	219	15	080AJ4 human immun
72	169	95.5	225	15	0991C1 human immun
73	169	95.5	225	15	0991B9 human immun
74	169	95.5	225	15	0991C2 human immun
75	169	95.5	225	15	0991C5 human immun
76	169	95.5	225	15	0991C0 human immun
77	169	95.5	357	15	078118 human immun
78	169	95.5	357	15	078156 human immun
79	169	95.5	357	15	078155 human immun
80	169	95.5	358	15	078140 human immun
81	169	95.5	358	15	078141 human immun
82	169	95.5	360	15	080DX2 human immun
83	169	95.5	392	15	080511 human immun
84	169	95.5	398	15	072603 human immun
85	169	95.5	421	15	080514 human immun
86	169	95.5	606	15	0906V8 human immun
87	169	95.5	679	15	091K02 human immun
88	169	95.5	797	15	003808 human immun
89	169	95.5	797	15	003810 human immun

90 168 95.5 799 15 Q03807

ALIGNMENTS

Q03807 human immun

RESULT 1

Q90052

PRELIMINARY; PRT; 132 AA.

AC Q90052
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MOI496;
RX MEDLINE=21322034; Pubmed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."
RL AIDs Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF31089; AAK92300.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15708 MW; 51D9DB8AED574FAB CRC64;

Query Match 96.0%; Score 169; DB 15; Length 132;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 36
Db 10 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 45

RESULT 2

Q7SLZ2

PRELIMINARY; PRT; 132 AA.

AC Q7SLZ2
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT970;
RA Gonzalez Perez M.P., Garcia Saiz A.,
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530024; AAP87755.1; -
DR Envelope protein.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15717 MW; CA7F0709A8949E33 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 132;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 36
Db 11 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 46

RESULT 3

Q7SM06

PRELIMINARY; PRT; 143 AA.

AC Q7SM06
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT1138;
RA Gonzalez Perez M.P., Garcia Saiz A.,
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530010; AAP87741.1; -
KM Envelope protein.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 17210 MW; 415F5E738FA76BE0 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 143;
Best Local Similarity 97.2%; Pred. No. 2.6e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 36
Db 11 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYLK 46

RESULT 4

Q7ZCD7

PRELIMINARY; PRT; 144 AA.

AC Q7ZCD7
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naïve patients infected with subtype B
and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185383; AAO65658.1; -
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318EBE CRC64;

Query Match 96.0%; Score 169; DB 15; Length 144;

Best Local Similarity 97.2%; Pred. No. 2.7e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 36
DB 24 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 59

RESULT 5

Q7ZCD6 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-2;
RA Roman F., Gonzalez D., Lambert C., Derco S., Fischer A., Baurith T.,
RA Staub T., Boule R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncomm mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185384; AA065659.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EBB CRC64;

Query Match 96.0%; Score 169; DB 15; Length 144;
Best Local Similarity 97.2%; Pred. No. 2.7e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 36
DB 24 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 59

RESULT 6

Q7SM03 PRELIMINARY; PRT; 153 AA.
AC Q7SM03;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT598;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
RT infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530013; AB87744.1; -
KW Envelope protein.
FT NON TER 1
FT NON TER 153
SQ SEQUENCE 153 AA; 18136 MW; 014FA9E1FFEC035 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 153;
Best Local Similarity 97.2%; Pred. No. 2.8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 36
DB 11 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 46

RESULT 7

Q78119 PRELIMINARY; PRT; 357 AA.
AC Q78119;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.,
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61356; CA43624.1; -
DR PIR; A53591; A53591.
DR PIR; S70422; S21996.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 357
SQ SEQUENCE 357 AA; 41118 MW; FE4CA7E122A8B6 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 357;
Best Local Similarity 97.2%; Pred. No. 6.9e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 36
DB 54 NNLRAIEAQOHLQLTWQIKOLQARIIVERYLK 89

RESULT 8

Q993A8 PRELIMINARY; PRT; 588 AA.
AC Q993A8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF21147; AA20295.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
DR EMBL: AF321144; AAK20292.1; -.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240AE8 CRC64;

Query Match
Best Local Similarity 96.0%; Score 169; DB 15; Length 588;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 496 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 531

RESULT 9
QY 0993A7 PRELIMINARY; PRT; 588 AA.
AC 0993A7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt1;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321148; AAK20296.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
DR EMBL: AF321148; AAK20296.1; -.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match
Best Local Similarity 96.0%; Score 169; DB 15; Length 588;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 496 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 531

RESULT 10
QY 0993B1 PRELIMINARY; PRT; 589 AA.
AC 0993B1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.

```

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RC STRAIN=1P8;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321144; AAK20292.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 589 589
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match
Best Local Similarity 96.0%; Score 169; DB 15; Length 589;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 496 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 531

RESULT 11
QY 0993A9 PRELIMINARY; PRT; 590 AA.
AC 0993A9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321146; AAK20294.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120, 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 590 590
SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;

Query Match
Best Local Similarity 96.0%; Score 169; DB 15; Length 590;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 497 NNILRAIEAQOHLQLTWQIKOLQARILAVERYLK 532

RESULT 12
QY 0993B0 PRELIMINARY; PRT; 616 AA.

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AC 0993B0;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCosta S.S.; Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DE EMBL: AF321145; AAK20293.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP41; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 616 AA; 69189 MW; 57ABE20F9A580A4F CRC64;
Query Match 96.0%; Score 169; DB 15; Length 616;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
Db 497 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 532
RESULT 13
ID 0993B2 PRELIMINARY; PRT; 618 AA.
AC 0993B2;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCosta S.S.; Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DE EMBL: AF321143; AAK20291.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP41; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AB CRC64;
Query Match 96.0%; Score 169; DB 15; Length 618;

Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
Db 499 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 534
RESULT 14
ID 090723 PRELIMINARY; PRT; 727 AA.
AC 090723;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Envelope polypotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RX MEDLINE=9272698; PubMed=10339592;
RA Hoffman T.L.; Labranche C.C.; Zhang W.; Canziani G.; Robinson J.;
RA Chaiken I.; Hoxie J.A.; Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent HIV-1 envelope protein."
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=11Bx;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C.; Hoffman T.L.; Romano J.; Haggarty B.S.; Edwards T.G.;
RA Matthews T.J.; Doms R.W.; Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus type 1 variant map outside regions required for coreceptor specificity."
RL J. Virol. 73:10310-10319 (1999).
DE EMBL: AF189158; AAF25627.1; -
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP41; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD626D26B9E66 CRC64;
Query Match 96.0%; Score 169; DB 15; Length 727;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
Db 548 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 583
RESULT 15
ID 070607 PRELIMINARY; PRT; 747 AA.
AC 070607;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW87-1;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12034; AAA76669.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 747 747
 SQ SEQUENCE 747 AA; 84250 MW; 732836A52245F14 CRC64;
 Query Match 96.0%; Score 169; DB 15; Length 747;
 Best Local Similarity 97.2%; Pred. No. 1.5e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 36
 Db 548 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 583
 RESULT 16
 Q70606 PRELIMINARY; PRT; 748 AA.
 ID Q70606;
 AC Q70606;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW881;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12032; AAA76668.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 747 747
 SQ SEQUENCE 747 AA; 84250 MW; 732836A52245F14 CRC64;
 Query Match 96.0%; Score 169; DB 15; Length 747;
 Best Local Similarity 97.2%; Pred. No. 1.5e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 748 748
 SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;
 Query Match 96.0%; Score 169; DB 15; Length 748;
 Best Local Similarity 97.2%; Pred. No. 1.5e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 36
 Db 549 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 584
 RESULT 17
 Q70604 PRELIMINARY; PRT; 752 AA.
 ID Q70604;
 AC Q70604;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RX MEDLINE=95127297; PubMed=7826699;
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RT "viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LW851;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12030; AAA76666.1; -.
 DR PIR; A53591; A53591.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 752 752
 SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
 Query Match 96.0%; Score 169; DB 15; Length 752;
 Best Local Similarity 97.2%; Pred. No. 1.5e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 36
 Db 553 NNTLRATIAEQHLLQLTWGIKQLQARILAVERYLK 588
 RESULT 18
 Q70605 PRELIMINARY; PRT; 752 AA.
 ID Q70605;
 AC Q70605;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AAA76667.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.0%; Score 169; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 553 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 588

RESULT 19
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AAA76670.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

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DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 752
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0B8F8 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 553 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 588

RESULT 20
Q90722 PRELIMINARY; PRT; 757 AA.
AC Q90722;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=99272698; PubMed=10339592;
RA Hoffman T.L., Labranche C.C., Zhang W., Canziani G., Robinson J.,
  Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
  HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IIBX;
RX MEDLINE=20027260; PubMed=10559349;
RA Labranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
  Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
  type 1 variant map outside regions required for coreceptor
  specificity.";
RL J. Virol. 73:10310-10319(1999).
DR EMBL: AF189159; AAF25628.1; -.
DR PIR: A53591; A53591.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR InterPro: IPR006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 757
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BD2E CRC64;

Query Match 96.0%; Score 169; DB 15; Length 757;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 548 NMLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 583

RESULT 21

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Q9DVL6
ID Q9DVL6 PRELIMINARY; PRT; 811 AA.
AC Q9DVL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX MEDLINE=97DC.KCD4;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D., Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E., "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1) group M genetic diversity in the Democratic Republic of Congo suggests that the HIV-1 pandemic originated in Central Africa." J. Virol. 74:10498-10507(2000).
RL EMBL: A1401037; CAC15045.1; -
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR000625; REV_protein.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00424; REV; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1 811
FT NON TER 1 811
SQ SEQUENCE 811 AA; 90894 MW; 13A2E13246117541 CRC64;
Query Match 96.0%; Score 169; DB 15; Length 811;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 22
ID Q73341 PRELIMINARY; PRT; 842 AA.
AC Q73341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX MEDLINE=BR/93/29;
RA Penny W.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H., Daniels R.S.; "env gene sequences of primary HIV type 1 isolates of subtypes B, C, D, E, and F obtained from the World Health Organization Network for HIV Isolation and Characterization"; AIDS Res. Hum. Retroviruses 12:741-747(1996).
RL EMBL: U39236; AAB37173.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1 842
FT NON TER 1 842
SQ SEQUENCE 842 AA; 94964 MW; 02B9CB76D3D1B9F1 CRC64;
Query Match 96.0%; Score 169; DB 15; Length 842;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 23
ID Q70895 PRELIMINARY; PRT; 842 AA.
AC Q70895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RX MEDLINE=98285725; PubMed=9621027;
RA Gao F., Robertson D.L., Carnuthers C.D., Morrison S.G., Jian B., Chen Y., Barre-Sinoussi F., Girard M., Srinivasan A., Abimku A.G., Shaw G.M., Sharp P.M., Hahn B.H.; "A comprehensive panel of near-full-length clones and reference sequences for non-subtype B isolates of human immunodeficiency virus type 1." J. Virol. 72:5680-5698(1998).
RL J. Virol. 72:5680-5698(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93br029;
RA Gao F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005495; MAD03179.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON TER 1 842
FT NON TER 1 842
SQ SEQUENCE 842 AA; 94810 MW; F82041BD932DCAD CRC64;
Query Match 96.0%; Score 169; DB 15; Length 842;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 24
ID Q73340 PRELIMINARY; PRT; 842 AA.
AC Q73340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR/93/29;
 RX MEDLINE=96303593; PubMed=8744585.
 RA Penny M.A., Thomas S.J., Douglas N.W., Ranbar S., Holmes H., Daniels R.S.;
 RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C, RT D, E, and F obtained from the World Health Organization Network for HIV Isolation and Characterization";
 RT AIDS Res. Hum. Retroviruses 12:741-747(1996).
 DR EMBL; U39235; AAB37172.1; -;
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 842 AA; 94906 MW; 607BAF2A47B91B8 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 842;
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAQOHLQTLTWQIKOLARILAVERYLK 36
 Db 539 NNLRAIEAQOHLQTLTWQIKOLARILAVERYLK 574

RESULT 25

ID O69996 PRELIMINARY; PRT; 847 AA.
 AC O69996;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S., Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M., Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from the human immunodeficiency virus type 1 sequence subtypes A through G. The RT and NIAID Networks for HIV Isolation and Characterization";
 RT J. Virol. 70:1651-1657(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA NIAID/NIH AIDS Variation Program;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=594;
 RA McEvilly M.M.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U08445; AAB04071.1; -.

DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 847 AA; 95602 MW; FCBCBA7AF446FB20 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 847;
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAQOHLQTLTWQIKOLARILAVERYLK 36
 Db 544 NNLRAIEAQOHLQTLTWQIKOLARILAVERYLK 579

RESULT 26

ID O78243 PRELIMINARY; PRT; 851 AA.
 AC O78243;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Env polypotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q., Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer RT chronically infected HUT-78 cellular clone";
 RT J. Viral Diseases 1:40-55(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9352106; PubMed=2765297;
 RA Federic M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B., Macchi B., Mangiano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non producer clones from HUT-78 infected with a patient HIV isolate";
 RT AIDS Res. Hum. Retroviruses 5:385-396(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tilti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B., Borsetti A., Saggio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not productive clone";
 RT Int. J. Immunopharmacol. 3:17-23(1990).
 RL EMBL; Z11530; CAA77628.1; -;
 DR PIR; A53591; A53591.
 DR PIR; S13288; S13288.
 DR PIR; S33985; S33985.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A376B9B7B98027 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 851;
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 36
DB      548 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 583

RESULT 27
ID      056566      PRELIMINARY;      PRT;      854 AA.
AC      056566;
RT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
EN      Envelope glycoprotein.
GN      ENV.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=PIH309;
RX      MEDLINE=99372987; PubMed=10445815;
RA      Ataman-Onal Y., Colffler C., Giraud A., Babic-Erecg A., Biron F.,
RA      Verrier B.;
RT      "Comparison of complete env gene sequences from individuals with
RT      asymptomatic primary HIV type 1 infection."
RL      AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
DR      EMBL: AF041132; ACC2523.1; -.
DR      GO: GO:0016021; C:Integral to membrane; IEA.
DR      GO: GO:0019028; C:Viral capsid; IEA.
DR      GO: GO:0019031; C:Viral envelope; IEA.
DR      GO: GO:0005198; F:Structural molecule activity; IEA.
DR      InterPro: IPR000328; Env_GP41.
DR      InterPro: IPR000777; GP120.
DR      Pfam: PF00516; GP120; 1.
DR      Pfam: PF00517; GP41; 1.
KM      AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ      SEQUENCE 854 AA; 97062 MW; 588012C83A0C3D2 CRC64;

Query Match      96.0%; Score 169; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 36
DB      551 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 586

RESULT 28
ID      085582      PRELIMINARY;      PRT;      854 AA.
AC      085582;
RT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
EN      Envelope polypeptide.
GN      ENV.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NL4-3;
RX      MEDLINE=86281827; PubMed=3016298;
RA      Adachi A., Gendelman H.E., Koenig S., Folke T., Willey R., Rabson A.,
RA      Martin M.A.;
RT      "Production of acquired immunodeficiency syndrome-associated
RT      retrovirus in human and nonhuman cells transfected with an infectious
RT      molecular clone."
RL      J. Virol. 59:284-291(1986).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C.E.;
RX      Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL      Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.

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RN      [3]
RP      SEQUENCE FROM N.A.
RA      Buckler C.E.;
RL      Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92219406; PubMed=1373204;
RA      Dai L.C., Litana R., Takahashi K., Ennis F.A.;
RT      "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
RT      gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T
RT      lymphocytes."
RL      J. Virol. 66:3151-3154(1992).
DR      EMBL: M19921; AAA44992.1; -.
DR      PIR: A53591; A53591.
DR      PIR: S13288; S13288.
DR      GO: GO:0016021; C:Integral to membrane; IEA.
DR      GO: GO:0019028; C:Viral capsid; IEA.
DR      GO: GO:0019031; C:Viral envelope; IEA.
DR      GO: GO:0005198; F:Structural molecule activity; IEA.
DR      InterPro: IPR000328; Env_GP41.
DR      InterPro: IPR000777; GP120.
DR      Pfam: PF00516; GP120; 1.
DR      Pfam: PF00517; GP41; 1.
KM      AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ      SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5555A CRC64;

Query Match      96.0%; Score 169; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 36
DB      551 NNLLRAIEAQOHLQLTWGQIKQIQAARI LAVERYLK 586

RESULT 29
ID      072502      PRELIMINARY;      PRT;      854 AA.
AC      072502;
RT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
EN      ENV polypeptide.
GN      ENV.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NL4-3;
RX      MEDLINE=96036482; PubMed=7483282;
RA      Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA      Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT      "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT      from primary virus cultures using the polymerase chain reaction."
RL      Virology 213:80-86(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NL4-3;
RX      MEDLINE=86281827; PubMed=3016298;
RA      Adachi A., Gendelman H.E., Koenig S., Folke T., Willey R., Rabson A.,
RA      Martin M.A.;
RT      "Production of acquired immunodeficiency syndrome-associated
RT      retrovirus in human and nonhuman cells transfected with an infectious
RT      molecular clone."
RL      J. Virol. 59:284-291(1986).
DR      EMBL: U26942; AAB60576.1; -.
DR      PIR: A53591; A53591.
DR      PIR: S13288; S13288.
DR      GO: GO:0016021; C:Integral to membrane; IEA.
DR      GO: GO:0019028; C:Viral capsid; IEA.
DR      GO: GO:0019031; C:Viral envelope; IEA.
DR      GO: GO:0005198; F:Structural molecule activity; IEA.

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DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT CONFLICT 214 214 H -> L (IN REF. 2).
 FT CONFLICT 530 530 A -> S (IN REF. 2).
 FT CONFLICT 739 739 G -> D (IN REF. 2).
 SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 96.0%; Score 169; DB 15; Length 854;
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQITVWQIKQLQARILAVERYLK 36
 DB 551 NNLRAIEAQOHLQITVWQIKQLQARILAVERYLK 586

RESULT 30

ID 090178 PRELIMINARY; PRT; 854 AA.
 AC 090178;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074930; PubMed=7983770;
 RA Fang H., Pincus S.H.;
 RT "Unique insertion sequence and pattern of CD4 expression in variants
 RT selected with immunotoxins from human immunodeficiency virus type 1-
 RT infected T cells."
 RL J. Virol. 69:75-81(1995).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Fang H., Pincus S.H.;
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an
 RT immunotoxin-resistant variant T cell line."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF070521; AAC28452.1; -.
 DR PIR: A53591; A53591.
 DR PIR: S13288; S13288.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 96.0%; Score 169; DB 15; Length 854;
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQITVWQIKQLQARILAVERYLK 36
 DB 551 NNLRAIEAQOHLQITVWQIKQLQARILAVERYLK 586

Search completed: June 2, 2004, 11:48:19
 Job time : 31.2283 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 ; Search time 13.3043 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336A-148
Perfect score: 176
Sequence: 1 NMLRAIEAQHLLQTLTWQIKQLQARILAVERYLK 36

Scoring table: BLOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	176	100.0	38 4	US-08-973-952-82	Sequence 82, App1
2	169	96.0	36 4	US-09-515-965A-1721	Sequence 1721, App
3	169	96.0	37 4	US-09-515-965A-1722	Sequence 1722, App
4	169	96.0	38 1	US-08-374-666-1	Sequence 1, App1
5	169	96.0	38 3	US-08-486-099-89	Sequence 89, App1
6	169	96.0	38 3	US-08-360-107A-99	Sequence 99, App1
7	169	96.0	38 3	US-08-360-107A-132	Sequence 132, App
8	169	96.0	38 3	US-08-484-223B-89	Sequence 89, App1
9	169	96.0	38 3	US-08-919-597-89	Sequence 89, App1
10	169	96.0	38 3	US-08-475-551A-89	Sequence 89, App1
11	169	96.0	38 3	US-08-471-913A-89	Sequence 89, App1
12	169	96.0	38 3	US-08-485-264A-89	Sequence 89, App1
13	169	96.0	38 3	US-09-082-279B-16	Sequence 16, App1
14	169	96.0	38 3	US-09-082-279B-507	Sequence 507, App
15	169	96.0	38 3	US-09-082-279B-604	Sequence 604, App
16	169	96.0	38 3	US-09-082-279B-661	Sequence 661, App
17	169	96.0	38 3	US-09-082-279B-662	Sequence 662, App
18	169	96.0	38 4	US-08-474-349A-89	Sequence 89, App1
19	169	96.0	38 4	US-08-474-349A-441	Sequence 441, App
20	169	96.0	38 4	US-09-315-304B-16	Sequence 16, App1
21	169	96.0	38 4	US-09-315-304B-507	Sequence 507, App
22	169	96.0	38 4	US-09-315-304B-604	Sequence 604, App
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24	169	96.0	38 4	US-09-315-304B-662	Sequence 662, App
25	169	96.0	38 4	US-08-255-208A-25	Sequence 25, App
26	169	96.0	38 4	US-08-470-896-89	Sequence 89, App1
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31	169	96.0	38 4	US-09-834-784-507	Sequence 507, App
32	169	96.0	38 4	US-09-834-784-604	Sequence 604, App
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39	169	96.0	38 4	US-09-515-965A-604	Sequence 604, App
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45	169	96.0	38 4	US-09-350-641C-661	Sequence 661, App
46	169	96.0	38 4	US-09-350-641C-662	Sequence 662, App
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57	169	96.0	41 3	US-08-485-551A-8	Sequence 8, App1
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61	169	96.0	41 3	US-09-082-279B-496	Sequence 496, App
62	169	96.0	41 3	US-09-082-279B-601	Sequence 601, App
63	169	96.0	41 3	US-09-082-279B-633	Sequence 633, App
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65	169	96.0	41 4	US-08-474-349A-8	Sequence 8, App1
66	169	96.0	41 4	US-09-315-304B-496	Sequence 496, App
67	169	96.0	41 4	US-09-315-304B-601	Sequence 601, App
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69	169	96.0	41 4	US-09-315-304B-661	Sequence 661, App
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85	169	96.0	41 4	US-09-350-641C-601	Sequence 601, App
86	169	96.0	41 4	US-09-350-641C-633	Sequence 633, App
87	169	96.0	41 4	US-09-350-641C-1163	Sequence 1163, App
88	169	96.0	44 1	US-08-374-666-10	Sequence 10, App1
89	169	96.0	44 4	US-08-464-003-10	Sequence 10, App1
90	169	96.0	45 3	US-09-082-279B-1164	Sequence 1164, App

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 100.0%; Score 176; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 2
US-09-515-965A-1721
Sequence 1721, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1721
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1721

Query Match 96.0%; Score 169; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.6e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 3
US-09-515-965A-1722
Sequence 1722, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.

APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1722
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1722

Query Match 96.0%; Score 169; DB 4; Length 37;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 4
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dan P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1

Query Match 96.0%; Score 169; DB 1; Length 38;

Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36

RESULT 5

US-08-486-099-89

; Sequence 89, Application US/08486099
; Patent No. 6013263

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: USA

; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids

; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-486-099-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36

RESULT 6

US-08-360-107A-99

; Sequence 99, Application US/08360107A
; Patent No. 6017536

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: USA

; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids

; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-360-107A-99

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36

RESULT 7

US-08-360-107A-132

; Sequence 132, Application US/08360107A
; Patent No. 6017536

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: USA

; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids

; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-360-107A-99

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36
Db 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLK 36

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQLARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTVMQIKQLARILAVERYLK 36

RESULT 8
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTVMQIKQLARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTVMQIKQLARILAVERYLK 36

RESULT 9
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36

RESULT 10

US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89
Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36

RESULT 12

US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36
DB 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36

RESULT 13
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petleway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36
DB 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36

RESULT 14
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 96.0%; Score 169; DB 3; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36
DB 1 NNLRAIEAQCHLLQLTWMOIKOLARILAVERYLK 36

RESULT 15
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match
Best Local Similarity 97.2%; Score 169; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36

RESULT 16
US-09-082-279B-604
Sequence 604, Application US/09082279B

PATENT NO. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match
Best Local Similarity 97.2%; Score 169; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36

RESULT 17
US-09-082-279B-661
Sequence 661, Application US/09082279B

PATENT NO. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-661

Query Match 96.0%; Score 169; DB 3; Length 38;

Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36
DB 2 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 37

RESULT 18
US-09-082-279B-662
Sequence 662, Application US/09082279B

PATENT NO. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ. ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 662
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-662

Query Match
Best Local Similarity 97.2%; Score 169; DB 3; Length 38;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 36
DB 3 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYLK 38

RESULT 19
US-08-474-349A-89
Sequence 89, Application US/08474349A

PATENT NO. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

RESULT 20
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Stephen R.
APPLICANT: Petteway, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

RESULT 21
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Wernicka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PASCSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-16

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

RESULT 22
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Wernicka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PASCSEQ for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-507

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36
DB 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36

RESULT 23

US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-604

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36
DB 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36

RESULT 24

US-09-315-304B-661
Sequence 661, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-661

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36
DB 2 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 37

RESULT 25

US-09-315-304B-662
Sequence 662, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:

APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 662
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-662

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 36
DB 3 NNLRAIEAOQHLLQLTWGIKQLOARILAVERYLK 38

RESULT 26

US-08-255-208A-25
Sequence 25, Application US/08255208A
Patent No. 6440656
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,208A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36
DB 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36

RESULT 27
US-08-470-896-89
Sequence 89, Application US/08470896
Patent No. 6479055

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36
DB 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36

RESULT 28
US-08-485-546A-89
Sequence 89, Application US/08485546A
Patent No. 6518013

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1,7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36
DB 1 NNLRAIEAQOHLLQLTWQIKOLQARIILAVERYLK 36

RESULT 29
US-09-796-202-11

; Sequence 11, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBUTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 1 NNLRLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

RESULT 30
US-09-834-784-16
; Sequence 16, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Mernicka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 96.0%; Score 169; DB 4; Length 38;
Best Local Similarity 97.2%; Pred. No. 1.7e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36
Db 1 NNLRLRAIEAQOHLQLTWQIKQLQARIILAVERYLK 36

Search completed: June 2, 2004, 11:52:38
Job time: 14.3043 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 47.6033 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336A-2
Perfect score: 187
Sequence: 1 NNILRAIEAQHLLQLTWQIKQLQARILLAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	100.0	38	2	AAR98408
2	187	100.0	38	4	AAB54785
3	187	100.0	38	4	AAB55005
4	187	100.0	38	4	AAB54970
5	187	100.0	38	4	AAB52244
6	187	100.0	38	4	AAB54785
7	187	100.0	38	5	AAO18771
8	182	97.3	37	3	AAAB14705
9	182	97.3	37	4	AAAB54969
10	181	96.8	37	4	AAAB14739
11	181	96.8	37	4	AAAB55004
12	180	96.3	38	2	AAAB5635
13	180	96.3	38	2	AAAB5636
14	180	96.3	38	2	AAAB7216
15	180	96.3	38	2	AAAB7216
16	180	96.3	38	3	AAAB8666
17	180	96.3	38	3	AAAB8730
18	180	96.3	38	3	AAAB8731
19	180	96.3	38	3	AAAB89145
20	180	96.3	38	3	AAAB89146
21	180	96.3	38	3	AAAB89243
22	180	96.3	38	3	AAAB14530
23	180	96.3	38	3	AAAB52824
24	180	96.3	38	3	AAAB52786
25	180	96.3	38	3	AAAB52823

26	180	96.3	38	4	AAAG3858	AAAG3858 Amino aci
27	180	96.3	38	4	AAAB92349	AAAB92349 Virus rel
28	180	96.3	38	4	AAAB77021	AAAB77021 Core poly
29	180	96.3	38	4	AAAB77085	AAAB77085 Core poly
30	180	96.3	38	4	AAAB77086	AAAB77086 Core poly
31	180	96.3	38	4	AAAB77596	AAAB77596 Core poly
32	180	96.3	38	4	AAAB77500	AAAB77500 Core poly
33	180	96.3	38	4	AAAB77624	AAAB77624 Core poly
34	180	96.3	38	4	AAU70185	AAU70185 HIV viral
35	180	96.3	38	4	AAU70184	AAU70184 HIV viral
36	180	96.3	38	4	AAAB5690	AAAB5690 DP107 pep
37	180	96.3	38	4	AAAB01489	AAAB01489 Viral cor
38	180	96.3	38	4	AAAB00505	AAAB00505 Viral DP1
39	180	96.3	38	4	AAAB00090	AAAB00090 Viral DP1
40	180	96.3	38	4	AAAB02077	AAAB02077 Viral cor
41	180	96.3	38	4	AAAB00025	AAAB00025 HIV-1 gp4
42	180	96.3	38	4	AAAB00089	AAAB00089 Viral DP1
43	180	96.3	38	4	AAAB00504	AAAB00504 Viral DP1
44	180	96.3	38	4	AAAB00629	AAAB00629 Viral DP1
45	180	96.3	38	4	AAAB00601	AAAB00601 RSV Fl pr
46	180	96.3	38	4	AAAB01980	AAAB01980 Viral cor
47	180	96.3	38	4	AAU12638	AAU12638 DP178-11k
48	180	96.3	38	4	AAU13053	AAU13053 DP178-11k
49	180	96.3	38	4	AAU13149	AAU13149 DP178-11k
50	180	96.3	38	4	AAU13177	AAU13177 DP178-11k
51	180	96.3	38	4	AAU12574	AAU12574 DP178-11k
52	180	96.3	38	4	AAU12639	AAU12639 DP178-11k
53	180	96.3	38	4	AAAB82962	AAAB82962 Anti-HIV
54	180	96.3	38	5	AAAB22292	AAAB22292 gp41 fusi
55	180	96.3	38	5	AAAB02097	AAAB02097 Hybrid po
56	180	96.3	38	6	AAAB01509	AAAB01509 Hybrid po
57	180	96.3	38	6	AAAB75976	AAAB75976 HIV-1 gp4
58	180	96.3	38	6	AAAB09553	AAAB09553 Peptide f
59	180	96.3	38	6	AAAB01245	AAAB01245 HIV-1 gp
60	180	96.3	38	7	AAAB09756	AAAB09756 DP-107 an
61	180	96.3	38	7	AAAB73011	AAAB73011 HIV gp41
62	180	96.3	38	7	AAAB52840	AAAB52840 DP-125 -
63	180	96.3	41	2	AAAB98406	AAAB98406 Peptide D
64	180	96.3	41	2	AAAB17019	AAAB17019 DP-178-11
65	180	96.3	41	2	AAAB27616	AAAB27616 Human imm
66	180	96.3	41	2	AAAB27622	AAAB27622 Human imm
67	180	96.3	41	3	AAAB97779	AAAB97779 Core poly
68	180	96.3	41	3	AAAB98240	AAAB98240 Core poly
69	180	96.3	41	3	AAAB98134	AAAB98134 Core poly
70	180	96.3	41	4	AAAB54791	AAAB54791 HIV anti
71	180	96.3	41	4	AAAB92250	AAAB92250 Virus rel
72	180	96.3	41	4	AAAB77553	AAAB77553 Core poly
73	180	96.3	41	4	AAAB78180	AAAB78180 Core poly
74	180	96.3	41	4	AAAB77489	AAAB77489 Core poly
75	180	96.3	41	4	AAAB02106	AAAB02106 Viral cor
76	180	96.3	41	4	AAAB01187	AAAB01187 Viral DP1
77	180	96.3	41	4	AAAB02636	AAAB02636 Viral cor
78	180	96.3	41	4	AAAB01969	AAAB01969 Viral cor
79	180	96.3	41	4	AAAG67047	AAAG67047 Control p
80	180	96.3	41	4	AAAB00493	AAAB00493 Viral DP1
81	180	96.3	41	4	AAAB02074	AAAB02074 Viral cor
82	180	96.3	41	4	AAAB00598	AAAB00598 Viral DP1
83	180	96.3	41	4	AAU14018	AAU14018 Control p
84	180	96.3	41	4	AAU13773	AAU13773 DP178-11k
85	180	96.3	41	4	AAU13146	AAU13146 DP178-11k
86	180	96.3	41	4	AAU13042	AAU13042 DP178-11k
87	180	96.3	41	5	AAO18828	AAO18828 HIV gp41
88	180	96.3	41	5	AAO18828	AAO18828 HIV gp41
89	180	96.3	41	5	AAO18829	AAO18829 HIV gp41
90	180	96.3	41	5	AAO1989	AAO1989 Hybrid po

ALIGNMENTS

RESULT 1
AAR98408 standard; peptide; 38 AA.

XX AAR98408;
 AC 16-OCT-2003 (revised)
 DT 17-FEB-1997 (first entry)
 XX DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.
 XX Anti-fusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM Influenza virus; hepatitis B virus.
 XX Human immunodeficiency virus 1.
 OS WO9619495-A1.
 XX PD 27-JUN-1996.
 XX PF 20-DEC-1995; 95WO-US016733.
 XX PR 20-DEC-1994; 94US-00360107.
 PR 06-JUN-1995; 95US-00470896.
 XX (UYDU-) UNIV DUKE.
 PA (TRIM-) TRIMERIS INC.
 XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
 PI Petteway SR, Langlois AJ;
 XX WPI; 1996-309517/31.
 DR Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 XX isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence
 PT search motif.
 PS Disclosure; Page 30; 471pp; English.
 XX The sequences given in AAR98398-408 represent peptides which exhibit
 CC anti-fusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALLMOT15, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 38 AA;
 Query Match 100.0%; Score 187; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.6e-17;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 DB 1 NNLRLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 RESULT 2
 ID AAB54785 standard; peptide; 38 AA.
 AC AAB54785;
 XX 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX HIV antiviral activity exhibiting peptide SEQ ID NO:2.
 XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 OS Human immunodeficiency virus 1.

XX WO200069902-A1.
 PN 23-NOV-2000.
 PD 17-MAY-2000; 2000MO-US013651.
 XX PF 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 PI WPI; 2001-007496/01.
 DR A modified peptide and a reactive group which is reactive with amino
 XX groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 PS Claim 6; Page 173; 211pp; English.
 XX The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB54783 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 38 AA;
 Query Match 100.0%; Score 187; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.6e-17;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLRLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 DB 1 NNLRLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 RESULT 3
 ID AAB55005 standard; peptide; 38 AA.
 AC AAB55005;
 XX 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX Anti-HIV peptide DP107 amino truncation peptide #35.
 XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM anti-fusogenic; mobile blood component; measles virus; MeV; SIV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 OS Human immunodeficiency virus 1.

not used in patent prosecution
20/2/2004

PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
XX
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
DR WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 139; 211pp; English.
XX
CC The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 187; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 NNTLRATIAEQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNTLRATIAEQOHLQLTWQIKQLQARILAVERYLKQ 38
XX
RESULT 4
AAB54970
ID AAB54970 standard; peptide; 38 AA.
XX
AC AAB54970;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX
DE Anti-HIV peptide DP107 carboxy truncation peptide #35.
XX
XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antifusogenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200069902-A1.
PN

XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
XX
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
DR WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 137; 211pp; English.
XX
CC The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
CC
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 187; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 NNTLRATIAEQOHLQLTWQIKQLQARILAVERYLKQ 38
Db 1 NNTLRATIAEQOHLQLTWQIKQLQARILAVERYLKQ 38
XX
RESULT 5
AAB92244
ID AAB92244 standard; peptide; 38 AA.
XX
AC AAB92244;
XX
DT 22-JUN-2001 (first entry)
DT 05-MAR-2001 (first entry)
XX
XX
DE Virus related peptide SEQ ID NO:1420.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; malimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
PD

XX 17-MAY-2000; 2000WO-US013576.
 XX
 PF 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONU-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thihaudeau K;
 XX WPI; 2001-112059/12.
 DR
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PS Disclosure; Page 662; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 38 AA;
 QY
 Db 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 RESULT 6
 AAU14011 ID AAU14011 standard; peptide; 38 AA.
 XX
 AC AAU14011;
 XX
 DT 11-SEP-2003 (revised)
 DT 21-NOV-2001 (first entry)
 XX
 DE DP107 peptide from HIV-1 transmembrane protein gp41.
 XX
 KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KM antifusogenic; antiviral; HIV transmission.
 XX
 OS Human immunodeficiency virus 1; isolate LAI.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..35
 FT /note= "Amino acids 1-35 can be optionally and serially
 FT deleted from the N-terminus"
 FT Misc-difference 4..38
 FT /note= "Amino acids 4-38 can be optionally and serially
 FT deleted from the C-terminus"
 XX
 PN WO200151673-A2.
 XX

PD 19-JUL-2001.
 XX
 PF 05-JUL-2000; 2000WO-US035727.
 XX
 PR 09-JUL-1999; 99US-00350841.
 XX
 PA (TRIM-) TRIMERIS INC.
 PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merricka G;
 XX WPI; 2001-442157/47.
 DR
 XX
 PT Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Page 33; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 38 AA;
 QY
 Db 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 1 NNLRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
 RESULT 7
 AA018771 ID AA018771 standard; peptide; 38 AA.
 XX
 AC AA018771;
 XX
 DT 29-OCT-2002 (first entry)
 DT
 XX
 DE HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
 XX
 KW Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
 KM gp41.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO200256902-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 17-DEC-2001; 2001WO-US048802.
 PF 19-DEC-2000; 2000US-0256657P.
 PR
 XX
 PA (SCHE) SCHERING CORP.
 XX

PI Baroudy BM;
 XX
 DR WPI; 2002-636513/58.
 XX
 PT Treatment of HIV infection in an individual involves administration of a
 PT combination of chemokine co-receptor five antagonist and a specified HIV
 PT envelope polypeptide.
 PS Disclosure; Page 34; 52pp; English.
 XX
 CC The present invention relates to a method of treating an HIV infection in
 CC an individual, which involves administering in combination a chemokine co-
 CC receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
 CC derivative. Other viral infections can also be treated using the method.
 CC The present sequence is a peptide derived from HIV and useful in the
 CC method of the invention
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 187; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.6e-17;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
 RESULT 8
 AAB14705
 ID AAB14705 standard; peptide; 37 AA.
 XX
 AC AAB14705;
 XX
 DT 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
 XX
 KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KW isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 XX
 PI Wild CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 PS Disclosure; Page 36; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralising antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)

CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 37 AA;
 Query Match 97.3%; Score 182; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKD 37
 Db 1 NNLLRAIEAQOHLLQLTWQIKQLQARILAVERYLKD 37
 RESULT 9
 AAB54969
 ID AAB54969 standard; peptide; 37 AA.
 XX
 AC AAB54969;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
 XX
 KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KW antitumorigenic; mobile blood component; measles virus; MeV; SIV;
 KW simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007496/01.
 XX
 CC A modified peptide and a reactive group which is reactive with amino
 CC groups, hydroxyl groups, or thiol groups on blood components to form
 CC stable covalent bonds useful for treatment of viral infections, e.g.
 CC human immunodeficiency virus.

XX PS Disclosure; Page 137; 211pp; English.

XX CC The present invention describes a modified anti-viral peptide (I)

XX CC comprising a peptide that exhibits anti-viral activity and a reactive

XX CC group which is reactive with amino groups, hydroxyl groups, or thiol

XX CC groups on blood components to form stable covalent bonds. (I) has anti-

XX CC viral and anti-fusogenic activities. (I) inhibits viral infection of

XX CC cells by inhibiting cell-cell fusion or free virus infection or to reduce

XX CC the level of membrane fusion events between two or more entities, e.g.,

XX CC virus-cell or cell-cell, relative to the level of membrane fusion that

XX CC occurs in the absence of the peptide. (I) is useful in the treatment of

XX CC patients who are suffering from viral infection, e.g., HIV, RSV, HPIV,

XX CC MeV, and SiV. (I) may be administered prophylactically to previously

XX CC uninfected individuals. This is useful in cases where an individual has

XX CC been subjected to a high risk of exposure to a virus. By bonding of long-

XX CC lived components of the blood, such as immunoglobulin, serum albumin, red

XX CC blood cells and platelets the activity is extended for days to weeks.

XX CC This is due to improved stability in vivo and a reduced susceptibility to

XX CC peptidase or protease degradation. This minimises the need for more

XX CC frequent, or even continual, administration of the peptides. AAB54784 to

XX CC AAB55431 represent peptides used in the exemplification of the present

XX CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 37 AA;

XX Query Match 97.3%; Score 182; DB 4; Length 37;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-16;

XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37

Db 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKD 37

RESULT 10

AAAB14739

ID AAB14739 standard; peptide; 37 AA.

XX AC AAB14739;

XX DT 12-SEP-2003 (revised)

XX DT 24-NOV-2000 (first entry)

XX DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #68.

XX KW HIV-1, gp41 N-helical domain; gp41 heptad repeat region; coiled coil;

XX KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;

XX KW humoral response; broad spectrum vaccine; anti-HIV;

XX KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;

XX KW isolate LAI.

XX OS Human immunodeficiency virus 1.

XX PN WO2000040616-A1.

XX PD 13-JUL-2000.

XX PF 10-JAN-2000; 2000WO-US000456.

XX PR 08-JAN-1999; 99US-0115404P.

XX PR 07-JAN-2000; 2000US-00480336.

XX PA (WILD/) WILD C.T.

XX PA (WEISS/) WEISS C.D.

XX PI WILD CT, Weiss CD;

XX DR WPI; 2000-465959/40.

XX PT Raising neutralizing antibody response to human immunodeficiency virus,

XX PT comprises administering a polypeptide capable of forming a stable coiled-

XX PT coil solution structure.

XX PS Disclosure; Page 38; 97pp; English.

XX CC Sequences AAB14672-B14739 represent peptides derived from the N-helical

XX CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,

XX CC isolate LAI. The invention relates to raising a neutralising antibody

XX CC response to a broad spectrum of HIV (human immunodeficiency virus)

XX CC strains and isolates, comprising the administration of a peptide which

XX CC corresponds to or mimics highly conserved portions of gp41 which are

XX CC important in mediating the process of viral entry into host cells. Such

XX CC peptides can correspond to or mimic the coiled coil solution structure of

XX CC the N-helical domain (the heptad repeat region), or can correspond or

XX CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-

XX CC helical segment), or the gp41 core 6-helix bundle, which is formed by the

XX CC interaction of the N- and C-helical domains of three gp41 proteins. The

XX CC peptides can be administered either singly or as a combination

XX CC (particularly a combination of N-helical and C-helical peptides), and can

XX CC be multimerised. For example, N- and C-helical domain peptides can be

XX CC alternately linked together to form a peptide which mimics the core 6-

XX CC helix bundle. Administration of the peptide(s) generates a humoral

XX CC response, with the production of antibodies against gp41 structures

XX CC involved in viral entry. As these portions of gp41 are well conserved,

XX CC such antibodies may be effective against a broad range of HIV strains and

XX CC isolates. The peptide compositions may be administered as a prophylactic

XX CC or therapeutic vaccine to generate antibodies which reduce or inhibit the

XX CC ability of HIV to infect uninfected cells. A composition comprising

XX CC polyclonal or monoclonal antibodies can be administered to reduce HIV

XX CC infection of uninfected cells. Antibodies raised against entry-relevant

XX CC gp41 structures may also be used therapeutically and as tools to further

XX CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to

XX CC standardise OS field)

XX SQ Sequence 37 AA;

XX Query Match 96.8%; Score 181; DB 3; Length 37;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-16;

XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38

Db 1 NNLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37

RESULT 11

AAAB55004

ID AAB55004 standard; peptide; 37 AA.

XX AC AAB55004;

XX DT 11-SEP-2003 (revised)

XX DT 05-MAR-2001 (first entry)

XX DE Anti-HIV peptide DP107 amino truncation peptide #34.

XX KW Long lasting fusion peptide inhibitor; viral infection; antiviral;

XX KW anti-fusogenic; mobile blood component; measles virus; MeV; SiV;

XX KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

XX KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX OS Human immunodeficiency virus 1.

XX PN WO200069902-A1.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US013651.

XX PR 17-MAY-1999; 99US-0134406P.

XX PR 10-SEP-1999; 99US-0153406P.

XX PA (CONU-) CONU/CHEM INC.

XX PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.
 DR A modified peptide and a reactive group which is reactive with amino
 XX groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 139; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptide. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 37 AA;
 Query Match 96.8%; Score 181; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 37
 RESULT 12
 AAR55635
 ID AAR55635 standard; peptide; 38 AA.
 XX
 AC AAR55635;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX
 DE DP-139 - DP-107 analogue.
 XX
 KW Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KW antiviral; gp41.
 XX
 OS Synthetic.
 XX
 PN WO9402505-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006769.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Wild CT, Matthews TJ, Bolognesi DP;
 XX WPI; 1994-048790/06.
 DR

XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Disclosure; Page 25; 38pp; English.
 XX
 CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 96.3%; Score 180; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 RESULT 13
 AAR55636
 ID AAR55636 standard; peptide; 38 AA.
 XX
 AC AAR55636;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)
 XX
 DE DP-140 - DP-107 analogue.
 XX
 KW Leucine zipper; HIV-1; human immunodeficiency virus;
 KW transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
 KW antiviral; gp41.
 XX
 OS Synthetic.
 XX
 PN WO9402505-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006769.
 XX
 PR 20-JUL-1992; 92US-00916540.
 PR 07-AUG-1992; 92US-00927532.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Wild CT, Matthews TJ, Bolognesi DP;
 XX WPI; 1994-048790/06.
 DR
 XX New peptides corresponding to HIV transmembrane protein - used for
 PT inhibiting infection of cells by an enveloped virus, partic. for
 PT inhibiting HIV-induced cell fusion.
 XX
 PS Disclosure; Page 25; 38pp; English.
 XX
 CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
 CC of forming a heterodimer with DP-107; or a multimer of these peptides can
 CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
 CC fusion. DP-107 is based on a highly conserved region in the transmembrane
 CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
 CC amphipathic alpha-helix with structural analogues in the TM proteins of
 CC several fusogenic viruses. Other peptides studied and DP-107 analogues
 CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
 CC correct PN field.)

CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38

RESULT 14
AAR47216
ID AAR47216 standard; peptide; 38 AA.

AC AAR47216;

DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (S58-S95).

XX Leucine zipper; HIV-1; human immunodeficiency virus;
KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.

XX Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 12

FT 12 of the sequence in Fig 1 is H; residue
FT 12 of the sequence in Table 4 is G"

XX WO9402505-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006769.

XX 20-JUL-1992; 92US-00916540.

XX 07-AUG-1992; 92US-00927532.

XX (UYDU-) UNIV DUKE.

XX Wild CT, Matthews TJ, Bolognesi DP;

XX WPI; 1994-048790/06.

XX New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.

XX Claim 1; Page 27; 38pp; English.

XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX

XX Sequence 38 AA;

Query Match 96.3%; Score 180; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38

RESULT 15
AAR27614
ID AAR27614 standard; peptide; 38 AA.

AC AAR27614;

DT 25-MAR-2003 (revised)

DT 22-DEC-1997 (first entry)

DE Human immunodeficiency virus gp41 derived peptide DP-107.

XX Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;
KM inhibition; induction; cell fusion; transmission; type 1.

XX Human immunodeficiency virus.

XX US5656480-A.

XX 12-AUG-1997.

XX 27-JAN-1995; 95US-00374666.

XX 20-JUL-1992; 92US-00916540.

XX 07-AUG-1992; 92US-00927532.

XX 19-JUL-1993; 93WO-US006769.

XX (UYDU-) UNIV DUKE.

XX Bolognesi DP, Wild CT, Matthews TJ;

XX WPI; 1997-414595/38.

XX Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
XX syncytia formation and transmission.

XX Claim 1; Col 13-14; 18pp; English.

XX The present human immunodeficiency virus (HIV) transmembrane glycoprotein
CC 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
CC cell fusion in a culture and cell free HIV transmission in a culture to a
CC human cell not infected with HIV, especially HIV type 1. (Updated on 25-
CC MAR-2003 to correct PF field.)

XX Sequence 38 AA;

Query Match 96.3%; Score 180; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38
DB 1 NNILRAIEAQOHLLQITWQIKQLARILAVERYLKDQ 38

RESULT 16
AAY88666
ID AAY88666 standard; peptide; 38 AA.

AC AAY88666;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 21.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.


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XX OS Unidentified.
XX PN WO9959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PR 20-MAY-1998; 98US-00082279.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX DR WPI; 2000-136792/12.
XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX PT comprises enhancer sequence.
XX PS Disclosure; Page 21; 124pp; English.
XX CC The invention relates to hybrid polypeptides comprising enhancer peptide
XX CC sequence linked to core polypeptides. The enhancer polypeptides are
XX CC derived from various retroviral envelope (gp41) protein sequences,
XX CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX CC pharmacokinetic properties such as increasing the half-life of any core
XX CC polypeptide that they are linked to. The core polypeptides are any
XX CC polypeptide that may be introduced into a living system and that can
XX CC function as a pharmacologically useful peptide for the treatment or
XX CC prevention of a disease. The core polypeptides are bioactive peptides
XX CC selected from a growth factor, cytokine, differentiation factor,
XX CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX CC factor. The peptides of the invention can be used for inhibiting viral
XX CC infection and can be used in anti-viral and anti-fusogenic treatments.
XX CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
XX CC be used in the invention. Some sequences among those indicated also
XX CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38

RESULT 17
AAY8730
ID AAY8730 standard; peptide; 38 AA.
AC AAY8730;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 85.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX PN WO9959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties

```

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PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX DR WPI; 2000-136792/12.
XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX PT comprises enhancer sequence.
XX PS Disclosure; Page 22; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX CC sequence linked to core polypeptides. The enhancer polypeptides are
XX CC derived from various retroviral envelope (gp41) protein sequences,
XX CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX CC pharmacokinetic properties such as increasing the half-life of any core
XX CC polypeptide that they are linked to. The core polypeptides are any
XX CC polypeptide that may be introduced into a living system and that can
XX CC function as a pharmacologically useful peptide for the treatment or
XX CC prevention of a disease. The core polypeptides are bioactive peptides
XX CC selected from a growth factor, cytokine, differentiation factor,
XX CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX CC factor. The peptides of the invention can be used for inhibiting viral
XX CC infection and can be used in anti-viral and anti-fusogenic treatments.
XX CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
XX CC be used in the invention. Some sequences among those indicated also
XX CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERTLKQ 38

RESULT 18
AAY8731
ID AAY8731 standard; peptide; 38 AA.
AC AAY8731;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 86.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX OS
XX PN WO9959615-A1.
XX PD 25-NOV-1999.
XX PF 20-MAY-1999; 99WO-US011219.
XX PR 20-MAY-1998; 98US-00082279.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX DR WPI; 2000-136792/12.
XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties

```

PT comprises enhancer sequence.
XX
XX Disclosure; Page 22; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 19
AAY89145
XX AAY89145 standard; peptide; 38 AA.
XX
XX AAY89145;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 583.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 30; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAY8651-Y9005 represent core polypeptide fragments that can

CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLLQLTWGIKQLQARIILAVERYLKDQ 38
Db 1 NNLRAIEAQOHLLQLTWGIKQLQARIILAVERYLKDQ 38

RESULT 20
AAY89146
XX AAY89146 standard; peptide; 38 AA.
XX
XX AAY89146;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 583.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 30; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAY8651-Y9005 represent core polypeptide fragments that can

CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQD 38
 DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQD 38

RESULT 21
 AAY89243
 ID AAY89243 standard; peptide; 38 AA.

AC AAY89243;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 681.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Nerutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

PS Disclosure; Page 32; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQD 38
 DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQD 38

RESULT 22
 AAB14530
 ID AAB14530 standard; peptide; 38 AA.

AC AAB14530;

DT 12-SEP-2003 (revised)

DT 24-NOV-2000 (first entry)

DE HIV-1 isolate LAI gp41 N-helical domain residues 558-595 (peptide P-17).

KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KW humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy.

OS Human immunodeficiency virus 1.

PN WO200040616-A1.

PD 13-JUL-2000.

PF 10-JAN-2000; 2000WO-US000456.

PR 08-JAN-1999; 99US-0115404P.

PR 07-JAN-2000; 2000US-00480336.

PA (WILD/) WILD C T.

PA (WEIS/) WEISS C D.

PI WILD CT, Weiss CD;

DR WPI; 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.

PS Claim 5; Page 56; 97pp; English.

XX Sequences AAB14529-B14531 and AAB14537-B14568 represent specifically
 CC claimed peptides derived from the N-helical domain of the gp41 envelope
 CC glycoprotein from a variety of HIV-1 isolates. The invention relates to
 CC raising a neutralizing antibody response to a broad spectrum of HIV
 CC (human immunodeficiency virus) strains and isolates, comprising the
 CC administration of a peptide which corresponds to or mimics highly
 CC conserved portions of gp41 which are important in mediating the process
 CC of viral entry into host cells. Such peptides can correspond to or mimic
 CC the coiled coil solution structure of the N-helical domain (the heptad
 CC repeat region), or can correspond or mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the gp41
 CC core 6-helix bundle, which is formed by the interaction of the N- and C-
 CC helical domains of three gp41 proteins. The peptides can be administered
 CC either singly or as a combination (particularly a combination of N-
 CC helical and C-helical peptides), and can be multimerised. For example, N-
 CC and C-helical domain peptides can be alternately linked together to form
 CC a peptide which mimics the core 6-helix bundle. Administration of the
 CC peptide(s) generates a humoral response, with the production of
 CC antibodies against gp41 structures involved in viral entry. As these
 CC portions of gp41 are well conserved, such antibodies may be effective
 CC against a broad range of HIV strains and isolates. The peptide
 CC compositions may be administered as a prophylactic or therapeutic vaccine
 CC to generate antibodies which reduce or inhibit the ability of HIV to
 CC infect uninfected cells. A composition comprising polyclonal or
 CC monoclonal antibodies can be administered to reduce HIV infection of
 CC uninfected cells. Antibodies raised against entry-relevant gp41
 CC structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to

CC standardise OS field)
XX
SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 23
AAB52824
ID AAB52824 standard; peptide; 38 AA.
XX
AC AAB52824;

XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX

DE T21/DP107 peptide fragment #101.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemoattractant.

XX Human immunodeficiency virus 1.

XX WO200066622-A1.

XX 09-NOV-2000.

PF 05-MAY-2000; 2000WO-US012371.

XX 05-MAY-1999; 99US-0132686P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

XX WPI; 2000-656493/63.

PT Administration of peptide agents with a sequence corresponding to a
partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
is used to modulate inflammation.

XX Disclosure; Page 28; 148pp; English.

XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemoattractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 24
AAB52786

ID AAB52786 standard; peptide; 38 AA.

XX AAB52786;

XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX

DE T21/DP107 peptide fragment #68.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemoattractant.

XX Human immunodeficiency virus 1.

XX WO200066622-A1.

XX 09-NOV-2000.

PF 05-MAY-2000; 2000WO-US012371.

XX 05-MAY-1999; 99US-0132686P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

XX WPI; 2000-656493/63.

PT Administration of peptide agents with a sequence corresponding to a
partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
is used to modulate inflammation.

XX Claim 12; Page 29; 148pp; English.

XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemoattractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38
1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKQ 38

RESULT 25
AAB52823
ID AAB52823 standard; peptide; 38 AA.
XX

XX AAB52823;

XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX

DE T21/DP107 peptide fragment #100.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemoattractant.

XX Human immunodeficiency virus 1.

XX WO200006622-A1.
 XX
 XX 09-NOV-2000.
 XX
 XX 05-MAY-2000; 2000MO-US012371.
 XX
 XX 05-MAY-1999; 99US-0132686P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
 XX
 XX WP1; 2000-656493/63.
 XX
 XX Administration of peptide agents with a sequence corresponding to a
 XX partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
 XX is used to modulate inflammation.
 XX
 XX Claim 15; Page 42; 148pp; English.
 XX
 XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
 XX helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
 XX located in the amino terminus of the gp41 ectodomain. gp41 plays a
 XX critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
 XX interacts with members of the formyl peptide receptor (FPR) family and
 XX thereby up-regulates an inflammatory response, and acts as a potent
 XX chemotactic and activator of human peripheral blood phagocytes (but
 XX not T cells). The present peptide can be used to modulate an inflammatory
 XX response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 XX Sequence 38 AA;

Query	1	NNILRAIEAOQHLLQLTWQGIKQLQARIIVERYLKDDQ	38
Db	1	NNILRAIEAOQHLLQLTWGIGIKQLQARIIVERYLKDDQ	38
Best Match			
Query Match			96.3%; Score 180; DB 3; Length 38;
Similarity			97.4%; Pred. No. 2,9e-16;
Matches	37;	Conservative	0; Mismatches 1; Indels 0; Gaps

RESULT 26	
AAG63858	
ID	AAG63858 standard; peptide; 38 AA.
XX	
AC	AAG63858;
XX	
DT	11-SEP-2003 (revised)
DT	29-OCT-2001 (first entry)
XX	
DE	Amino acid sequence of a HIV-1 gp41 peptide fragment.
XX	
KM	HIV-1; isolate LAI; gp41; viral entry; envelope protein; glycoprotein.
XX	
XX	viral infection; antiviral.
OS	Human immunodeficiency virus 1.
XX	
PN	MO200159457-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001MO-US004030.
XX	
PR	10-FEB-2000; 2000US-0181543P.
PR	28-SEP-2000; 2000US-0235901P.
XX	
PA	(PANA-) PANACOS PHARM INC.
XX	
PI	Wild CT, Allaway GP;
XX	
DR	WPI; 2001-522493/57.
XX	
PT	Screening for inhibitors of viral entry structure formation by

PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
its formation.
XX
PS Disclosure; Page 23; 68pp; English.
PV

The present sequence represents a fragment of a Human immunodeficiency virus type 1 (HIV-1) isolate LAI gp41 protein. The peptide is used to raise antibodies for use in the method of the invention. The specification describes a method of screening for inhibitors of viral entry structure formation. The method comprises contacting a viral envelope protein or glycoprotein (e.g. gp41) with a triggering agent and a candidate compound to form a mixture, and measuring the effect that the candidate compound has on the formation of conformational intermediates. The effect of the candidate compound can be measured by antibody binding to these conformational intermediates. The compounds identified by the method are useful as inhibitors for inhibiting or preventing viral infection and to treat humans infected with HIV-1 or other viruses. This antiviral compounds can also be used to inactivate viruses in body fluids, e.g. blood or blood compounds used for therapeutic purposes. The assay is also useful for detecting antibodies in virus-infected individuals or virus-infected body fluids or tissues that inhibit entry-relevant conformational changes in one or more viral envelope proteins or glycoproteins. The presence of the antibodies in infected individuals or samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 38 AA;

Query Match	96.3%	Score 180;	DB 4;	Length 38;
Best Local Similarity	97.4%	Pred. No. 2.9e-16;		
Matches 37;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

Dy 1 NNLLRAIEAQQHLLQLTWGKIQKLQARILAVERYLKDQ 38

Ddb 1 NNLLRAIEAQQHLLQLTWGKIQKLQARILAVERYLKDQ 38

RESULT 27
AAB92349
ID AAB92349 standard; peptide; 38 AA.

DT 22-JUN-2001 (first entry)

DE Virus related peptide SEQ ID NO:1525.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimide; maleimide group; amino
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 15-OCT-1999; 99US-0159783P.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibault K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 704; 733bp; English.
 PS
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidease activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptideases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptideases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 96.3%; Score 180; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 RESULT 28
 AAB77021
 ID AAB77021 standard; peptide; 38 AA.
 AC AAB77021;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Core polypeptide T21.
 XX
 KM Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KM fusion-related disorder; bacterial infection; viral infection.
 XX
 OS Unidentified.
 PN WO200103723-A1.
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018772.
 XX
 PR 09-JUL-1999; 99US-00350641.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;
 DR WPI; 2001-147136/15.
 XX
 PT New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX
 PS Disclosure; Page 30; 151bp; English.
 XX
 CC The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the

CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 96.3%; Score 180; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLKDQ 38
 RESULT 29
 AAB77085
 ID AAB77085 standard; peptide; 38 AA.
 AC AAB77085;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Core polypeptide T95.
 XX
 KM Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KM fusion-related disorder; bacterial infection; viral infection.
 XX
 OS Unidentified.
 PN WO200103723-A1.
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018772.
 XX
 PR 09-JUL-1999; 99US-00350641.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;
 DR WPI; 2001-147136/15.
 XX
 PT New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX
 PS Disclosure; Page 31; 151bp; English.
 XX
 CC The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the
 CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral

CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used

XX
 SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLKDQ 38
 Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLKDQ 38

RESULT 30

AAB77086 standard; peptide; 38 AA.

XX AAB77086;

XX 19-APR-2001 (first entry)

XX Core polypeptide T86.

XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KM antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KM fusion-related disorder; bacterial infection; viral infection.

XX Unidentified.

XX WO200103723-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000MO-US018772.

XX 09-JUL-1999; 99US-00350641.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Nerutka G, Anwer MK, Lambert DM;

XX WPI; 2001-147136/15.

XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.

XX Disclosure; Page 31; 151pp; English.

XX The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the
 CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side

CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used

XX
 SQ Sequence 38 AA;

Query Match 96.3%; Score 180; DB 4; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLKDQ 38
 Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLKDQ 38

Search completed: June 2, 2004, 11:41:41
 Job time : 50.6033 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:33:58 / Search time 14.0435 Seconds
(without alignments)
139.694 Million cell updates/sec

Title: US-09-657-336a-2

Perfect score: 187
Sequence: 1 NMLRAIEAQHILQLTWQIKQARILAVERYLKDQ 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 90 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187	100.0	38	4	US-08-973-952-82
2	180	96.3	38	1	US-08-374-666-1
3	180	96.3	38	3	US-08-486-099-89
4	180	96.3	38	3	US-08-360-107A-99
5	180	96.3	38	3	US-08-360-107A-132
6	180	96.3	38	3	US-08-484-223B-89
7	180	96.3	38	3	US-08-919-597-89
8	180	96.3	38	3	US-08-475-668A-89
9	180	96.3	38	3	US-08-485-551A-89
10	180	96.3	38	3	US-08-471-913A-89
11	180	96.3	38	3	US-08-485-264A-89
12	180	96.3	38	3	US-08-982-279B-16
13	180	96.3	38	3	US-08-982-279B-507
14	180	96.3	38	3	US-09-082-279B-604
15	180	96.3	38	4	US-08-474-349A-89
16	180	96.3	38	4	US-08-474-349A-441
17	180	96.3	38	4	US-09-315-304B-16
18	180	96.3	38	4	US-09-315-304B-507
19	180	96.3	38	4	US-09-315-304B-604
20	180	96.3	38	4	US-08-255-208A-25
21	180	96.3	38	4	US-08-470-896-89
22	180	96.3	38	4	US-08-485-546A-89
23	180	96.3	38	4	US-09-796-202-11
24	180	96.3	38	4	US-09-834-784-16
25	180	96.3	38	4	US-09-834-784-507
26	180	96.3	38	4	US-09-834-784-604
27	180	96.3	38	4	US-08-464-003-1

28	180	96.3	38	4	US-09-779-451-2	Sequence 2, App1
29	180	96.3	38	4	US-09-515-965A-16	Sequence 16, App1
30	180	96.3	38	4	US-09-515-965A-507	Sequence 507, App1
31	180	96.3	38	4	US-09-515-965A-604	Sequence 604, App1
32	180	96.3	38	4	US-09-350-641C-16	Sequence 16, App1
33	180	96.3	38	4	US-09-350-641C-507	Sequence 507, App1
34	180	96.3	38	4	US-09-350-641C-604	Sequence 604, App1
35	180	96.3	41	1	US-08-073-028-8	Sequence 8, App1
36	180	96.3	41	1	US-08-374-666-9	Sequence 9, App1
37	180	96.3	41	1	US-08-471-913A-8	Sequence 8, App1
38	180	96.3	41	3	US-08-485-551A-8	Sequence 8, App1
39	180	96.3	41	3	US-08-485-551A-8	Sequence 8, App1
40	180	96.3	41	3	US-08-484-223B-8	Sequence 8, App1
41	180	96.3	41	3	US-08-484-223B-242	Sequence 242, App1
42	180	96.3	41	3	US-08-484-223B-243	Sequence 243, App1
43	180	96.3	41	3	US-08-475-597-8	Sequence 8, App1
44	180	96.3	41	3	US-08-475-597-8	Sequence 8, App1
45	180	96.3	41	3	US-08-485-551A-8	Sequence 8, App1
46	180	96.3	41	3	US-08-471-913A-8	Sequence 8, App1
47	180	96.3	41	3	US-08-554-616-8	Sequence 8, App1
48	180	96.3	41	3	US-08-485-264A-8	Sequence 8, App1
49	180	96.3	41	3	US-09-082-279B-496	Sequence 496, App1
50	180	96.3	41	3	US-09-082-279B-601	Sequence 601, App1
51	180	96.3	41	3	US-09-082-279B-633	Sequence 633, App1
52	180	96.3	41	3	US-09-082-279B-1163	Sequence 1163, App1
53	180	96.3	41	4	US-08-474-349A-8	Sequence 8, App1
54	180	96.3	41	4	US-09-315-304B-496	Sequence 496, App1
55	180	96.3	41	4	US-09-315-304B-601	Sequence 601, App1
56	180	96.3	41	4	US-09-315-304B-633	Sequence 633, App1
57	180	96.3	41	4	US-09-315-304B-1163	Sequence 1163, App1
58	180	96.3	41	4	US-08-470-896-8	Sequence 8, App1
59	180	96.3	41	4	US-08-973-952-8	Sequence 8, App1
60	180	96.3	41	4	US-08-485-546A-8	Sequence 8, App1
61	180	96.3	41	4	US-08-485-546A-8	Sequence 8, App1
62	180	96.3	41	4	US-09-834-784-496	Sequence 496, App1
63	180	96.3	41	4	US-09-834-784-601	Sequence 601, App1
64	180	96.3	41	4	US-09-834-784-633	Sequence 633, App1
65	180	96.3	41	4	US-09-834-784-1163	Sequence 1163, App1
66	180	96.3	41	4	US-08-464-003-3	Sequence 3, App1
67	180	96.3	41	4	US-08-464-003-9	Sequence 9, App1
68	180	96.3	41	4	US-09-515-965A-496	Sequence 496, App1
69	180	96.3	41	4	US-09-515-965A-601	Sequence 601, App1
70	180	96.3	41	4	US-09-515-965A-633	Sequence 633, App1
71	180	96.3	41	4	US-09-515-965A-1163	Sequence 1163, App1
72	180	96.3	41	4	US-09-350-641C-496	Sequence 496, App1
73	180	96.3	41	4	US-09-350-641C-601	Sequence 601, App1
74	180	96.3	41	4	US-09-350-641C-633	Sequence 633, App1
75	180	96.3	41	4	US-09-350-641C-1163	Sequence 1163, App1
76	180	96.3	44	1	US-08-374-666-10	Sequence 10, App1
77	180	96.3	44	4	US-08-464-003-10	Sequence 10, App1
78	180	96.3	45	3	US-09-082-279B-1164	Sequence 1164, App1
79	180	96.3	45	4	US-09-315-304B-1164	Sequence 1164, App1
80	180	96.3	45	4	US-09-834-784-1164	Sequence 1164, App1
81	180	96.3	45	4	US-09-779-451-9	Sequence 9, App1
82	180	96.3	45	4	US-09-515-965A-1164	Sequence 1164, App1
83	180	96.3	45	4	US-09-350-641C-1164	Sequence 1164, App1
84	180	96.3	49	4	US-09-796-202-3	Sequence 3, App1
85	180	96.3	51	3	US-09-082-279B-745	Sequence 745, App1
86	180	96.3	51	4	US-09-315-304B-745	Sequence 745, App1
87	180	96.3	51	4	US-09-834-784-745	Sequence 745, App1
88	180	96.3	51	4	US-09-515-965A-745	Sequence 745, App1
89	180	96.3	51	4	US-09-350-641C-745	Sequence 745, App1
90	180	96.3	52	3	US-09-082-279B-1119	Sequence 1119, App1

ALIGNMENTS

RESULT 1
US-08-973-952-82
; Sequence 82, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:

APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/08/973,952A
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: 08/481,957
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 82
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-08-973-952-82

Query Match 100.0%; Score 187; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,6e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38
Db 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38

RESULT 2
US-08-374-666-1
Sequence 1, Application US/08374666
Patent No. 5656480
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,666
FILING DATE: 27-JAN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-374-666-1

Query Match 96.3%; Score 180; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38
Db 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38

RESULT 3
US-08-486-099-89
Sequence 89, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38
Db 1 NNLRRAIEAOQHLLQLTWQIKOLQARILAVERYLKQD 38

RESULT 4
US-08-360-107A-99
Sequence 99, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-99

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 NNILRAIEAQOHLQLTWGIKQIARILAVERYLKQ 38
1 NNILRAIEAQOHLQLTWGIKQIARILAVERYLKQ 38

RESULT 5
US-08-360-107A-132
Sequence 132, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-132

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 NNILRAIEAQOHLQLTWGIKQIARILAVERYLKQ 38
1 NNILRAIEAQOHLQLTWGIKQIARILAVERYLKQ 38

RESULT 6
US-08-484-223B-89
Sequence 89, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-2238-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 7
US-08-919-597-89
Sequence 89, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 8
US-08-475-668A-89
Sequence 89, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38
Db 1 NNILRAIEAQOHLLQLTWQIKQLQARILAVERYLKDQ 38

RESULT 9
US-08-485-551A-89
Sequence 89, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERTKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERTKQ 38

RESULT 10
US-08-471-913A-89
Sequence 89, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERTKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERTKQ 38

RESULT 11
US-08-485-264A-89
Sequence 89, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-89

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 12
US-09-082-279B-16
Sequence 16, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-16

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 13
US-09-082-279B-507
Sequence 507, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-507

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 14
US-09-082-279B-604
Sequence 604, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-604

Query Match 96.3%; Score 180; DB 3; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38
Db 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLKQ 38

RESULT 15
US-08-474-349A-89
Sequence 89, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-89

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 16
US-08-474-349A-441
Sequence 441, Application US/08474349A
Patent No. 6333395

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petreway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

TITLE OF INVENTION: VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-024

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 441:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-441

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 17
US-09-315-304B-16
Sequence 16, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Amner, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 16

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-16

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38
DB 1 NNLRAIEAQOHLQLTWQIKOLQARIILAVERYLKQ 38

RESULT 18
US-09-315-304B-507
Sequence 507, Application US/09315304B
Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Amner, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 507

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial Sequence

```
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-507

Query Match          96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 19
US-09-315-304B-604
Sequence 604, Application US/09315304B
Patent No. 6148568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315, 304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082, 279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-604

Query Match          96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 20
US-08-255-208A-25
Sequence 25, Application US/08255208A
Patent No. 6440656
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
```

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255, 208A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-25

Query Match          96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38
Db 1 NNLLRAIEAQOHLQLTWGKIQQLARILAVERYLKDQ 38

RESULT 21
US-08-470-896-89
Sequence 89, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470, 896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
```


LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-896-89

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 22
US-08-485-546A-89
Sequence 89, Application US/08485546A
Patent No. 6518013

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-546A-89

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 23
US-09-796-202-11
Sequence 11, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SUPRATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 24
US-09-834-784-16
Sequence 16, Application US/09834784
Patent No. 6562787

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guttridge, Kelly
APPLICANT: Metucka, Gene
APPLICANT: Amer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-16

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38
DB 1 NNLRAIEAOQHLLQLTWQIKOLQARILAVERYLKQ 38

RESULT 25
US-09-834-784-507
Sequence 507, Application US/09834784
Patent No. 6562787

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-507

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38
Db 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38

RESULT 26
US-09-834-784-604
Sequence 604, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-604

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38
Db 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38

RESULT 27
US-08-464-003-1
Sequence 1, Application US/08464003
Patent No. 6573078
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,003
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-464-003-1

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38
Db 1 NMLRAIEAQOHLQLTVMQIKQLQARILAVERYLKQ 38

RESULT 28
US-09-779-451-2
Sequence 2, Application US/09779451
Patent No. 6605427
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-2

Query Match 96.3%; Score 180; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: June 2, 2004, 11:48:34 ; Search time 33.163 Seconds
(without alignments)
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Title: US-09-657-336a-148
Perfect score: 176
Sequence: 1 NMLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database :

Published Applications AA:*
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15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	38	14	US-10-252-136-82 Sequence 82, Appl
2	169	96.0	36	15	US-10-005-305-129 Sequence 129, App
3	169	96.0	37	15	US-10-005-305-130 Sequence 130, App
4	169	96.0	38	9	US-09-796-202-11 Sequence 11, Appl
5	169	96.0	38	9	US-09-779-451-2 Sequence 2, Appl
6	169	96.0	38	9	US-09-912-824-2 Sequence 2, Appl
7	169	96.0	38	10	US-09-493-346-2 Sequence 2, Appl
8	169	96.0	38	12	US-10-267-682-89 Sequence 89, Appl
9	169	96.0	38	12	US-10-267-748-89 Sequence 89, Appl
10	169	96.0	38	12	US-09-809-060-6 Sequence 6, Appl
11	169	96.0	38	12	US-09-809-060-7 Sequence 7, Appl
12	169	96.0	38	12	US-10-663-589-3 Sequence 3, Appl
13	169	96.0	38	12	US-10-681-879-2 Sequence 2, Appl
14	169	96.0	38	12	US-09-828-615-2 Sequence 2, Appl
15	169	96.0	38	14	US-10-116-797-2 Sequence 2, Appl

16	169	96.0	38	14	US-10-323-314-11 Sequence 11, Appl
17	169	96.0	38	14	US-10-414-192-1 Sequence 1, Appl
18	169	96.0	38	14	US-10-351-641-16 Sequence 16, Appl
19	169	96.0	38	14	US-10-351-641-507 Sequence 507, Appl
20	169	96.0	38	14	US-10-351-641-604 Sequence 604, App
21	169	96.0	38	14	US-10-351-641-661 Sequence 661, App
22	169	96.0	38	14	US-10-351-641-662 Sequence 662, App
23	169	96.0	38	15	US-10-005-305-165 Sequence 165, App
24	169	96.0	38	15	US-10-005-305-202 Sequence 202, App
25	169	96.0	38	15	US-10-005-305-203 Sequence 203, App
26	169	96.0	38	15	US-10-420-194-1234 Sequence 1234, Ap
27	169	96.0	38	16	US-10-664-021-2 Sequence 2, Appl
28	169	96.0	38	16	US-10-671-316-2 Sequence 8, Appl
29	169	96.0	41	12	US-10-267-682-8 Sequence 8, Appl
30	169	96.0	41	12	US-10-267-748-8 Sequence 8, Appl
31	169	96.0	41	12	US-10-663-589-30 Sequence 30, Appl
32	169	96.0	41	12	US-10-663-589-33 Sequence 35, Appl
33	169	96.0	41	12	US-10-663-589-35 Sequence 3, Appl
34	169	96.0	41	14	US-10-414-192-3 Sequence 3, Appl
35	169	96.0	41	14	US-10-414-192-9 Sequence 496, App
36	169	96.0	41	14	US-10-351-641-496 Sequence 601, App
37	169	96.0	41	14	US-10-351-641-601 Sequence 633, App
38	169	96.0	41	14	US-10-351-641-633 Sequence 1163, Ap
39	169	96.0	41	14	US-10-351-641-1163 Sequence 27, Appl
40	169	96.0	41	16	US-10-664-021-27 Sequence 36, Appl
41	169	96.0	41	16	US-10-671-316-27 Sequence 9, Appl
42	169	96.0	44	12	US-10-663-589-36 Sequence 10, Appl
43	169	96.0	44	14	US-10-414-192-10 Sequence 9, Appl
44	169	96.0	45	9	US-09-779-451-9 Sequence 9, Appl
45	169	96.0	45	12	US-09-809-060-50 Sequence 29, Appl
46	169	96.0	45	12	US-10-663-589-29 Sequence 50, Appl
47	169	96.0	45	12	US-10-663-589-29 Sequence 1164, Ap
48	169	96.0	45	14	US-10-351-641-1164 Sequence 26, Appl
49	169	96.0	45	16	US-10-664-021-26 Sequence 26, Appl
50	169	96.0	45	16	US-10-671-316-26 Sequence 26, Appl
51	169	96.0	48	14	US-10-263-103-26 Sequence 3, Appl
52	169	96.0	49	9	US-09-796-202-3 Sequence 26, Appl
53	169	96.0	49	12	US-10-663-589-26 Sequence 26, Appl
54	169	96.0	49	16	US-10-323-314-3 Sequence 23, Appl
55	169	96.0	49	16	US-10-664-021-23 Sequence 23, Appl
56	169	96.0	49	16	US-10-671-316-23 Sequence 23, Appl
57	169	96.0	51	12	US-10-663-589-27 Sequence 27, Appl
58	169	96.0	51	14	US-10-351-641-745 Sequence 745, App
59	169	96.0	51	16	US-10-664-021-24 Sequence 24, App
60	169	96.0	51	16	US-10-671-316-24 Sequence 24, Appl
61	169	96.0	52	14	US-10-351-641-1119 Sequence 1119, Ap
62	169	96.0	53	14	US-10-351-641-955 Sequence 955, App
63	169	96.0	53	14	US-10-351-641-1062 Sequence 1062, Ap
64	169	96.0	53	9	US-09-779-451-1 Sequence 1, Appl
65	169	96.0	55	12	US-09-809-060-14 Sequence 14, Appl
66	169	96.0	57	15	US-10-438-691-1 Sequence 1, Appl
67	169	96.0	59	16	US-10-664-021-1 Sequence 1, Appl
68	169	96.0	59	16	US-10-671-316-1 Sequence 1, Appl
69	169	96.0	60	12	US-10-663-589-1 Sequence 1, Appl
70	169	96.0	63	12	US-10-267-682-201 Sequence 201, App
71	169	96.0	63	12	US-10-267-748-201 Sequence 201, App
72	169	96.0	63	14	US-10-252-136-54 Sequence 54, Appl
73	169	96.0	101	14	US-10-263-103-31 Sequence 31, Appl
74	169	96.0	103	14	US-10-263-103-29 Sequence 29, Appl
75	169	96.0	103	14	US-10-263-103-32 Sequence 32, Appl
76	169	96.0	103	15	US-10-438-691-3 Sequence 3, Appl
77	169	96.0	105	14	US-10-263-103-28 Sequence 28, Appl
78	169	96.0	105	14	US-10-263-103-30 Sequence 30, Appl
79	169	96.0	108	15	US-10-263-103-33 Sequence 33, Appl
80	169	96.0	113	15	US-10-438-691-4 Sequence 4, Appl
81	169	96.0	177	14	US-10-040-349B-2 Sequence 2, Appl
82	169	96.0	138	9	US-09-854-816-88 Sequence 88, Appl
83	169	96.0	138	9	US-09-854-816-89 Sequence 89, Appl
84	169	96.0	200	14	US-10-263-103-25 Sequence 25, Appl
85	169	96.0	200	15	US-10-438-691-8 Sequence 8, Appl
86	169	96.0	222	14	US-10-059-271-81 Sequence 81, Appl
87	169	96.0	234	14	US-10-059-271-82 Sequence 82, Appl
88	169	96.0	256	14	US-10-059-271-97 Sequence 97, Appl

89 169 96.0 268 9 US-09-854-816-16
90 169 96.0 268 9 US-09-854-816-17

ALIGNMENTS

Sequence 16, Appl
Sequence 17, Appl

RESULT 1
US-10-252-136-82
; Sequence 82, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-82

Query Match 100.0%; Score 176; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 2
US-10-005-305-129
; Sequence 129, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-129

Query Match 96.0%; Score 169; DB 15; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.3e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 3
US-10-005-305-130
; Sequence 130, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-130

Query Match 96.0%; Score 169; DB 15; Length 37;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 4
US-09-796-202-11
; Sequence 11, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUBLATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(38)
; OTHER INFORMATION: DP107
US-09-796-202-11

Query Match 96.0%; Score 169; DB 9; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYLK 36

RESULT 5
US-09-779-451-2
; Sequence 2, Application US/09779451

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; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-779-451-2
;
Query Match          96.0%; Score 169; DB 9; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
US-09-912-824-2
; Sequence 2, Application US/09912824
; Patent No. US20020106374A1
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF HIV-1 INFECTION
; FILE REFERENCE: 2048/62942-B
; CURRENT APPLICATION NUMBER: US/09/912,824
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 Peptide
; US-09-912-824-2
;
Query Match          96.0%; Score 169; DB 9; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
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NNILRAIEAQOHLQLTWGIKOLQARIIAVERYLK 36
Db
1 NNILRAIEAQOHLQLTWGIKOLQARIIAVERYLK 36

RESULT 7
US-09-493-346-2
; Sequence 2, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olsson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
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; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
; US-09-493-346-2
;
Query Match          96.0%; Score 169; DB 10; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 NNILRAIEAQOHLQLTWGIKOLQARIIAVERYLK 36
NNILRAIEAQOHLQLTWGIKOLQARIIAVERYLK 36
Db
1 NNILRAIEAQOHLQLTWGIKOLQARIIAVERYLK 36

RESULT 8
US-10-267-682-89
; Sequence 89, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-267-682-89
;
Query Match          96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36

RESULT 9
US-10-267-748-89
Sequence 89, Application US/10267748
Publication No. US2004052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matchews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:

US-10-267-748-89

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36

RESULT 10
US-09-809-060-6
Sequence 6, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies Against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-6

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36

RESULT 11
US-09-809-060-7
Sequence 7, Application US/09809060
Publication No. US20020010317A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
Neutralizing Antibodies Against Fusion-Active
TITLE OF INVENTION: Regions of HIV Envelope Proteins
FILE REFERENCE: 1900.0260001
CURRENT APPLICATION NUMBER: US/09/809,060
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/189,981
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 38
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-7

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQHLLQLTWQIKQLQARILAVERYLK 36

RESULT 12
US-10-653-589-3
Sequence 3, Application US/10663589
Publication No. US2004006357A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/653,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin version 3.2

SEQ ID NO 3
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-3

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 13
US-10-681-879-2
Sequence 2, Application US/10681879
Publication No. US20040062767A1
GENERAL INFORMATION:
APPLICANT: Olson, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/10/681,879
CURRENT FILING DATE: 2003-10-09/493,346
PRIOR APPLICATION NUMBER: US/09/493,346
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DP107 peptide
US-10-681-879-2

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 14
US-09-828-615-2
Sequence 2, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-2

Query Match 96.0%; Score 169; DB 12; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 15
US-10-116-797-2
Sequence 2, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C
APPLICANT: Maddon, Paul J
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-2

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 16
US-10-323-314-11
Sequence 11, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SUBSTITUTED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 38
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
OTHER INFORMATION: DP107
US-10-323-314-11

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 17
US-10-414-192-1
Sequence 1, Application US/10414192
Publication No. US20030181382A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Matthews, Thomas J.
APPLICANT: Bolognesi, Dani P.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT HIV REPLICATION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,192
FILING DATE: 15-Apr-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-414-192-1

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 18
US-10-351-641-16
Sequence 16, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Core polypeptide
US-10-351-641-16

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 19
US-10-351-641-507
Sequence 507, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 507
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-507

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36
DB 1 NNLRAIEAQOHLQLTWQIKOLQARILAVERYLK 36

RESULT 20
US-10-351-641-604
Sequence 604, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Amer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 604
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-604

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 21
US-10-351-641-661
Sequence 661, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 661
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-661

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
Db 2 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 37

RESULT 22
US-10-351-641-662
Sequence 662, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641

CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 662
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-662

Query Match 96.0%; Score 169; DB 14; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
Db 3 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 38

RESULT 23
US-10-005-305-165
Sequence 165, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 165
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-165

Query Match 96.0%; Score 169; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQLQARILAVERYLK 36

RESULT 24
US-10-005-305-202
Sequence 202, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
APPLICANT: Secretary, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1

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CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 202
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-202

Query Match          96.0%; Score 169; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36

RESULT 25
US-10-005-305-203
Sequence 203, Application US/10005305
Publication No. US20030203841A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, represented by the
SECRETARY, Department of Health and Human Services
TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
TITLE OF INVENTION: OF HUMAN PHAGOCYTE
TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
FILE REFERENCE: NIH171.001C1
CURRENT APPLICATION NUMBER: US/10/005,305
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: PCT/US00/12371
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,686
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-005-305-203

Query Match          96.0%; Score 169; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36

RESULT 26
US-10-420-194-1234
Sequence 1234, Application US/10420194
Publication No. US20040006035A1
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: MCSwigen, Jim
APPLICANT: Blact, Larry
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Mediated Disruption of HIV Fusogenic Peptide
TITLE OF INVENTION: Interactions
FILE REFERENCE: MBH02-305-A (400/011)
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CURRENT APPLICATION NUMBER: US/10/420,194
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US 03/05190
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/398,036
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/374,722
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1234
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 1234
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV gp41 peptide sequences
NAME/KEY: PEPTIDE
LOCATION: (1)..(38)
US-10-420-194-1234

Query Match          96.0%; Score 169; DB 15; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 NNLRAIEAQOHLQLTWQIKQARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWGIKQARILAVERYLK 36

RESULT 27
US-10-664-021-2
Sequence 2, Application US/10664021
Publication No. US2004007637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: HIV-Derived HRI Peptides Modified to Form Stable Trimers, and
TITLE OF INVENTION: Their Use in Therapy to Inhibit Transmission of Human
TITLE OF INVENTION: Immunodeficiency Virus
FILE REFERENCE: TRM-001
CURRENT APPLICATION NUMBER: US/10/664,021
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,514
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 2
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-664-021-2

Query Match          96.0%; Score 169; DB 16; Length 38;
Best Local Similarity 97.2%; Pred. No. 2,4e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 36
Db 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 36

RESULT 28
US-10-671-316-2
Sequence 2, Application US/10671316
Publication No. US20040091855A1
GENERAL INFORMATION:

APPLICANT: Trimeris, Inc.

TITLE OF INVENTION: Method for production of antivirals by use of HIV-derived HRI
TITLE OF INVENTION: peptides, and trimers formed therefrom
FILE REFERENCE: Tm-002

CURRENT APPLICATION NUMBER: US/10/671.316

CURRENT FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: 60/414,515

PRIOR FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.2

SEQ ID NO 2

LENGTH: 38

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: synthesized

US-10-671-316-2

Query Match 96.0%; Score 169; DB 16; Length 38;

Best Local Similarity 97.2%; Pred. No. 2.4e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 36

Db 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 36

RESULT 29
US-10-267-682-8
Sequence 8, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petleway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267.682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484.223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-267-682-8

Query Match 96.0%; Score 169; DB 12; Length 41;

Best Local Similarity 97.2%; Pred. No. 2.7e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 36

Db 4 NNLRAIEAQOHLQLTWQIKOLARILAVERYLK 39

RESULT 30
US-10-267-748-8
Sequence 8, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petleway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267.748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484.223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: <unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-267-748-8

Query Match 96.0%; Score 169; DB 12; Length 41;
Best Local Similarity 97.2%; Pred. No. 2.7e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRLRAIEAQQHLLQLTWQIKQLQARIHIAVERYLK 36
DB 4 NNLRLRAIEAQQHLLQLTWGIKQLQARIHIAVERYLK 39

Search completed: June 2, 2004, 12:29:24
Job time: 33.163 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 11:28:22 ; Search time 43.8451 Seconds
(without alignments)
225.548 Million cell updates/sec

Title: US-09-657-336a-149
Sequence: 1 NMLRAIEAQOHLLQLTWQIKQLQARILAVERYL 35

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	171 100.0	35 3	AAB14703	Aab14703 HIV-1 Iso
2	171 100.0	35 4	AAB54967	Aab54967 Anti-HIV
3	171 100.0	36 3	AAB14704	Aab14704 HIV-1 Iso
4	171 100.0	36 4	AAB54968	Aab54968 Anti-HIV
5	171 100.0	37 3	AAB14705	Aab14705 HIV-1 Iso
6	171 100.0	37 4	AAB54969	Aab54969 Anti-HIV
7	171 100.0	38 2	AAR98408	Aar98408 DP107 cor
8	171 100.0	38 4	AAB54785	Aab54785 HIV antiiv
9	171 100.0	38 4	AAB55005	Aab55005 Anti-HIV
10	171 100.0	38 4	AAB54970	Aab54970 Anti-HIV
11	171 100.0	38 4	AAB92244	Aab92244 Virus rel
12	171 100.0	38 4	AAU14011	Aau14011 DP107 pep
13	171 100.0	38 5	AAO18771	Aao18771 HIV gp41
14	167 97.7	34 4	AAB14702	Aab14702 HIV-1 Iso
15	167 97.7	34 4	AAB54966	Aab54966 Anti-HIV
16	165 96.5	37 3	AAB14739	Aab14739 HIV-1 Iso
17	165 96.5	37 4	AAB55004	Aab55004 Anti-HIV
18	164 95.9	35 3	AAB52749	Aab52749 T21/DP107
19	164 95.9	36 3	AAB52750	Aab52750 T21/DP107
20	164 95.9	37 3	AAB52751	Aab52751 T21/DP107
21	164 95.9	38 2	AAR55635	Aar55635 DP-139 -
22	164 95.9	38 2	AAR55636	Aar55636 DP-140 -
23	164 95.9	38 2	AAR47216	Aar47216 DP-107 -
24	164 95.9	38 2	AAW27614	Aaw27614 Human Imm
25	164 95.9	38 3	AAY88666	Aay88666 Core poly

26	164 95.9	38 3	AAY88730	Aay88730 Core poly
27	164 95.9	38 3	AAY88731	Aay88731 Core poly
28	164 95.9	38 3	AAY89251	Aay89251 Core poly
29	164 95.9	38 3	AAY89145	Aay89145 Core poly
30	164 95.9	38 3	AAY89146	Aay89146 Core poly
31	164 95.9	38 3	AAY89243	Aay89243 Core poly
32	164 95.9	38 3	AAB14530	Aab14530 HIV-1 Iso
33	164 95.9	38 3	AAB52824	Aab52824 T21/DP107
34	164 95.9	38 3	AAB52786	Aab52786 T21/DP107
35	164 95.9	38 3	AAB52823	Aab52823 T21/DP107
36	164 95.9	38 4	AAG63858	Aag63858 Amino aci
37	164 95.9	38 4	AAB92349	Aab92349 Virus rel
38	164 95.9	38 4	AAB77021	Aab77021 Core poly
39	164 95.9	38 4	AAB77653	Aab77653 Core poly
40	164 95.9	38 4	AAB77085	Aab77085 Core poly
41	164 95.9	38 4	AAB77086	Aab77086 Core poly
42	164 95.9	38 4	AAB77596	Aab77596 Core poly
43	164 95.9	38 4	AAB77652	Aab77652 Core poly
44	164 95.9	38 4	AAB77500	Aab77500 Core poly
45	164 95.9	38 4	AAB77624	Aab77624 Core poly
46	164 95.9	38 4	AAB77654	Aab77654 Core poly
47	164 95.9	38 4	AAU70185	Aau70185 HIV viral
48	164 95.9	38 4	AAU70184	Aau70184 HIV viral
49	164 95.9	38 4	AAB85690	Aab85690 DP107 pep
50	164 95.9	38 4	AAB01489	Aab01489 Viral cor
51	164 95.9	38 4	AAB00505	Aab00505 Viral DP1
52	164 95.9	38 4	AAB00090	Aab00090 Viral DP1
53	164 95.9	38 4	AAB00657	Aab00657 Viral cor
54	164 95.9	38 4	AAB02077	Aab02077 Viral cor
55	164 95.9	38 4	AAB00025	Aab00025 HIV-1 gp4
56	164 95.9	38 4	AAB00089	Aab00089 Viral DP1
57	164 95.9	38 4	AAB00504	Aab00504 Viral DP1
58	164 95.9	38 4	AAB02136	Aab02136 Viral cor
59	164 95.9	38 4	AAB00658	Aab00658 Viral DP1
60	164 95.9	38 4	AAB02135	Aab02135 Viral cor
61	164 95.9	38 4	AAB00629	Aab00629 Viral cor
62	164 95.9	38 4	AAB00659	Aab00659 Viral DP1
63	164 95.9	38 4	AAB00601	Aab00601 RSV Fl pr
64	164 95.9	38 4	AAB01980	Aab01980 Viral cor
65	164 95.9	38 4	AAB02134	Aab02134 Viral cor
66	164 95.9	38 4	AAU13207	Aau13207 DP178-1ik
67	164 95.9	38 4	AAU12638	Aau12638 DP178-1ik
68	164 95.9	38 4	AAU13205	Aau13205 DP178-1ik
69	164 95.9	38 4	AAU13053	Aau13053 DP178-1ik
70	164 95.9	38 4	AAU13149	Aau13149 DP178-1ik
71	164 95.9	38 4	AAU13177	Aau13177 DP178-1ik
72	164 95.9	38 4	AAU12574	Aau12574 DP178-1ik
73	164 95.9	38 4	AAU13206	Aau13206 DP178-1ik
74	164 95.9	38 4	AAU12639	Aau12639 DP178-1ik
75	164 95.9	38 4	AAB82962	Aab82962 Anti-HIV
76	164 95.9	38 5	AAB82297	Aab82297 gp41 fusi
77	164 95.9	38 5	AAB82292	Aab82292 gp41 fusi
78	164 95.9	38 5	AAB82097	Aab82097 Hybrid po
79	164 95.9	38 5	AAB82156	Aab82156 Hybrid po
80	164 95.9	38 5	AAB82155	Aab82155 Hybrid po
81	164 95.9	38 5	AAB82154	Aab82154 Hybrid po
82	164 95.9	38 5	AAB82153	Aab82153 Hybrid po
83	164 95.9	38 6	ABG75976	Abg75976 HIV-1 gp4
84	164 95.9	38 6	ABU09553	Abu09553 Peptide I
85	164 95.9	38 7	ABO10245	Abu09553 Peptide I
86	164 95.9	38 7	ADG99756	Adg99756 DP-107 an
87	164 95.9	38 7	ADG73011	Adg73011 HIV gp41
88	164 95.9	41 2	AAR52840	Aar52840 DP-125 -
89	164 95.9	41 2	AAR98406	Aar98406 Peptide D
90	164 95.9	41 2	AAW17019	Aaw17019 DP-178-1i

ALIGNMENTS

RESULT 1
ID AAB14703 standard; peptide; 35 AA.

XX AAB14703;
 AC 12-SEP-2003 (revised)
 DT 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #32.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 XX WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000MO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 PR 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 PA (WEIS/) WEISS C D.
 PI
 XX WILD CT, Weiss CD;
 DR WPI; 2000-465959/40.
 PT
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 XX
 PS Disclosure; Page 36; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralizing antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond to or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerised. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic
 CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX Sequence 35 AA;
 SQ

Query Match 100.0%; Score 171; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.5e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQHLLQLTWQIKOLARILAVERYL 35
 Db 1 NNILRAIEAQHLLQLTWQIKOLARILAVERYL 35
 XX
 XX AAB54967 standard; peptide, 35 AA.
 AC AAB54967;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #32.
 XX
 XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antitumorigenic; mobile blood component; measles virus; MeV; STV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 XX WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 XX (CONV-) CONJUCHEM INC.
 PA
 PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 PI WPI; 2001-007496/01.
 DR
 XX
 XX A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 137; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and STV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 XX Sequence 35 AA;
 SQ

Query Match 100.0%; Score 171; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.5e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNILRAIEAQHLLQLTWQIKOLARILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERYL 35

RESULT 3
AAB14704
ID AAB14704 standard; peptide; 36 AA.
XX
AC AAB14704;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #33.
XX
KW HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KW core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KW humoral response; broad spectrum vaccine; anti-HIV;
KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KW isolate LAI.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200040616-A1.
XX
PD 13-JUL-2000.
XX
PF 10-JAN-2000; 2000MO-US000456.
XX
PR 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
PA (WILD/) WILD C T.
PA (WEIS/) WEISS C D.
XX
PI Wild CT, Weiss CD;
XX
DR WPI; 2000-465959/40.
XX
PT Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX Disclosure; Page 36; 97pp; English.

Sequences AAB1672-B1473 represent peptides derived from the N-helical domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B, isolate LAI. The invention relates to raising a neutralizing antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of gp41 which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond or mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-helical segment), or the gp41 core 6-helix bundle, which is formed by the interaction of the N- and C-helical domains of three gp41 proteins. The peptides can be administered either singly or as a combination (particularly a combination of N-helical and C-helical peptides), and can be multimerised. For example, N- and C-helical domain peptides can be alternately linked together to form a peptide which mimics the core 6-helix bundle. Administration of the peptide(s) generates a humoral response, with the production of antibodies against gp41 structures involved in viral entry. As these portions of gp41 are well conserved, such antibodies may be effective against a broad range of HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to standardise OS field)

XX
SQ Sequence 36 AA;
XX
Query Match 100.0%; Score 171; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERYL 35
Db 1 NNLRAIEAQOHLQLTWQIKQLQARILLAVERYL 35

RESULT 4
AAB54968
ID AAB54968 standard; peptide; 36 AA.
XX
AC AAB54968;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE Anti-HIV peptide DP107 carboxy truncation peptide #33.
XX
KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antitumorigenic; mobile blood component; measles virus; MeV; STV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200069902-A1.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013651.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boujdellab N, Robitaille M, Malner PG;
XX
DR WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 137; 211pp; English.

The present invention describes a modified anti-viral peptide (I) comprising a peptide that exhibits anti-viral activity and a reactive group which is reactive with amino groups, hydroxyl groups, or thiol groups on blood components to form stable covalent bonds. (I) has anti-viral and anti-fusogenic activities. (I) inhibits viral infection of cells by inhibiting cell-cell fusion or free virus infection or to reduce the level of membrane fusion events between two or more entities, e.g., virus-cell or cell-cell, relative to the level of membrane fusion that occurs in the absence of the peptide. (I) is useful in the treatment of patients who are suffering from viral infection, e.g. HIV, RSV, HPIV, MeV, and STV. (I) may be administered prophylactically to previously uninfected individuals. This is useful in cases where an individual has been subjected to a high risk of exposure to a virus. By bonding of long-lived components of the blood, such as immunoglobulin, serum albumin, red blood cells and platelets the activity is extended for days to weeks. This is due to improved stability in vivo and a reduced susceptibility to peptidase or protease degradation. This minimises the need for more frequent, or even continual, administration of the peptides. AAB54784 to AAB55331 represent peptides used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;
 Query Match 100.0%; Score 171; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.7e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35

RESULT 5
 AAB14705
 AAB14705 standard; peptide; 37 AA.

AC AAB14705;
 XX
 DT 12-SEP-2003 (revised)
 XX 24-NOV-2000 (first entry)
 XX
 DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #34.
 XX
 KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
 KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
 KM humoral response; broad spectrum vaccine; anti-HIV;
 KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
 KM isolate LAI.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200040616-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 10-JAN-2000; 2000WO-US000456.
 XX
 PR 08-JAN-1999; 99US-0115404P.
 XX 07-JAN-2000; 2000US-00480336.
 XX
 PA (WILD/) WILD C T.
 XX (WEIS/) WEISS C D.
 XX
 PI WILD CT, Weiss CD;
 XX
 DR WPI; 2000-465959/40.
 XX
 PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprising administering a polypeptide capable of forming a stable coiled-
 PT coil solution structure.
 PT
 PS Disclosure; Page 36; 97pp; English.
 XX
 CC Sequences AAB14672-B14739 represent peptides derived from the N-helical
 CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
 CC isolate LAI. The invention relates to raising a neutralizing antibody
 CC response to a broad spectrum of HIV (human immunodeficiency virus)
 CC strains and isolates, comprising the administration of a peptide which
 CC corresponds to or mimics highly conserved portions of gp41 which are
 CC important in mediating the process of viral entry into host cells. Such
 CC peptides can correspond to or mimic the coiled coil solution structure of
 CC the N-helical domain (the heptad repeat region), or can correspond to or
 CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
 CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
 CC interaction of the N- and C-helical domains of three gp41 proteins. The
 CC peptides can be administered either singly or as a combination
 CC (particularly a combination of N-helical and C-helical peptides), and can
 CC be multimerized. For example, N- and C-helical domain peptides can be
 CC alternately linked together to form a peptide which mimics the core 6-
 CC helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains and
 CC isolates. The peptide compositions may be administered as a prophylactic

CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
 CC ability of HIV to infect uninfected cells. A composition comprising
 CC polyclonal or monoclonal antibodies can be administered to reduce HIV
 CC infection of uninfected cells. Antibodies raised against entry-relevant
 CC gp41 structures may also be used therapeutically and as tools to further
 CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
 CC standardise OS field)

SQ Sequence 37 AA;
 Query Match 100.0%; Score 171; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 4.8e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERYL 35

RESULT 6
 AAB54969
 AAB54969 standard; peptide; 37 AA.

AC AAB54969;
 XX
 DT 11-SEP-2003 (revised)
 XX 05-MAR-2001 (first entry)
 XX
 DE Anti-HIV peptide DP107 carboxy truncation peptide #34.
 XX
 KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KM antifeusogenic; mobile blood component; measles virus; MeV; SiV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200069902-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 XX 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille W, Milner PG;
 XX
 DR WPI; 2001-007496/01.
 XX
 CC A modified peptide and a reactive group which is reactive with amino
 CC PT groups, hydroxyl groups, or thiol groups on blood components to form
 CC PT stable covalent bonds useful for treatment of viral infections, e.g.
 CC PT human immunodeficiency virus.
 XX
 PS Disclosure; Page 137; 211pp; English.
 XX
 CC The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SiV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red

CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC proteolysis or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 37 AA;

Query Match 100.0%; Score 171; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 4,9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYL 35
1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYL 35

RESULT 7

AAR98408 AAR98408 standard; peptide; 38 AA.

XX AAR98408;

XX 16-OCT-2003 (revised)
DT 17-FEB-1997 (first entry)

DE DP107 corresponds to residues 558-595 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
KW ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
KW Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX WO9619495-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-US016733.

XX 20-DEC-1994; 94US-00360107.

XX 06-JUN-1995; 95US-00470896.

XX (UYDU-) UNIV DUKE.
PA (TRIM-) TRIMERIS INC.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
PI Peteway SR, Langlois AJ;
XX WPI; 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence
PT search motif.

XX Disclosure; Page 30; 471pp; English.

XX The sequences given in AAR98398-408 represent peptides which exhibit
CC antifusogenic activity, antiviral capability and/or the ability to
CC modulate intracellular processes involving coiled-coil peptide
CC structures. These peptides are recognised by the ALLMOT15, 107x178x4 and
CC PLZIP search motifs. These peptides may be used to inhibit the
CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYL 35

DB 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYL 35

RESULT 8
AAB54785 AAB54785 standard; peptide; 38 AA.

XX AAB54785;

XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)

DE HIV antiviral activity exhibiting peptide SEQ ID NO:2.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antifusogenic; mobile blood component; measles virus; MeV; SiV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus 1.

XX WO200069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013651.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Dufresne RP, Boudjelal N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

XX Claim 6; Page 173; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SiV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC proteolysis or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLQLTWQIKQLQARILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYL 35

RESULT 9

AAB55005 ID AAB55005 standard; peptide; 38 AA.

XX AAB55005;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 amino truncation peptide #35.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antitumorigenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.

XX WO200069902-A1.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013651.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

PS Disclosure; Page 139; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 4.9e-16; Mismatches 0; Indels 0; Gaps 0;

DB 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYL 35

RESULT 10
AAB54970 ID AAB54970 standard; peptide; 38 AA.

XX AAB54970;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP107 carboxy truncation peptide #35.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
XX antitumorigenic; mobile blood component; measles virus; MeV; SIV;
XX simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
XX human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.

XX WO200069902-A1.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013651.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.

PS Disclosure; Page 137; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptide. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 38 AA;

Query Match 100.0%; Score 171; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 4.9e-16; Mismatches 0; Indels 0; Gaps 0;

DB 1 NNLRAIEAQOHLQLTWQIKOLARILAVERYL 35

RESULT 11
 AAB92244
 ID AAB92244 standard; peptide; 38 AA.
 XX AAB92244;
 AC
 XX 22-JUN-2001 (first entry)
 DT
 XX
 DE Virus related peptide SEQ ID NO:1420.
 OS
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 OS
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000MO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 662; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 171; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYL 35
 DB 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYL 35

RESULT 12
 AAU14011
 ID AAU14011 standard; peptide; 38 AA.
 XX
 AC AAU14011;

XX 11-SEP-2003 (revised)
 DT 21-NOV-2001 (first entry)
 XX
 DE DP107 peptide from HIV-1 transmembrane protein gp41.
 XX
 KM Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KW antitumorogenic; antiviral; HIV transmission.
 XX
 OS Human immunodeficiency virus 1; isolate LAI.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..35
 FT /note="amino acids 1-35 can be optionally and serially
 FT deleted from the N-terminus"
 FT Misc-difference 4..38
 FT /note="amino acids 4-38 can be optionally and serially
 FT deleted from the C-terminus"
 XX
 PN WO200151673-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 05-JUL-2000; 2000MO-US035727.
 XX
 PR 09-JUL-1999; 99US-00350841.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Mernitka G;
 XX
 DR WPI; 2001-442157/47.
 XX
 PT Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitumorogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Page 33; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU1559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antitumorogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents the DP107 peptide. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 171; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYL 35
 DB 1 NNILRAIEAQOHLLQLTWQIKOLQARILAVERYL 35

RESULT 13
 AA018771
 ID AA018771 standard; peptide; 38 AA.
 XX

AA018771;
29-OCT-2002 (first entry)
HIV gp41 protein DP-107 region derived peptide SEQ ID NO: 2.
Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
gp41.
Human immunodeficiency virus.
WO200256902-A2.
25-JUL-2002.
17-DEC-2001; 2001WO-US048802.
19-DEC-2000; 2000US-0256657P.
(SCHE) SCHERING CORP.
Baroudy BM;
WPI; 2002-636513/68.
Treatment of HIV infection in an individual involves administration of a
combination of chemokine co-receptor five antagonist and a specified HIV
envelope polypeptide.
Disclosure; Page 34; 52pp; English.
The present invention relates to a method of treating an HIV infection in
an individual, which involves administering in combination a chemokine co-
receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
derivative. Other viral infections can also be treated using the method.
The present sequence is a peptide derived from HIV and useful in the
method of the invention
Sequence 38 AA;
Query Match 100.0%; Score 171; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,9e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 NNILRAIEAQOHLTLTWQIKOLQARILAVERYL 35
1 NNILRAIEAQOHLTLTWQIKOLQARILAVERYL 35
RESULT 14
AAB14702
ID AAB14702 standard; peptide; 34 AA.
AC AAB14702;
XX
DT 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE HIV-1 isolate LAI gp41 N-helical domain peptide P-17, fragment #31.
XX
KM HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M; subtype B;
KM isolate LAI.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200040616-A1.
XX
PD 13-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US000456.

08-JAN-1999; 99US-0115404P.
07-JAN-2000; 2000US-00480336.
(WILD/) WILD C T.
(WEIS/) WEISS C D.
WILD CT, Weiss CD;
WPI; 2000-465959/40.
Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
coil solution structure.
Disclosure; Page 36; 97pp; English.
Sequences AAB14672-B14739 represent peptides derived from the N-helical
domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
isolate LAI. The invention relates to raising a neutralizing antibody
response to a broad spectrum of HIV (human immunodeficiency virus)
strains and isolates, comprising the administration of a peptide which
corresponds to or mimics highly conserved portions of gp41 which are
important in mediating the process of viral entry into host cells. Such
peptides can correspond to or mimic the coiled coil solution structure of
the N-helical domain (the heptad repeat region), or can correspond or
mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
helical segment), or the gp41 core 6-helix bundle, which is formed by the
interaction of the N- and C-helical domains of three gp41 proteins. The
peptides can be administered either singly or as a combination
(particularly a combination of N-helical and C-helical peptides), and can
be multimerised. For example, N- and C-helical domain peptides can be
alternately linked together to form a peptide which mimics the core 6-
helix bundle. Administration of the peptide(s) generates a humoral
response, with the production of antibodies against gp41 structures
involved in viral entry. As these portions of gp41 are well conserved,
such antibodies may be effective against a broad range of HIV strains and
isolates. The peptide compositions may be administered as a prophylactic
or therapeutic vaccine to generate antibodies which reduce or inhibit the
ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
infection of uninfected cells. Antibodies raised against entry-relevant
gp41 structures may also be used therapeutically and as tools to further
elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
standardise OS field)
Sequence 34 AA;
Query Match 97.7%; Score 167; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 NNILRAIEAQOHLTLTWQIKOLQARILAVERY 34
1 NNILRAIEAQOHLTLTWQIKOLQARILAVERY 34
RESULT 15
AAB54966
ID AAB54966 standard; peptide; 34 AA.
AC AAB54966;
XX
DT 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE Anti-HIV peptide DP107 carboxy truncation peptide #31.
XX
KM Long lasting fusion peptide inhibitor; viral infection; antiviral;
KM antitumorigenic; mobile blood component; measles virus; MeV; SIV;
KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.
PN WO200063902-A1.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013651.
XX
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG.
PI WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
XX
PS Disclosure; Page 137; 21pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC Mev, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobulin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB54431 represent peptides used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 34 AA:
Query Match 97.7%; Score 167; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERY 34
DB 1 NNLRAIEAQOHLQLTWQIKQLQARILAVERY 34
RESULT 16
AAB14739
ID AAB14739 standard; peptide; 37 AA.
XX
XX AAB14739;
XX
XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
XX HIV-1 isolate IAI gp41 N-helical domain peptide P-17, fragment #68.
XX
XX HIV-1; gp41 N-helical domain; gp41 heptad repeat region; coiled coil;
KM core 6-helix bundle; viral entry inhibition; immunogenic; antibody;
KM humoral response; broad spectrum vaccine; anti-HIV;
KM envelope glycoprotein; prophylaxis; therapy; group M, subtype B;
XX isolate IAI.
XX

OS Human immunodeficiency virus 1.
XX
XX PN WO200040616-A1.
XX
XX 13-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000456.
XX
XX 08-JAN-1999; 99US-0115404P.
PR 07-JAN-2000; 2000US-00480336.
XX
XX (WILD/) WILD C. T.
PA (WEIS/) WEISS C. D.
XX
XX WILD CT, Weiss CD;
PI WPI; 2000-465959/40.
XX
XX Raising neutralizing antibody response to human immunodeficiency virus,
PT comprises administering a polypeptide capable of forming a stable coiled-
PT coil solution structure.
XX
XX
PS Disclosure; Page 38; 97pp; English.
XX
XX Sequences AAB14672-B14739 represent peptides derived from the N-helical
CC domain of the gp41 envelope glycoprotein from HIV-1 group M, subtype B,
CC isolate IAI. The invention relates to raising a neutralising antibody
CC response to a broad spectrum of HIV (human immunodeficiency virus)
CC strains and isolates, comprising the administration of a peptide which
CC corresponds to or mimics highly conserved portions of gp41 which are
CC important in mediating the process of viral entry into host cells. Such
CC peptides can correspond to or mimic the coiled coil solution structure of
CC the N-helical domain (the heptad repeat region), or can correspond or
CC mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-
CC helical segment), or the gp41 core 6-helix bundle, which is formed by the
CC interaction of the N- and C-helical domains of three gp41 proteins. The
CC peptides can be administered either singly or as a combination
CC (particularly a combination of N-helical and C-helical peptides), and can
CC be multimerised. For example, N- and C-helical domain peptides can be
CC alternately linked together to form a peptide which mimics the core 6-
CC helix bundle. Administration of the peptide(s) generates a humoral
CC response, with the production of antibodies against gp41 structures
CC involved in viral entry. As these portions of gp41 are well conserved,
CC such antibodies may be effective against a broad range of HIV strains and
CC isolates. The peptide compositions may be administered as a prophylactic
CC or therapeutic vaccine to generate antibodies which reduce or inhibit the
CC ability of HIV to infect uninfected cells. A composition comprising
CC polyclonal or monoclonal antibodies can be administered to reduce HIV
CC infection of uninfected cells. Antibodies raised against entry-relevant
CC gp41 structures may also be used therapeutically and as tools to further
CC elucidate the mechanism of HIV cell entry. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
XX
SQ Sequence 37 AA:
Query Match 96.5%; Score 165; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLRRAIEAQOHLQLTWQIKQLQARILAVERY 35
DB 1 NLRRAIEAQOHLQLTWQIKQLQARILAVERY 34
RESULT 17
AAB55004
ID AAB55004 standard; peptide; 37 AA.
XX
XX AAB55004;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX

DE Anti-HIV peptide DP107 amino truncation peptide #34.
 XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 XX antifusogenic; mobile blood component; measles virus; MeV; SiV;
 KM simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;
 KM human respiratory syncytial virus; human immunodeficiency virus; HIV.
 OS Human immunodeficiency virus 1.
 XX WO200069902-A1.
 XX 23-NOV-2000.
 XX 17-MAY-2000; 2000WO-US013651.
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX (CONT-) CONJUCHEM INC.
 PA Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 PI WPI; 2001-007496/01.
 DR A modified peptide and a reactive group which is reactive with amino
 XX groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 PS Disclosure; Page 139; 211pp; English.
 XX The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPiV,
 CC MeV, and SiV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC XX
 SQ Sequence 37 AA;
 Query Match 96.5%; Score 165; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.1e-15;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
 Db 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYL 34
 RESULT 18
 AAB52749
 ID AAB52749 standard; peptide; 35 AA.
 XX AAB52749;
 XX 12-SEP-2003 (revised)
 DT 23-FEB-2001 (first entry)
 XX T21/DP107 peptide fragment #31.

XX Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
 KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
 KM chemottractant.
 XX Human immunodeficiency virus 1.
 OS WO200066622-A1.
 XX 09-NOV-2000.
 XX 05-MAY-2000; 2000WO-US012371.
 PR 05-MAY-1999; 99US-0132686P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
 PI WPI; 2000-656493/63.
 DR Administration of peptide agents with a sequence corresponding to a
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
 PT is used to modulate inflammation.
 XX Claim 12; Page 28; 149pp; English.
 XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
 CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
 CC located in the amino terminus of the gp41 ectodomain. gp41 plays a
 CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
 CC interacts with members of the formyl peptide receptor (FPR) family and
 CC thereby up-regulates an inflammatory response, and acts as a potent
 CC chemottractant and activator of human peripheral blood phagocytes (but
 CC not T cells). The present peptide can be used to modulate an inflammatory
 CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
 CC XX
 SQ Sequence 35 AA;
 Query Match 95.9%; Score 164; DB 3; Length 35;
 Best Local Similarity 97.1%; Pred. No. 4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
 Db 1 NLLRAIEAQOHLQLTWQIKQLQARILAVERYL 35
 RESULT 19
 AAB52750
 ID AAB52750 standard; peptide; 36 AA.
 XX AAB52750;
 XX 12-SEP-2003 (revised)
 DT 23-FEB-2001 (first entry)
 XX T21/DP107 peptide fragment #32.
 DE Antiinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
 KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
 KM chemottractant.
 XX Human immunodeficiency virus 1.
 OS WO200066622-A1.
 XX 09-NOV-2000.
 XX 05-MAY-2000; 2000WO-US012371.
 PR 05-MAY-1999; 99US-0132686P.
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang JM, Oppenheim JU, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2000-656493/63.
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Claim 12; Page 28; 148pp; English.
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. GP41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 36 AA;

Query Match 95.9%; Score 164; DB 3; Length 36;
Best Local Similarity 97.1%; Pred. No. 4.2e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARIILAVERYL 35
DB 1 NNILRAIEAQOHLLQLTWQIKQLQARIILAVERYL 35

RESULT 20
AAB52751
ID AAB52751 standard; peptide; 37 AA.
XX
XX AAB52751;
XX
XX 12-SEP-2003 (revised)
DT 23-FEB-2001 (first entry)
XX
XX T21/DP107 peptide fragment #33.
DE
XX
XX Antinflammatory; T21/DP107; gp41 ectodomain; HIV-1 fusion;
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;
KM chemottractant.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200066622-A1.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000MO-US012371.
PF
XX
XX 05-MAY-1999; 99US-0132686P.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Wang JM, Oppenheim JU, Su S, Gong W, Gao J, Murphy PM;
PI WPI; 2000-656493/63.
DR
XX
XX Administration of peptide agents with a sequence corresponding to a
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor antagonist
PT is used to modulate inflammation.
XX
XX Claim 12; Page 28; 148pp; English.
PS
XX
XX The present sequence is a peptide fragment of T21/DP107. T21/DP107 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T21/DP107 is
CC located in the amino terminus of the gp41 ectodomain. GP41 plays a

CC critical role in the fusion of HIV-1 and host cell membranes. T21/DP107
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemottractant and activator of human peripheral blood phagocytes (but
CC not T cells). The present peptide can be used to modulate an inflammatory
CC response in a subject. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 37 AA;

Query Match 95.9%; Score 164; DB 3; Length 37;
Best Local Similarity 97.1%; Pred. No. 4.3e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARIILAVERYL 35
DB 1 NNILRAIEAQOHLLQLTWQIKQLQARIILAVERYL 35

RESULT 21
AAR55635
ID AAR55635 standard; peptide; 38 AA.
XX
XX AAR55635;
XX
XX 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
XX DP-139 - DP-107 analogue.
DE
XX
XX Leucine zipper; HIV-1; human immunodeficiency virus;
KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.
XX
XX Synthetic.
OS
XX
XX WO9402505-A1.
PN
XX
XX 03-FEB-1994.
PD
XX
XX 19-JUL-1993; 93WO-US006769.
PF
XX
XX 20-JUL-1992; 92US-00916540.
PR 07-AUG-1992; 92US-00927532.
XX
XX (UYDU-) UNIV DUKE.
PA
XX
XX Wild CT, Matthews TJ, Bolognesi DP;
PI
XX
XX WPI; 1994-048790/06.
DR
XX
XX New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.
XX
XX Disclosure; Page 25; 38pp; English.
PS
XX
XX Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct PN field.)
CC
XX
SQ Sequence 38 AA;

Query Match 95.9%; Score 164; DB 2; Length 38;
Best Local Similarity 97.1%; Pred. No. 4.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNILRAIEAQOHLLQLTWQIKQLQARIILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYL 35

RESULT 22

AAR55636

ID AAR55636 standard; peptide; 38 AA.

AC AAR55636;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-140 - DP-107 analogue.

KM Leucine zipper; HIV-1; human immunodeficiency virus;
KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.

OS Synthetic.

PN W09402505-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93MO-US006769.

PR 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

PA (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

PT New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.

PS Disclosure; Page 25; 38pp; English.

CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 38 AA;

XX Query Match 95.9%; Score 164; DB 2; Length 38;

XX Best Local Similarity 97.1%; Pred. No. 4.4e-15;

XX Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYL 35

RESULT 23

AAR47216

ID AAR47216 standard; peptide; 38 AA.

AC AAR47216;

DT 25-MAR-2003 (revised)

DT 25-JUL-1994 (first entry)

DE DP-107 - HIV-1 TM protein (558-595).

XX Leucine zipper; HIV-1; human immunodeficiency virus;
KM transmembrane protein; TM; inhibition; cell fusion; alpha-helix;
KM antiviral; gp41.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 12 /note="Residue 12 of the sequence in Fig 1 is H; residue
FT 12 of the sequence in Table 4 is G"

PN W09402505-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93MO-US006769.

PR 20-JUL-1992; 92US-00916540.

PR 07-AUG-1992; 92US-00927532.

PA (UYDU-) UNIV DUKE.

PI Wild CT, Matthews TJ, Bolognesi DP;

DR WPI; 1994-048790/06.

PT New peptides corresponding to HIV transmembrane protein - used for
PT inhibiting infection of cells by an enveloped virus, partic. for
PT inhibiting HIV-induced cell fusion.

PS Claim 1; Page 27; 38pp; English.

CC Peptide DP-107 (AAR47216); a peptide comprising 14-60 amino acids capable
CC of forming a heterodimer with DP-107; or a multimer of these peptides can
CC be contacted with an HIV-infected cell to inhibit HIV- induced cell
CC fusion. DP-107 is based on a highly conserved region in the transmembrane
CC protein (TM) of HIV-1 (gp41) which was predicted to form an extended
CC amphipathic alpha-helix with structural analogues in the TM proteins of
CC several fusogenic viruses. Other peptides studied and DP-107 analogues
CC are given in AAR52839-48 and AAR55633-37. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 38 AA;

XX Query Match 95.9%; Score 164; DB 2; Length 38;

XX Best Local Similarity 97.1%; Pred. No. 4.4e-15;

XX Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYL 35

Db 1 NNLRAIEAQOHLQLTWGIKOLQARIILAVERYL 35

RESULT 24

AAM27614

ID AAM27614 standard; peptide; 38 AA.

AC AAM27614;

DT 25-MAR-2003 (revised)

DT 22-DEC-1997 (first entry)

DE Human immunodeficiency virus gp41 derived peptide DP-107.

KM Human immunodeficiency virus; HIV; transmembrane; glycoprotein 41; gp41;

KM inhibition; induction; cell fusion; transmission; type 1.

OS Human immunodeficiency virus.

PN US5656480-A.

PD 12-AUG-1997.

XX 27-JAN-1995; 95US-00374666.
XX
XX 20-JUL-1992; 92US-00916540.
XX 07-AUG-1992; 92US-00927532.
XX 19-JUL-1993; 93WO-US006769.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Bolognesi DP, Wild CT, Matchews TJ;
XX WPI; 1997-414595/38.
XX
XX Peptide(s) derived from HIV trans-membrane protein gp41 - inhibit HIV
XX syncytia formation and transmission.
XX
XX Claim 1; Col 13-14; 18pp; English.
XX
XX The present human immunodeficiency virus (HIV) transmembrane glycoprotein
XX 41 (gp41) derived peptide (DP-107), can be used to inhibit HIV induced
XX cell fusion in a culture and cell free HIV transmission in a culture to a
XX human cell not infected with HIV, especially HIV type 1. (updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 38 AA;
SQ
Query Match 95.9%; Score 164; DB 2; Length 38;
Best Local Similarity 97.1%; Pred. No. 4.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYL 35
1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYL 35
Db
RESULT 25
AAV88666
ID AAV88666 standard; peptide; 38 AA.
XX
XX AAV88666;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 21.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 21; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are

CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAV88651-Y0055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
XX Sequence 38 AA;
SQ
Query Match 95.9%; Score 164; DB 3; Length 38;
Best Local Similarity 97.1%; Pred. No. 4.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYL 35
1 NNLRAIEAQOHLQLTVMQIKQLQARILAVERYL 35
Db
RESULT 26
AAV88730
ID AAV88730 standard; peptide; 38 AA.
XX
XX AAV88730;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 85.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO959615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 22; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;
 Best Local Similarity 97.1%; Pred. No. 4.4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
 Db

RESULT 27
 AAY88731
 ID AAY88731 standard; peptide; 38 AA.
 XX
 AC AAY88731;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 86.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 XX anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO9959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

XX Disclosure; Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;

Best Local Similarity 97.1%; Pred. No. 4.4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
 Db

RESULT 28
 AAY89251
 ID AAY89251 standard; peptide; 38 AA.
 XX
 AC AAY89251;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 741.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 XX anti-fusogenic; differentiation factor; interleukin; interferon;
 XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO9959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merucka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence.

XX Disclosure; Page 33; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 38 AA;

Query Match 95.9%; Score 164; DB 3; Length 38;
 Best Local Similarity 97.1%; Pred. No. 4.4e-15;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 35
 4 NNLRAIEAQOHLQLTWTWQIKQLQARILAVERYL 38
 Db

RESULT 29

AAV89145
ID AAV89145 standard; peptide: 38 AA.
XX
AC AAV89145;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 583.
XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
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PA (TRIM-) TRIMERIS INC.
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CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAV8851-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 38 AA;
XX
QY
Db 1 NNLIRATEAQOHLQLTWGKIKOLQARILAVERYL 35
1 NNLIRATEAQOHLQLTWGKIKOLQARILAVERYL 35
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity 97.1%; Score 164; DB 3; Length 38;
Query Match 95.9%; Pred. No. 4.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULTS
AAV89146
ID AAV89146 standard; peptide: 38 AA.
XX
AC AAV89146;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 583.
XX

KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
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OS Unidentified.
XX
PN WO959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
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PA (TRIM-) TRIMERIS INC.
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SQ Sequence 38 AA;
XX
QY
Db 1 NNLIRATEAQOHLQLTWGKIKOLQARILAVERYL 35
1 NNLIRATEAQOHLQLTWGKIKOLQARILAVERYL 35
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity 97.1%; Score 164; DB 3; Length 38;
Query Match 95.9%; Pred. No. 4.4e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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